Science
Review

*Compiling the year's research uses of
data accessed through the
Global Biodiversity Information Facility*

2016

Foreword

The phrase '*free and open access to biodiversity data*' that appears on GBIF.org is more than a slogan.

Making data open and accessible to users without them having to ask for permission dramatically reduces the "transaction costs" associated with accessing data. Rather than negotiating with multiple data providers, a researcher can simply get the data and explore it. Such an exploration might lead to a dead end, but the cost of failure is low, because we haven't wasted time negotiating access for something that ultimately didn't work out. The fewer obstacles we put in the way of researchers, the more varied and innovative the uses that are likely to emerge.

This is reflected in this year's *Science Review*, which documents a growing body of research that hinges on free and open access to biodiversity data from the GBIF network. The 57 additional papers in 2015 represent a 17 per cent annual increase, amounting to an additional peer-reviewed use of GBIF-mediated data each week.

As befits a global organization, the geographic diversity of authors using GBIF-mediated data has broadened. Based on authors' host institutions, the number of papers produced by researchers working in China, Mexico, Spain, Brazil and Colombia now nearly matches and sometimes exceeds the output from their peers in Germany, Australia, France and Switzerland. The regional totals support the notion that these are general trends, with researchers from Asia (+44), North America (+51) and Latin America (+57) each co-authoring dozens more papers than in 2014. One hopes that activities to fill data gaps like the data mobilization projects supported by the EU-funded Biodiversity Information for Development programme (BID) will see returns in more active use by researchers in Africa, the Caribbean and the Pacific.

A major use of GBIF-mediated data is modelling species distributions, which is to be expected given the nature of the data. Estimating current distributions, and predicting how they might change in the future, is a staple of GBIF-based science and has obvious practical applications to areas such as invasive species, vectors of human disease, and food crops.

GBIF-mediated data also underpins basic, curiosity-driven research. Increasingly we are also seeing meta-analyses of biodiversity data, such as the paper included here, "Synthetic datasets and community tools for the rapid testing of ecological hypotheses", whose authors include Miguel Araújo, a past winner of GBIF's Ebbe Nielsen Prize. The abstract is worth quoting:

> *The increased availability of both open ecological data, and software to interact with it, allows the fast collection and integration of information at all spatial and taxonomic scales. This offers the opportunity to address macroecological questions in a cost-effective way.*

In other words, "free and open access to biodiversity data" enables approaches to the study of diversity that are not otherwise possible. The publications gathered here are a testimony to the benefits of open data.

ROD PAGE
Chair, GBIF Science Committee

Vice Chairs : Mark Costello, Anders G. Finstad &
Philippe Grandcolas
Members: Elizabeth Arnaud & Guy Cochrane

About the *Science Review*

The GBIF *Science Review* provides an annual survey drawn from the Secretariat's ongoing literature tracking programme, which identifies research uses and citations of biodiversity information accessed through GBIF's global infrastructure. The peer-reviewed articles summarized in the following pages offer a partial but instructive view of research investigations enhanced and supported by free open access data that the GBIF network of members and publishers make available.

This year, we introduce two new conventions. The first is to identify open-access scientific articles using the symbol ⓐ. We think this step is both valuable and practical for those interested in reading the research at a time of institutional journal subscriptions.

In addition, to keep pace with the ever-expanding bibliographic tables (and reduce printing costs), we have decoupled the comprehensive list of the year's uses, publishing them instead in a companion *Science Review* Sourcebook, available at gbif.org/science-review-sourcebook-2016.

As in previous years, the categories used here are intended to help readers navigate the major subject areas of GBIF-assisted research, despite the fact that some papers may cut across multiple topics. For clarity's sake, articles appear under only one category in the *Review*. Countries assigned to authors are based on the location of the institutions identified in the author information, while funding information included for the highlighted papers draws upon the papers' acknowledgements.

Those interested in sharing research uses that have escaped our attention can write to us at communication@gbif.org.
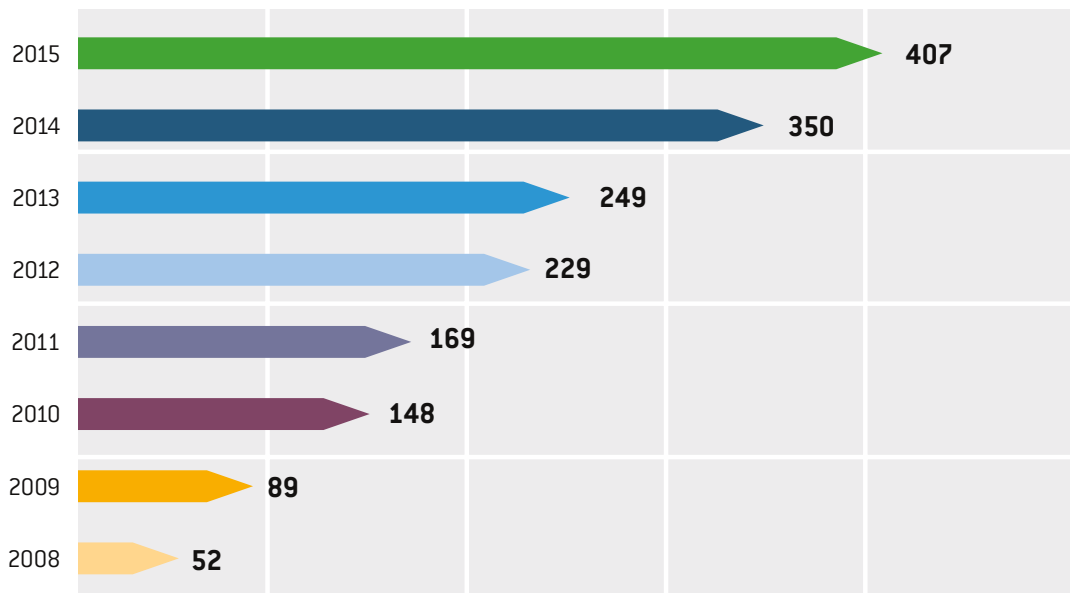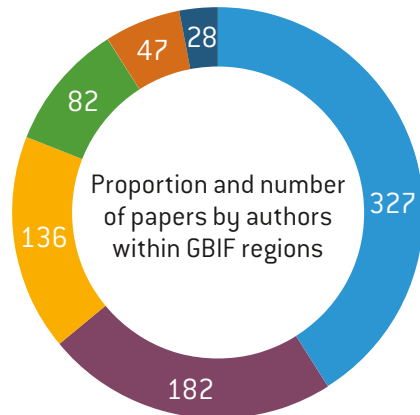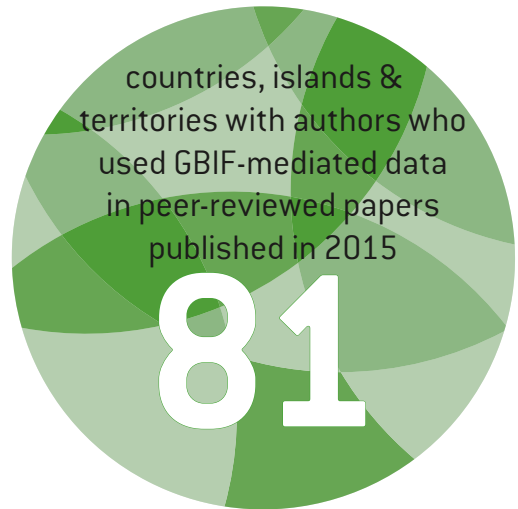
CONTENTS

Uses and trends

These visualizations of the use of GBIF-mediated data serve to show not just the growing number of peer-reviewed publications appearing each year, but also the increasing number of countries, islands and territories whose institutions host authors who apply the data in their research articles. Each trend highlights the GBIF network's widening sphere of influence and impact on scientific research related to the biological domain.

ANNUAL NUMBER OF PEER-REVIEWED ARTICLES USING GBIF-MEDIATED DATA

Year	Value
2015	407
2014	350
2013	249
2012	229
2011	169
2010	148
2009	89
2008	52

NUMBER OF ARTICLES WITH AUTHORS BY COUNTRY/ISLAND/TERRITORY

163 United States

59 United Kingdom

44 Germany

38 Australia

36 China

33 Mexico

32 Spain

30 Brazil

24 France

23 Colombia

22 Switzerland

19 Belgium

17 Canada

16 Netherlands

15 Sweden

14 Chile • Denmark • Italy

12 Norway

10 South Africa

9 New Zealand

8 Austria • India • Russian Federation

7 Argentina

6 Peru • Poland • Portugal • Singapore

5 Costa Rica • Czech Republic • **Thailand**

4 Benin • Bolivia • Ecuador • Japan • Panama • Saudi Arabia

3 Iran • Kenya • Pakistan • Taiwan • Ecuador • Zimbabwe

2 Estonia • Greece • Hungary • Iceland • Indonesia • Israel • Nigeria • South Korea

1 Bahamas • Bangladesh • Belize • Bulgaria • Burkina Faso • Cameroon • Croatia • Dominican Republic • French Guiana • Ghana • Greenland • Ireland • Kuwait • Luxembourg • Malaysia • Namibia • Nepal • Oman • Philippines • Puerto Rico • Romania • Rwanda • Slovenia • Slovakia • Suriname • Uganda • Uruguay • Venezuela

countries, islands & territories with authors who used GBIF-mediated data in peer-reviewed papers published in 2015

81

Proportion and number of papers by authors within GBIF regions

28
47
82
327
136
182

| GBIF Regions | Asia | Africa | Europe | Latin America | North America | Oceania |

Invasive alien species

MANGROVE FOREST, ANDAMAN ISLANDS, INDIA. ADHIKARI, TIWARY & BARIK (2015) IDENTIFY BOTH THE ANDAMANS AND INDIA'S MANGROVES AS LIKELY INVASION HOTSPOTS. CC BY-NC 2007 AMRE https://flic.kr/p/3frJfX

INVASIVE HOTSPOTS OF INDIA

Adhikari D, Tiwary R & Barik SK (2015) Modelling Hotspots for Invasive Alien Plants in India. *PLoS ONE* 10(7): e0134665. doi:10.1371/journal.pone.0134665
Author country: India

Identifying areas vulnerable to invasive alien species (IAS) is a prerequisite to controlling invasion. This study combines bioclimatic data with GBIF-mediated occurrences to model climatic niches for 155 invasive alien plants in India. After using the models to generate climatic suitability maps, the researchers overlaid terrestrial ecoregions and anthropogenic biomes. The resulting 'IAS hotspots' represent places where more than 50 per cent of an ecoregion overlaps with climatically suitable areas for multiple invasive species containing at least three anthropogenic biome types. These hotspots occur in 19 of 47 Indian ecoregions and coincide with major biodiversity hotspots such as Western Ghats, Indo-Burma, and Eastern Himalaya along with other forest reserves, islands, and coastal mangrove forests.

DISTRIBUTION VS. ABUNDANCE

Bradley BA (2016) Predicting abundance with presence-only models. Landscape Ecology 31(1): 19-30. doi:10.1007/s10980-015-0303-4
Author country: United States
Research funding: National Institute of Food and Agriculture,

USDA, Massachusetts Agricultural Experiment Station, Massachusetts Department of Environmental Conservation

This study examines 15 invasive plants in the US to argue that models based on occurrence data alone may be good indicators of species distribution, but poor predictors of species abundance. The author suggests that the latter instead requires abundance surveys as these data are effective predictors of species abundance.

PREDICTING THE RANGE OF AN INVASIVE MARINE SPECIES

Byers JE, Smith R, Pringle J et al. (2015) Invasion Expansion: Time since introduction best predicts global ranges of marine invaders. *Scientific Reports* 5: 12436. doi:10.1038/srep12436
Author countries: United States, Australia, New Zealand
Research funding: Macquarie University; University of New South Wales; U.S. National Science Foundation

What's the best way of predicting the range of an invasive marine species? This study points to the simplest of explanations: time since introduction. Researchers compiled a database of GBIF-mediated occurrences as well as traits and environmental variables for 138 invasive, coastal marine invertebrates in either Australia, New Zealand, or the United States. Estimating the total length of coastal range for each species, they found time since

introduction to be the most important variable in predicting the range. On average, invasive species expand their range at about 400 km per decade. But since time after introduction can only be measured after an invasion occurs, the calculation doesn't help in avoiding or managing invasions. The message is clearly that identifying vulnerable areas is the best means of protecting against invasion.

PLANT REPRODUCTIVE STRATEGIES AND NICHE DYNAMICS

By way of understanding the mechanics of the niche shifts common to many plant invasions, this study investigates whether the different reproductive strategies used by alien plants affect their ability to expand their individual niches. Using GBIF-mediated occurrences as well as climate data, researchers modeled the niche dynamics of 13 flowering plants that rely on sexual reproduction and compared them with plants that rely on asexual reproduction. The matched plants were either from the same genus or tribe. Surprisingly, they find no significant differences between the two groups. The assumption that sexual reproduction and the genetic recombination involved in this process would allow for more pronounced changes in niche dynamics does not hold up. In fact, their results indicate that adaptive evolution is not the predominant driver of niche dynamics.

DOES GLOBALIZATION INCREASE SPECIES NATURALIZATION?

This study identified all invasive plants in Australia, using GBIF-mediated occurrences to map their distributions prior to introduction 'down under'. Using the purpose and pathway of introduction to identify patterns in naturalization, their results show that 12% of total Australian flora is naturalized—but just two families account for more than a third. Originating mainly from Europe (47.4%), 65% of the plants were

introduced as ornamentals, but now more than a third of the naturalized plants are classified as weeds.

The overall results indicate a long-term shift in the plants' origins and uses, starting from food originating in Europe, through food and ornamentals from North America, to ornamental and accidental species from South Africa. Despite these changes, species introduction has remained more or less constant at the rate of around 20 species per year since 1880.

EPACRIS LONGIFOLIA, CC BY-NC 2015 ERI HTTP://WWW.INATURALIST.ORG/PHOTOS/2028647

ASSESSING TRANSFERABILITY OF SPECIES DISTRIBUTION MODELS

Anticipating and responding to the spread of invasive species in new environments often hinges on analyses of species distribution models. The authors begin by noting cases where convenient methodological assumptions have oversimplified and distorted the consistency with which species invade environments that resemble their preferred native habitats—a concept known as 'ecological niche transferability'. Building their models with a range of bioclimatic variables and GBIF-mediated data for 13 well-documented invasives, the authors compare the observed ranges for the species in both their native and invaded habitats with modelled predictions. Their results highlight the invaders' varied responses and

broadly suggest that niche transferability depends largely on the dynamics of species interactions in a given region. This finding emphasizes the importance of preventative controls while calling attention to the value of modelling niche transferability to guide post-invasion management measures.

COLLECTING AND SHARING (DATA ON) INVASIVE AQUATIC SPECIES

(a) Fuller P & Neilson ME (2015) The U.S. Geological Survey's Nonindigenous Aquatic Species Database: over thirty years of tracking introduced aquatic species in the United States (and counting). *Management of Biological Invasions* 6(2): 159-170. doi:10.3391/mbi.2015.6.2.06
Author country: United States
Research funding: U.S. Geological Survey; U.S. Fish and Wildlife Service; U.S. Environmental Protection Agency; U.S. National Oceanic and Atmospheric Administration

The US Geological Survey's Nonindigenous Aquatic Species (NAS) program has monitored, recorded, and analysed occurrences of alien freshwater organisms in the United States since the 1980s. The records draw from a number of sources, including 12,000 records from the GBIF network, all maintained in a publicly accessible online database (http://nas.er.usgs.gov) where users can search, display and map species by state, temporal range or other variables. The database has been used in a number of different studies, and distribution maps have appeared in many publications and news outlets. USGS also publishes the 260,000 records of the NAS database as a dataset on GBIF.org (see doi:10.15468/ijccz9).

HOW DOES THE HUMAN FOOTPRINT AFFECT DISTRIBUTION OF INVASIVE SPECIES?

(a) Gallardo B, Zieritz A & Aldridge DC (2015) The importance of the human footprint in shaping the global distribution of terrestrial, freshwater and marine invaders. *PLoS ONE* 10(5): e0125801. doi:10.1371/journal.pone.0125801
Author countries: United Kingdom, Spain
Research funding: European Union; Spanish Ministerio de Economía y Competitividad

By focusing on a portion of Europe that includes Great Britain, France, Belgium and the Netherlands, this study examines the influence of environmental and anthropogenic factors on global distribution of invasive species. Researchers created species distribution models (SDMs) of 72 invasive species (terrestrial plants and animals as well as freshwater and marine organisms), using GBIF-mediated and climatic data, geophysical variables, and five anthropogenic variables as proxies of the human footprint. They found temperature to be the most important overall factor, accounting for about half the distribution in the terrestrial and freshwater species. However, human footprint measures like closeness to ports or roads explained as much as a quarter of the distribution. All models showed a consistently correlation to human habitat use and identified urban areas close to major ports as hotspots for potential invasion.

ONCE AN INVADER, ALWAYS AN INVADER?

Gallien L, Saladin B, Boucher FC, Richardson DM & Zimmermann NE (2016) Does the legacy of historical biogeography shape current invasiveness in pines? *New Phytologist* 209(3): 1096-1105. doi:10.1111/nph.13700
Author countries: Switzerland, South Africa
Research funding: National Research Foundation, South Africa; Swiss National Science Foundation

How does the long-term history of species relate their current invasiveness? This study tries to answer that question by examining closely the genus *Pinus*, as it is one of the best-studied invasive clades. The researchers initially construct a new phylogeny of the whole genus, and use Pine distribution data based among others on GBIF mediated occurrences, to create a biogeographic history of all the *Pinus* species. The researchers find that invasive pines belong to lineages that had a tendency to colonize more regions in the past than non-invasive pines. The colonization history and thus invasiveness is, however, not correlated with any specific morphological trait. In fact, the researchers found no evidence that invaders had higher tolerance to e.g. extreme climates than non-invaders. However, they do show that lineages that moved most across biogeographical regions had faster rates of niche evolution.

SCOTS PINE (*PINUS SYLVESTRIS*). CC BY-SA 2015 SHINYPHOTOSCOTLAND
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DIFFERENT GENES, DIFFERENT NICHES

Ciona intestinalis is a highly successful invasive marine invertebrate that originated in Northern Europe, but has spread to all over the world. Recently, the genetic complex known as *C. intestinalis* has been found to correspond at least two distinct species. In Chile, the species is restricted to northern regions of the country, but may eventually find its way to important aquaculture centres in the south. Using GBIF-mediated occurrences and climate data, the researchers modeled ecological niches and found suitable habitats in both central and southern regions. They also did field sampling to validate the models, and indeed verified that southern regions of Chile had already been invaded. Their results also indicate that not only are there genetically distinct subgroups of *C. intestinalis*, but these also have different environmental preferences.

TRACKING NATURALIZED PLANTS WORLDWIDE

Combining GBIF-mediated occurrences with data from a novel database, the Global Naturalized Alien Flora (GloNAF), this study seeks to identify and quantify the spread and distribution of naturalized plant species worldwide. The researchers present an analysis of 13,168 naturalized vascular plants in 843 non-overlapping regions covering 83 per cent of the Earth's land surface. They determine number of native species per continent, and find that at least 3.9 per cent of all known vascular plants have been naturalized outside their native ranges. The biggest recipients of naturalized species from other continents by area are Australasia and Pacific Islands, and the major donors are the temperate regions of Europe and Asia. The study suggests that plant invasions overall have been a Northern-to-Southern hemisphere phenomenon rather than one from the Old World to the New.

COMMON RAGWEED (*AMBROSIA ARTEMISIIFOLIA*). CC BY-NC-SA 2014 DENDROICA CERULEA https://flic.kr/p/oLiKdK

DISTRIBUTION OF RAGWEED

Common ragweed (*Ambrosia artemisiifolia* L.) is an invasive species that causes allergies in 10-20 per cent of humans and thus presents a significant public health challenge. This study's physiological model performs well, with the plant's potential distribution corresponding with GBIF-mediated occurrences in both the native North American range and the invasive range in Europe. However, the model also predicts a much larger potential range for ragweed than currently observed, in part due to improved estimates on the amount and timing of pollen release.

STOWAWAY INVADERS

Cargo ships transport an estimated 10,000 marine species in ballast water worldwide. This study uses 22,550 GBIF-mediated occurrences to predict the spread of 18 non-indigenous species (NIS) along shipping routes and weigh the factors that might make potential habitat suitable for them in the Baltic Sea and Northeast Atlantic. The study finds that temperature and sea-ice concentration determine habitat suitability for 61 per cent of species, while salinity surprisingly accounts for only 11 per cent. This finding cuts against current practices for ships exchanging ballast water, where salinity remains the standard parameter for assessing NIS risk. The study also identifies potential NIS hotspots in shallow parts of the Baltic, where ships should avoid exchanging ballast water, pointing instead to the middle of the North Sea as a "cold spot" more suitable for ballast-water discharge with lower risk for spread of NIS.

INVADERS IN AQUARIUMS

One billion ornamental fish from more than 5,000 species are traded around the world every year. In Mexico, 60 per cent of native fish extinctions correlate with the presence of non-native species, so this study sought to identify high-risk ornamental fish to prevent future invasions. Using GBIF-mediated occurrences along with other data researchers employed a risk analysis method called Fish Invasiveness Screening Kit (FISK) and calibrated it for use with analysed 368 species of freshwater aquarium fish. Their results identify the top 30 invasive species—classifying 17 of them as high-risk invaders—and highlight the importance of identifying high-risk species to inform policy makers, implement monitoring programs and educate traders and pet-shop owners.

GREEN FROG (*LITHOBATES CLAMITANS*). CC BY-NC 2013 REIGH LEBLANC
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CLIMATE IS NOT THE ONLY PREDICTOR OF INVASION

Examining two anuran invasions of wetlands in British Columbia, Canada, this study evaluates the performance of occupancy models versus ecological niche models (ENMs) for predicting invasive ranges. The researchers used GBIF-mediated occurrences for both the green frog (*Lithobates clamitans*) and American bullfrog (*Lithobates catesbeianus*) to build the distribution models and compared them with occupancy models. They discovered that while ENMs perform well in predicting the invasive ranges of a climate-driven species like the green frog, they are less reliable with habitat specialists such as the American bullfrog, for which the occupancy model performs better. The researchers conclude by pointing out that relying on climate data can be helpful for predicting occurrences of invasive species, it might not tell the whole story.

CLOSE RELATIVES ARE BETTER INVADERS

Park DS & Potter D (2015). Why close relatives make bad neighbours: phylogenetic conservatism in niche preferences and dispersal disproves Darwin's naturalization hypothesis in the thistle tribe. *Molecular Ecology* 24(12): 3181-3193. doi:10.1111/mec.13227
Author country: United States
Research funding: U.S. National Science Foundation

The number of exotic plants naturalized in the United States far exceeds that of any other group of organisms. In this study of Cardueae thistles, researchers used GBIF-mediated occurrences to do ecological niche modelling of non-native species in the California Floristic Province. Results showed that the more closely related introduced thistles are to native species, the more likely they are to be invasive. Successful invaders also showed greater levels of niche overlap with native thistles than non-invasive species. The study also examined traits related to dispersal properties, finding that invasive thistles have longer bristles, and shorter and lighter seed than non-invasive counterparts. The conclusions make a case against Darwin's naturalization hypothesis, supporting the idea instead that plant invaders closely related to native species are not at a disadvantage.

INVADING AT A SNAIL'S PACE

ⓐ Rekha Sarma R, Munsi M & Neelavara Ananthram A (2015) Effect of Climate Change on Invasion Risk of Giant African Snail (*Achatina fulica* Férussac, 1821: Achatinidae) in India. *PLoS ONE* 10(11): e0143724. doi:10.1371/journal.pone.0143724
Author country: India
Research funding: India Department of Science and Technology

In this study, researchers used GBIF-mediated occurrences to create an ecological niche model that maps the current and future patterns in India of the giant African snail (*Achatina fulica*), considered one of the world's worst invasive species. Native to East Africa, the snail is known to consume 50 species of plants, regularly outcompetes native snails, and carries pathogens that cause disease in humans. 60 per cent of India faces invasion, and this study revealed three high-risk invasion hotspots: western India, parts of peninsular India, and

eastern India. Models under future climate scenarios predict that these regions will be even more prone to invasion, highlighting the country's need to control this noxious species.

SERPENTS' TALES: ASSESSING INVASION RISK OF INTRODUCED SNAKES IN THE BALEARIC ISLANDS

ⓐ Silva-Rocha I, Salvi D, Sillero N, Mateo JA & Carretero MA (2015) Snakes on the Balearic islands: an invasion tale with implications for native biodiversity conservation. *PLoS ONE* 10(4): e0121026. doi:10.1371/journal.pone.0121026
Author countries: Portugal, Spain
Research funding: Conselho Nacional de Desenvolvimento Científico e Tecnológico

Although the long chequered history of human interaction with the Balearic Islands has presented countless opportunities for biological invasion, this paper focuses on four recently introduced species: the horseshoe whip snake (*Hemorrhois hippocrepis*), the Montpellier snake (*Malpolon monspessulanus*), the false smooth snake (*Macroprotodon mauritanicus*) and the ladder snake (*Rhinechis scalaris*).

The authors analysed mitochondrial DNA from tissue samples to understand the snakes' origins and invasive pathways. Then, relying primarily on GBIF-mediated data to understand the native distribution of each species, they estimated their current and future habitat suitability in this Mediterranean archipelago. These combined molecular and ecological analyses suggest that the nursery trade in olive trees may be the sole source of each invasion, and that climate change might improve conditions for these already widespread alien species.

GIANT AFRICAN SNAIL (*ACHATINA FULICA*) FEEDING ON A SURINAM CHERRY (*EUGENIA UNIFLORA*). CC BY 2015 SCOT NELSON
https://flic.kr/p/rvqRjC

invasives

ASSESSING WEED RISK ASSESSMENTS

Authorities often rely on weed risk assessments (WRAs) to determine the invasive potential when considering a non-native plant species for introduction. The parameters and limits of the models used differ between countries, and in this study, researchers used 40 species of crops and invasive species to compare the WRAs used in the United States and Australia. Both models failed to distinguish weeds from crops, judging major crops like barley, rice, canola, and alfalfa to be high-risk. In one model, cereal rye scored higher than kudzu, a prodigious invader in the Southeastern U.S. The results reveal serious weaknesses in the WRAs and recommend caution in applying these models. The authors suggest additional screening such as field testing as a complementary method for assessing invasion risk.

ARCTIC INVASION THREATS FROM BALLAST WATER

Ships transport myriad marine organisms around the world in ballast water that may, when exchanged, introduce foreign species that become invasive in suitable areas. This study surveyed ballast water of eight foreign ships landing at the Norwegian archipelago of Svalbard, carrying out morphological and molecular analyses of the organisms on board. GBIF-mediated data provided information on the global distribution of the identified species and, in combination with climatic data, served to predict whether suitable niches exist around Svalbard. While these results showed that only one of 23 species had invasive potential, future climate scenarios increase the ranks of likely invaders to six species.

WATERS OF SVALBARD IN THE NORWEGIAN ARCTIC, CC BY-NC-ND 2014 NEIL MORALEE HTTPS://FLIC.KR/P/M9JGQC

Climate change

PLATYRRHINUS LINEATUS, CC BY-SA 2010 DESMODUS
HTTPS://COMMONS.WIKIMEDIA.ORG/WIKI/FILE:PLATYRRHINUS.JPG

THE EFFECT OF CLIMATE CHANGE ON THE BATS OF THE BRAZILIAN CERRADO

Ⓐ Aguiar LMS, Bernard B, Ribeiro V, Machado RB & Jones G (2016) Should I stay or should I go? Climate change effects on the future of Neotropical savannah bats. *Global Ecology and Conservation* 5: 22-33. doi:10.1016/j.gecco.2015.11.011
Author countries: Brazil, United Kingdom
Research funding: CNPq

Covering more than two million square kilometers and nearly a quarter of Brazil, the tropical ecoregion known as the Cerrado biome is the most biologically diverse savannah in the world and home to more than 250 species of mammals, including many bats. In this study, researchers combined more than 13,000 GBIF-mediated records with present and future climate data to model distributions for 116 of the Cerrado's bats. Their results suggest that unless these species can move to new suitable areas, climate change will cause 36 different species to lose more than 80 per cent of their suitable habitat. If, on the other hand, the bats of the Cerrado migrate into newly suitable areas, as many as two thirds of them will lose less than 20 per cent. Overall, the models predict that future habitat shifts of an average 281 km, mainly to the southeast.

PREDICTIONS TO INFORM CONSERVATION PLANNING IN ALASKA

Ⓐ Baltensperger AP & Huettmann F (2015) Predicted Shifts in Small Mammal Distributions and Biodiversity in the Altered Future Environment of Alaska: An Open Access Data and Machine Learning Perspective. *PLoS ONE* 10(7): e0132054.

doi:10.1371/journal.pone.0132054
Author country: United States
Research funding: University of Alaska Fairbanks

This study uses GBIF-mediated occurrences to create bioclimatic distribution models of 17 small mammals across Alaska. Combining the models with climate scenarios for the year 2100, the researchers predicted an average loss of suitable habitat of about 20 per cent and a northward shift of 111 km for species living in cold-climate, northern and interior regions. Species in the continental and southern regions, however, are to gain on average about 30 per cent more habitat. Their shifts are mixed with about half moving north and the other half moving south. The study predicts that Alaskan biodiversity hotspots in general will shift northward, inland, and upward—critical findings for future management strategies that also highlight the significance of reducing greenhouse gas emissions to halt climate change.

CLIMATE CHANGE MAY ALREADY AFFECT BIRDS

Bateman BL, Pidgeon AM, Radeloff VC et al (2015) The pace of past climate change vs. potential bird distributions and land use in the United States. Global Change Biology. doi:10.1111/gcb.13154
Author countries: United States, Australia
Research funding: U.S. National Aeronautics and Space Administration; James Cook University

Researchers analysed 60 years of GBIF-mediated occurrence across 285 land-bird species in the contiguous United States (excluding Alaska and Hawaii). More than five million records were cross-referenced with data on weather conditions from the same period, creating models predicting how changes in climate affect breeding-bird distributions. The results showed that these distributions are shifting at an average speed of 1.27 km/year, double the global estimates. Surprisingly, the direction of these shifts is not just northward, but also westward in 27.4% of species. While average temperature is the most important factor in long-term changes, short-term precipitation and extreme conditions also influence many species. Predicted increases in species richness in the Midwest and East hinge on whether these areas can sustain the affected species in the future in lands continuously developed by humans.

PREDICTING THE FATE OF EUCALYPTS

Ⓐ Booth TH, Broadhurst L, Pinkard E et al. (2015) Native forests and climate change: Lessons from eucalypts. *Forest Ecology and Management* 347:18-29. doi:10.1016/j.foreco.2015.03.002
Author countries: Australia
Research funding: CSIRO

This review analyses studies on the potential effect of climate change on natural stands of eucalypts of Australia. The genus *Eucalyptus* includes 100 species, none of which have been listed as extinct since the early 20th century, though 50 are now considered vulnerable or endangered. Climate change will make trees like eucalypts less likely to evolve or disperse, so predicting their ability to tolerate new climatic conditions is key to understanding their future.

The authors analysed numerous studies and used global occurrence data accessed via GBIF in BIOCLIM and MAXENT models that highlight the importance of considering not only natural distributions but also climatic adaptability. They conclude that changing climates will make prediction of species interactions, pest and diseases particularly challenging.

PREDICTING CHANGES TO PLANT RICHNESS AND DIVERSITY IN MADAGASCAR

Ⓐ Brown KA, Parks KE, Bethell CA, Johnson SE & Mulligan M (2015) Predicting plant diversity patterns in Madagascar: understanding the effects of climate and land cover change in a biodiversity hotspot. *PLoS ONE* 10(4): e0122721. doi:10.1371/journal.pone.0122721
Author countries: United Kingdom, Canada
Research funding: Madagascar National Parks, Madagascar Institute pour la Conservation des Ecosystèmes Tropicaux, Institute for the Conservation of Tropical Environments, Madagascar Biodiversity Partnership

EASTERN SHINGLEBACK (*TILIQUA RUGOSA*). CC BY-NC 2015 JOHN SULLIVAN
HTTP://WWW.INATURALIST.ORG/PHOTOS/2664222

Climate and land cover changes have the potential, both alone and together, to reshape terrestrial plant communities in tropical settings like the megadiverse island nation of Madagascar. Hoping to distinguish the combined and individual impacts of these two major drivers of changes, the authors modelled future shifts in species richness based on GBIF-mediated data for 828 genera and 2,186 species of plants in Madagascar, then quantified the changes by elevation and within the country's major ecoregions.

The results show that climate and land cover shifts will produce large-scale impacts on species diversity and richness, but with heterogeneous effects that forecast gains in certain regions. What seems worryingly consistent, though, is that the high-altitude ericoid thickets of Madagascar's four major mountains, with their high levels of endemism, will be highly vulnerable under any and all scenarios.

THE VULNERABILITY OF AUSTRALIAN SKINKS

Cabrelli AL & Hughes L (2015) Assessing the vulnerability of Australian skinks to climate change. *Climatic Change* 130(2): 223-233. doi:10.1007/s10584-015-1358-6
Author country: Australia
Research funding: Macquarie University

This study introduces a framework for assessing species' vulnerability to climate change, using Australian skinks as a case study to integrate projections of environmental niche models with indices of vulnerability. Skinks represent the largest group of reptiles in Australia, numbering almost 400 species. The researchers found that by 2050, more than 70 per cent of the skinks are projected to experience significant contractions in habitat, and 21 species stand to lose all suitable habitat. However, when assessing overall vulnerability, the researchers discovered that many species expected to lose habitat possess traits that make them very resilient to environmental changes. Other species less affected by habitat loss lack the same traits and may actually be more threatened. Those few species projected to lose nearly all habitat and with limited resilience to changes emerge as the primary focus for conservation efforts.

ANCIENT HOLLOW OAKS

Ⓐ Gough LA, Sverdrup-Thygeson A, Milberg P et al. Specialists in ancient trees are more affected by climate than generalists. *Ecology and Evolution* 5(23): 5632-5641. doi:10.1002/ece3.1799
Author countries: Norway, United Kingdom, Sweden
Research funding: Norwegian Environment Agency

BUFF-TAILED BUMBLEBEE(*BOMBUS TERRESTRIS*), CC BY 2012 DAVE YOUNG
HTTPS://WWW.FLICKR.COM/PHOTOS/DCYSURFER/6650123517

Ancient hollow oak trees are one of the most important habitats for insect biodiversity in Europe and North America. The old trees support numerous beetle species, and this study investigates how climate change will affect this community. Researchers surveyed 300 hollow oaks at 100 sites, grouped observed species as generalists or specialists, and used GBIF-mediated occurrences to cluster the species identified by geographical distribution. They then created models to predict the effects of future climate scenarios, finding that specialist beetles will be far more affected by changes in temperature and precipitation than generalists, indicating that halting the decline of hollow-oak habitats may be important to counter the effects of climate change.

INSECT INFESTATIONS OF SWEDISH FORESTS

The forest industry in Sweden sustains large financial losses every year due to insect infestations. Since climate change may increase the range of certain pest species, this study aimed to predict potential outbreak candidates. Using GBIF-mediated occurrences the researchers created models of potential distribution of 30 prospective pest species in the year 2070, which predict significant expansions of the distribution ranges across most species. Certain insects are likely to increase their geographic range by more than 90 per cent, and only a single species expects to see

its range contract. These results combined with the potential stressor of a warmer climate points to bleak prospects for present-day Swedish trees and forests.

BUMBLEBEES AND CLIMATE CHANGE

Bumblebees are important global providers of ecological services. This study used more than 360,000 GBIF-mediated occurrence records from Europe and North America to evaluate the impacts of climate change on the future of the bumblebee. The researchers found rapid losses of habitats in southern areas, but without any corresponding northward expansions. They tested whether these changes were associated with either pesticide or land-use changes, but find evidence that neither relate to shifts in bumblebee ranges. The study suggests assisted relocation of bumblebee colonies to new areas to alleviate the range losses caused by climate change.

RECEDING HARE LINES: CLIMATE CHANGE IMPACTS ON LAGOMORPHS

Species distribution models are frequently used to predict the impact of climate change on individual species' bioclimatic niches, but this study uses a novel framework to assess the bioclimatic future of an entire mammalian order (Lagomorpha) comprising hares, rabbits and pikas. Using a total of 139,000 occurrences mostly from the GBIF network, they modelled future distributions for 58 species, finding that by 2080, nearly one third of the Earth's area will experience loss of lagomorph species. On average, all three families will exhibit 1.1° shifts towards the poles and 165-meter increases in elevation by 2100. With their limited ability to move, species living on islands or in high altitudes are likely to suffer greater impacts. The study finally calls for minimizing gaps in our knowledge of Lagomorpha in order to predict and possibly prevent future extinctions.

MONARCH BUTTERFLY (*DANAUS PLEXIPPUS*). CC BY-NC 2010 EPICNOM
https://flic.kr/p/8m4uFV

USING MILKWEED TO PREDICT THE FUTURE OF THE MONARCH

ⓐ Lemoine NP (2015) Climate change may alter breeding ground distributions of eastern migratory monarchs (*Danaus plexippus*) via range expansion of Asclepias host plants. *PLoS ONE* 10(2): e0118614. doi:10.1371/journal.pone.0118614
Author country: United States
Research funding: Smithsonian Institution; Florida International University

The monarch, perhaps the most familiar North American butterfly, relies exclusively on milkweed plants (*Asclepias* spp.) for food in its larval stages. This study investigates the effects of climate change on the host plants and, consequently, the butterfly. Combining climate projections with 24,000 occurrences, including records from the GBIF network, the study's author modelled future distributions of milkweed and monarchs in the eastern United States, showing that optimal habitat for milkweed will shift north. What remains uncertain is whether monarchs will follow. Many factors, including genetics, control their migratory patterns, so this vegetation shift may present longer migration distances that could negatively impact the species.

TWO FOR ONE: PROTECT MOUNTAIN TAPIRS BY PROTECTING CLOUD FOREST

ⓐ Ortega-Andrade HM, Prieto-Torres DA, Gómez-Lora I & Lizcano DJ (2015) Ecological and geographical analysis of the distribution of the mountain tapir (*Tapirus pinchaque*) in Ecuador: importance of protected areas in future scenarios of global warming. *PLoS ONE* 10(3): e0121137. doi:10.1371/journal.pone.0121137
Author countries: Mexico, Ecuador, Venezuela, Spain
Research funding: Ecuadorian Ministry of Environment

The critically endangered mountain tapir (*Tapirus pinchaque*) is restricted to cloud forest and alpine tundra ecosystems between 1,400 and 4,700 meters above sea level in Colombia, Ecuador and northeastern Peru. Using GBIF-mediated occurrences, researchers modelled the tapir's distribution in Ecuador, evaluating the effects of future climate change scenarios on its habitats. The results reveal a general pattern of shifts toward higher elevations, reductions in area occupied by the animals, and, in some cases, complete loss of suitable habitat, and human activities may further imperil *T. pinchaque*. This study highlights the importance of informing the designation of protected areas that conserve unique and irreplaceable natural habitats.

WHICH MARINE SPECIES WILL COPE WITH RISING TEMPERATURES?

Stuart-Smith RD, Edgar GJ, Barrett NS, Kininmonth SJ & Bates AE (2015) Thermal biases and vulnerability to warming in the world's marine fauna. *Nature* 528: 88-92. doi:10.1038/nature16144
Author countries: Australia, Sweden, United Kingdom
Research funding: Australian Research Council; Institute for Marine and Antarctic Studies; Marine Biodiversity Hub; Ian Potter Foundation; CoastWest; National Geographic Society; Conservation International; Wildlife Conservation Society Indonesia: The Winston Churchill Memorial Trust; Australian-American Fulbright Commission; ASSEMBLE Marine

What do we know about the thermal needs and biases of marine animal communities? This study used nearly 400,000 GBIF-mediated occurrences to analyse and model thermal distributions of 3,900 species of shallow-water marine fish and mobile macro-invertebrates. After compiling community temperature indices (CTIs) that test for thermal bias of marine communities against environmental temperatures, the researchers' results showed that CTIs of most communities are either higher

MOUNTAIN TAPIR (*TAPIRUS PINCHAQUE*),CC BY 2009 DAVID SIFRY
https://flic.kr/p/6AhWaK

climate change

climate change

or lower than compared to the mean sea surface temperatures—meaning that some communities can likely handle increasing temperatures without significant loss of species, while others may be more threatened. The study identifies three ecoregions— the Gulf of Thailand, southwestern Caribbean, and North Cape of New Zealand—where warming is expected to exceed the upper limit of 50 per cent of the present species by 2025. Importantly, the locations with highest predicted loss of species align not with locations of greatest warming, but rather with areas of the highest level of thermal bias.

SPECIES TRAITS, WARMING OCEANS AND RANGE SHIFTS IN MARINE SPECIES

Sunday JM, Pecl GT, Frusher S et al. (2015) Species traits and climate velocity explain geographic range shifts in an ocean-warming hotspot. *Ecology Letters* 18(9): 944-53. doi:10.1111/ele.12474

Author countries: Canada, Australia, United Kingdom
Research funding: Australian National Network in Marine Science; NSERC; Australian Research Council; National Environmental Research Program, Australia; Fisheries Research and Development Corporation; Marie Curie International Incoming Fellowship; European Union

Increasingly strong currents in the coastal waters of eastern Australia have produced temperature increases three to four times greater than the global average in the region, triggering many range extensions. In this study, researchers test the theory that the traits related to invasion success are also predictors of range extensions. GBIF-mediated occurrences of 50 regional fish and 53 invertebrate species helped the researchers estimate the latitudinal range sizes. Analysing the changes alongside climate data and five other traits, they found that, although climate explains 23 per cent of the variation in range shifts, taking species traits into account increases this by 2.5 times, highlighted by the fact that the most rapid range extensions occur in omnivores with high adult mobility and large latitudinal range.

IS CLIMATE CHANGE THE MOST IMPORTANT CAUSE OF BIODIVERSITY LOSS?

Tejedor Garavito N, Newton AC, Golicher D & Oldfield S (2015) The Relative Impact of Climate Change on the Extinction Risk of Tree Species in the Montane Tropical Andes. *PLoS ONE* 10(7): e0131388. doi:10.1371/journal.pone.0131388

Author country: United Kingdom
Research funding: Bournemouth University; Franklinia Foundation

What is the relative impact of climate change on extinction risk compared to other threats? This study tries to answer this by using GBIF-mediated occurrences to model the distributions of 129 tree species endemic to the upper montane tropical Andes, and project these into future climate scenarios. Their results indicate that by the year 2080, reductions in the population size of between 36 and 46 species will qualify them as threatened. Compared against other criteria considered in IUCN Red List assessments, climate change increases the risk of extinction by 15 per cent—a finding that contradicts previous suggestions that climate change is the most important cause of biodiversity loss. This conclusion highlights the need to consider other threats when developing conservation strategies.

ARCTIC WARMING TO ENABLE TRANSOCEANIC SPECIES EXCHANGE

Wisz MS, Broennimann O, Grønkjær P et al. (2015) Arctic warming will promote Atlantic–Pacific fish interchange. *Nature Climate Change* 5: 261-265. doi:10.1038/nclimate2500

Author countries: Denmark, Greenland, Switzerland, France
Research funding: Danish Agency for Science, Technology and Innovation; European Union; NAACOS (Denmark); Canada Excellence Research Chair

The Atlantic and Pacific are connected by the Northeast and the Northwest Passage, but unsuitable conditions above the Arctic Circle have thus far prevented the interchange of marine biota between oceans. The present study simulates the spread of species under future climate conditions, creating

climate change

LINGCOD (*OPHIODON ELONGATUS*), CC BY 2012 ED BIERMAN https://flic.kr/p/dqjMBG

ecological niche models for 515 fish species based on GBIF-mediated occurrences and climate projections. In the most conservative simulation, results showed that by 2100, 13 species from the Pacific will have reached the Atlantic, whereas 16 species will have traveled the other way, with the vast majority finding suitable passage through the Northeast Passage. Though the consequences of these exchanges are difficult to predict, it is likely that they will increase beyond the year 2100 due to continued warming in the Arctic.

SEEDS OF CHANGE: CHANGING PLANT RANGES IN ALBERTA

Zhang J, Nielsen SE, Stolar J, Chen Y & Thuiller W (2015) Gains and losses of plant species and phylogenetic diversity for a northern high-latitude region. *Diversity and Distributions* 21(12): 1441-1454 doi:10.1111/ddi.12365
Author countries: Canada, Denmark, France
Research funding: Climate Change and Emissions Management Corporation; Alberta Biodiversity Monitoring Institute; Canada's Oil Sands Innovation Alliance; European Research Council; TEEMIO

In this study, researchers used 160,000 occurrences (27,000 from the GBIF network) to model ecological niches of 1,500 seed plants in the Canadian province of Alberta. When combined with future climate data, they found that by the 2080s, 24 per cent of species may lose more than 80 per cent of their habitat, but 35 per cent may double their suitable range. But overall, they predict that species richness and phylogenetic diversity will increase in most areas, except for the Rocky Mountains. The study suggests that analysis of the evolutionary history of species may offer new opportunities when prioritizing conservation efforts.

Species conservation and protected areas

GROUNDWORK: TOWARDS A GLOBAL UNDERSTANDING OF AT-RISK PLANTS

While global assessments of extinction risks for birds, mammals, amphibians and other groups are available to help guide their conservation, no similar baseline has existed for plants, despite the fundamental role they play in the biosphere. The IUCN Sampled Red List Index unveiled here offers the first accurate view of how threatened plants are around the world.

Drawing on specimen collections from the world's herbaria, including records accessed through GBIF, the authors assessed a 7,000-species sample from five major plant groups to represent the world's nearly 380,000 described plant species. Reaching the conclusion that more than one in five plants already faces the threat of extinction - a risk that is generally twice as high in the tropics - the authors argue that the world cannot afford this scale of loss, and that we must all work together to conserve what we have.

USING HISTORICAL DATA TO SAVE THE EUROPEAN EEL

The IUCN Red List lists the European eel (*Anguilla anguilla*) as critically endangered, with habitat restrictions from dam building cited among the causes of the species' collapse. By combining GBIF-mediated data with 16th- and 19th-century records on freshwater fish in Spain, the authors created current and historical distribution models for the Iberian Peninsula. After locating the region's dams in the distribution models, the authors calculated the importance of each dam in contributing to recovery of eel habitats. They concluded that making just 12 dams permeable to eels could restore access to 40 per cent of the animals' historic range, while modifications to 76 dams could achieve an 80 per cent recovery.

PROTECTING MESOAMERICAN FORESTS

Mesoamerica is home to almost 5,000 endemic plants and 8 per cent of the world's biodiversity, but how well are protected areas safeguarding the region's different forest types? Using species distribution models for 1,224 native tree species in Mesoamerica using 742,000 GBIF-mediated occurrences, this study found that about a quarter of Mesoamerican forest types are represented in protected areas, but only 5 per cent of its imperiled dry forests. They identified several novel high-value forest conservation areas (FCAs) that have regrettably little overlap with existing protected areas—in fact, more than half of the identified FCAs fall outside protected areas, particularly in Mexico's dry and coniferous forests and Panama's moist forest. Researchers hope the study's findings can guide expansion of the region's network of protected areas.

EUROPEAN EEL (*ANGUILLA ANGUILLA*), PUBLIC DOMAIN VIA THE NATIONAL LIBRARY OF THE NETHERLANDS HTTP://J.MP/2DMPEBN

species conservation

IDENTIFYING VULNERABLE SPECIES OF EASTERN MEXICO'S MONTANE CLOUD FOREST

Esperón-Rodríguez M & Barradas VL (2015) Comparing environmental vulnerability in the montane cloud forest of eastern Mexico: A vulnerability index. *Ecological Indicators* 52: 300–310. doi:10.1016/j.ecolind.2014.12.019
Author country: Mexico
Research funding: Universidad Nacional Autónoma de México; CONACyT-México

In this study, researchers combined physical traits, climate variables and potential distributions of 11 tree species to create a vulnerability index for species in the montane cloud forest of Mexico. Their results identify the most vulnerable species as American sweetgum (*Liquidambar styraciflua*) and the least vulnerable, *Persea longipes*.

REFLECTING LOCAL ADAPTATIONS IN SPECIES DISTRIBUTION MODELS

Hällfors MH, Liao J, Dzurisin JDK et al. (2016) Addressing potential local adaptation in species distribution models implications for conservation under climate change. *Ecological Applications* 26(4): 1154-1169. doi:10.1890/15-0926.1
Author countries: Finland, United States
Research funding: LUOVA; U.S. National Science Foundation; U.S. National Park Service

This paper develops case studies of two butterflies to address uncertainty surrounding local adaptation in species distributions models. Using GBIF-mediated occurrences for the Karner blue butterfly (*Lycaeides melissa samuelis*) and the Siberian primrose (*Primula nutans*), researchers built population-based models and whole-species models. The modelled results differed significantly, suggesting that important population-specific climatic conditions may be lost in whole-species models. The authors interpret their findings to recommend using population-based models rather than whole-species models where experimental studies suggest the presence of local adaptations. Failing to do so may lead to conservation management mistakes.

INTEGRATING EVOLUTIONARY HISTORY INTO CONSERVATION PLANNING

ⓐ Huang D & Roy K (2015) The future of evolutionary diversity in reef corals. *Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences* 370(1662): 20140010. doi:10.1098/rstb.2014.0010
Author countries: Singapore, United States
Research funding: Wildlife Reserves Singapore; U.S. National Science Foundation

One third of the world's reef-building corals face heightened extinction risks due to climate change and

KARNER BLUE BUTTERFLY (*LYCAEIDES MELISSA SAMUELIS*), CC BY 2011 USFWSMIDWEST https://flic.kr/p/9gp9ec

human impact, but not all species are equally affected. In this study, researchers used GBIF-mediated data and other sources to perform extinction analyses based on phylogenetic metrics and geographical distributions. Their results showed the highest proportion of threatened species in the most species-rich ecoregions, but threat to these regions is buffered by their evolutionary redundancy. So despite the comparative threat proportion, such areas face minimal loss of phylogenetic diversity—highlighting the need for integrating evolutionary history into conservation planning

GLOBAL IMPACT OF NATIONAL EFFORTS TO PROTECT VERTEBRATE DIVERSITY IN BRAZIL

ⓐ Jenkins CN, Alves MAS, Uezu A & Vale MM (2015) Patterns of Vertebrate Diversity and Protection in Brazil. *PLoS ONE* 10(12): e0145064. doi:10.1371/journal.pone.0145064
Author country: Brazil
Research funding: Ciência Sem Fronteiras; Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq); Fundação Carlos Chagas Filho de Amparo à Pesquisa do Estado do Rio de Janeiro (FAPERJ); MCTI

As one of the world's megadiverse countries, Brazil has great importance for global conservation. Researchers

relied on data from a number of sources, including GBIF.org, to map the vertebrate diversity of Brazil. The study attributes the highest values to the Amazon and the Atlantic Forest and finds that these regions are home to most threatened bird and mammal species. Endemics peak in the Atlantic Forest, and the authors recommend expanding protection and restoration efforts in the region. They also highlight a lack of occurrence data in certain regions of Brazil, urging wider support of initiatives that improve the collection and sharing of free and open biodiversity data.

ENDANGERED AMPHIBIANS OF THE MEXICAN MONTANE CLOUD FOREST

(a) Meza-Parral Y & Pineda E (2015) Amphibian diversity and threatened species in a severely transformed neotropical region in Mexico. *PLoS ONE* 10(3): e0121652. doi:10.1371/journal.pone.0121652
Author country: Mexico
Research funding: Instituto de Ecología, Mexico

The tropical montane cloud forest of Veracruz, Mexico, is home to several range-restricted endangered amphibians. Conducting ten field studies in the region, researchers recorded 895 observations of 16 species, half of which are under extinction threat. Based on their analysis on past records (including GBIF-mediated data), the authors calculate that their observations represent only 37% of the 43 amphibian species historically recorded in this now highly fragmented region.

HUMANS PRESSURE LAGOMORPHS

Verde Arregoitia LD, Leach K, Reid N & Fisher DO (2015) Diversity, extinction, and threat status in Lagomorphs. *Ecography* 38(11): 1155-1165. doi:10.1111/ecog.01063
Author countries: Australia, United Kingdom
Research funding: Consejo Nacional de Ciencia y Tecnología (CONACYT); Queen's Univ. Belfast; Natural Heritage Research Partnership; Northern Ireland Environment Agency; Australian Research Council

One quarter of all Lagomorpha—the taxonomic order that includes pikas, rabbits, hares and jackrabbits—are threatened with extinction. This study examined the phylogeny of lagomorphs and, combined with GBIF-mediated occurrences, attempted to draw parallels between evolutionary properties and patterns of diversity and extinction risk. But researchers found no apparent evolutionary traits associated with extinction risk, and no link between either climate or range size and number of species per genus. Instead, the discovery that the strongest

SWAMP RABBIT (*SYLVILAGUS AQUATICUS*), CC BY -NC 2016
DONNA POMEROY HTTP://WWW.INATURALIST.ORG/PHOTOS/3449961

predictor of extinction risk is habitats with high human population densities led them to conclude that severe man-made pressures override ecological, biological, and geographic variation in present lagomorphs.

USE OF PESTICIDES IN SPECIAL AREAS OF CONSERVATION

Wagner N, Mingo V, Schulte U & Lötters S (2015) Risk evaluation of pesticide use to protected European reptile species. *Biological Conservation* 191: 667-673. doi:10.1016/j.biocon.2015.08.002
Author country: Germany
Research funding: German Research Foundation

The European Union created Special Areas of Conservation (SACs) to protect 900 named species on sites managed to support their ecological needs. However, agricultural land use is permitted in these areas, raising the question of pesticide impact on the protection targets. Based on data from GBIF and other sources, researchers created a species-specific risk index for the reptiles that inhabit SACs and evaluated occurrence probability, physiology, and life-history aspects. The results showed that half of the species at above-average risk by pesticide use are already on the IUCN Red List and that all SAC turtle species are at high risk—findings that argue for the inclusion of pesticide risk assessments in future SAC management plans.

Biodiversity and human health

MONITORING SHIFTING MOSQUITO RANGES TO REDUCE MALARIA INCIDENCE

ⓐ Alimi TO, Fuller DO, Qualls WA et al. (2015) Predicting potential ranges of primary malaria vectors and malaria in northern South America based on projected changes in climate, land cover and human population. *Parasites & Vectors* 8: 431. doi:10.1186/s13071-015-1033-9
Author countries: United States, Colombia, Brazil
Research funding: U.S. National Institutes of Health

The countries of northern South America have taken effective public-health measures recently to control malaria in the region. But a changing climate combined with the continued growth of human populations will continue to provide environments conducive to *Anopheles darlingi* and *Anopheles nuneztovari s.l.*, two mosquitos among the area's most dominant disease vectors.

By modeling GBIF-mediated and other mosquito occurrence data and malaria incidence under future climate scenarios, this study unpacks how and where the disease vectors' ranges may expand even if infections continue to decline. Both mosquitos thrive in altered environments—*An. nuneztovari s.l.* on the fringes of disturbed land, *An. darlingi* wherever human blood meals go—so ongoing monitoring of disease vectors and incidence could help those planning and managing public health initiatives quickly target potential and emerging high-risk areas.

POTENTIAL OF SUB-SAHARAN AFRICAN PLANTS AGAINST HIV

Chingwaru W, Vidmar J & Kapewangolo PT (2015) The potential of sub-Saharan African plants in the management of Human Immunodeficiency Virus infections: a review. *Phytotherapy Research* 29(10): 1452-1487. doi:10.1002/ptr.5433
Author countries: Zimbabwe, Slovenia, Namibia

Plant products are frequently the source of new drug discoveries, providing 25 per cent of all traditional drugs. In 2015, about 5,700 people worldwide contracted HIV each day, two thirds of whom live in sub-Saharan Africa, where traditional herbal medicine plays an integral public health role. This paper reviews the HIV-inhibitory potential of Sub-Saharan African plants, highlighting the importance of additional research to identify and validate candidates for HIV treatment and prevention, using GBIF-mediated data to verify the occurrence of plants in the region.

TAKING MALARIA TREATMENT AND PREVENTION TO TRANSMISSION AREAS

Gwitira I, Murwira A, Zengeya FM, Masocha M & Mutambu S (2015) Modelled habitat suitability of a malaria causing vector (*Anopheles arabiensis*) relates well with human malaria incidences in Zimbabwe. *Applied Geography* 60: 130-138. doi:10.1016/j.apgeog.2015.03.010
Author country: Zimbabwe

In hope of contributing to better, more effective strategies for controlling of malaria, the authors developed a habitat suitability model for *Anopheles arabiensis*, one of the disease's vectors, using occurrence records from GBIF.org and other sources. The results showed a positive if weak correlation between suitable habitat for *A. arabiensis* and disease incidences recorded by Zimbabwean health facilities, suggesting the model's potential utility as an indicator in prioritizing disease prevention or treatment efforts.

ANTICIPATING RANGE SHIFTS IN MOSQUITO-BORNE ARBOVIRUSES

ⓐ Kraemer MUG, Sinka ME, Duda KA et al. (2015) The global distribution of the arbovirus vectors *Aedes aegypti* and *Ae. albopictus*. *eLife* 4: e08347. doi:10.7554/eLife.08347
Author countries: United Kingdom, United States, Brazil, Sweden, Belgium, Indonesia, Chinese Taipei
Research funding: German Academic Exchange Service; Bill & Melinda Gates Foundation; the Rhodes Trust; U.S. NASA; U.S. National Institutes of Health; the Wellcome Trust; VBORNET; European Commission; University of Oxford; U.S. Department of Homeland Security.

Dengue and chikungunya are mosquito-borne viral infections that have become increasingly widespread public health threats over the past 50 years. Using GBIF-mediated records to remove sampling bias, this

TIGER MOSQUITO (*AEDES ALBOPICTUS*), CC BY-NC-ND 2010 AFPMB
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study updated known and predicted distributions of *Aedes aegypti* and *Ae. albopictus*, the species most responsible for transmitting arboviruses to humans. By showing that both now inhabit all continents—and may yet have room to expand their ranges further, particularly *Ae. albopictus*—these findings provide a baseline understanding of the factors in their geographical spread and health-planning measures that might help control it.

ASSESSING RISK OF LASSA FEVER IN WEST AFRICA

ⓐ Mylne AQN, Pigott DM, Longbottom J et al. (2015) Mapping the zoonotic niche of Lassa fever in Africa. *Transactions of the Royal Society of Tropical Medicine and Hygiene* 109(8): 483-92. doi:10.1093/trstmh/trv047
Author countries: United Kingdom, United States
Research funding: Bill & Melinda Gates Foundation; the Rhodes Trust; University of Oxford; the Wellcome Trust; U.S. Department of Homeland Security; U.S. National Institutes of Health; European Commission

Lassa fever is a difficult-to-diagnose viral illness that claims an estimated 5,000 lives annually in West Africa. With previous research having pinpointed the Natal multimammate mouse (*Mastomys natalensis*) as the virus' animal host, the authors used more than 2 million GBIF-mediated records for all members of the family Muridae to model the host species' distribution.

Combining the model with known locations of Lassa infection in humans and animals, the results highlight an at-risk population of 37.7 million people in 14 West African countries—including four that have yet to report any cases—where conditions are suitable for transmission of the fever. This concluding paper in a series that also mapped the zoonotic niche of the Ebola, Marburg and Crimean-Congo viruses offers a spatial guide for future surveillance, diagnosis and treatment of Lassa fever, potentially enabling more rapid public health responses in the sub-Saharan regions susceptible to this acute viral illness.

MAPPING THE NICHE OF CHAGAS PARASITE

ⓐ Ramsey JM, Peterson AT, Carmona-Castro O et al. (2015) Atlas of Mexican Triatominae (Reduviidae: Hemiptera) and vector transmission of Chagas disease. *Memórias do Instituto Oswaldo Cruz* 110(3): 339-52. doi:10.1590/0074-02760140404
Author countries: Mexico, United States

All 31 species of assassin bug (subfamily Triatominae) found in Mexico are known carriers of *Trypanosoma cruzi*, the parasite responsible for Chagas disease in humans. In this study, researchers used occurrence data from sources including GBIF to model the 19 most abundant triatomine species as well as *T. cruzi*. The

results show the potential for the parasite to occur in 91.2 per cent of Mexico, exposing almost 100 million Mexicans to at least one of the vector species. Based on a parasite transmission model, they conclude that human communities in nine out of 32 states in Mexico are at risk of infection. As many as 2 million Mexicans are currently infected, and the study suggests that without immediate actions on public health, those numbers will only rise.

DATES ON DATE PALM (*PHOENIX DACTYLIFERA*), CC BY-NC 2006
MARTIN LABAR https://flic.kr/p/abWeW

FEEDING THE WORLD WITH DATES?

Shabani F, Kumar L, Nojoumian AH, Esmaeili A & Toghyani M (2015) Projected future distribution of date palm and its potential use in alleviating micronutrient deficiency. *Journal of the Science of Food and Agriculture* 96(4) 1132-1140. doi:10.1002/jsfa.7195
Author countries: Australia, Iran

Worldwide, billions of people are suffering from micronutrient deficiencies with serious health effects. 100 grams of date flesh could meet half their dietary micronutrient requirements. Using GBIF and other sources for data on date palm (*Phoenix dactylifera*), this study predicts that regions suffering most from such deficiencies may become highly suitable for date palm cultivation in the near future.

human health

DEER MOUSE (*PEROMYSCUS MANICULATUS*), CC BY 2010 USFWS https://flic.kr/p/aNW87t

MODELING THE NICHE OF PLAGUE

(a) Walsh M & Haseeb MA (2015) Modeling the ecologic niche of plague in sylvan and domestic animal hosts to delineate sources of human exposure in the western United States. *PeerJ* 3:e1493. doi:10.7717/peerj.1493
Author country: United States

Yersinia pestis, the bacterium responsible for bubonic and pneumonic plague in humans, also causes disease in rodents like deer mouse (*Peromyscus maniculatus*). The western United States has one of the largest concentrations of plague in the modern world, and this study set out to model *Y. pestis* infections occurring in the region not only in the wild but also domestic animals. Using 95,000 GBIF-mediated occurrences combined with confirmed animal plague cases, researchers created models of potential disease reservoirs and found that the most important factors in predicting infection outbreaks are the presence of deer mouse, altitude, precipitation and proximity to developed land. These results may prove useful in highlighting geographic areas at high risk for transmission of plague from animals to humans.

SNAKES BITING THEIR WAY FURTHER NORTH AND SOUTH

Yañez-Arenas C ,Peterson AT, Rodríguez-Medina K & Barve N (2016) Mapping current and future potential snakebite risk in the new world. *Climatic Change* 134(4): 697-711. doi:10.1007/s10584-015-1544-6
Author country: United States
Research funding: CONACYT

This study used GBIF-mediated occurrences to predict future snakebite risk from 90 venomous snake taxa across the Americas, where 300,000 bites occur each year. The study forecasts that climate change will expand areas of snakebite risk northward to Canada and southward to Argentina and Chile, the latter a country not yet inhabited by venomous snakes.

*See all **biodiversity and human health** citations in the Science Review Sourcebook, p.10*

Food, farming and biofuels

HEY, JOE: THE FUTURE OF COFFEE

Coffea arabica, or Arabica coffee, accounts for 75-80 per cent of the world's production of coffee. Previous studies estimate that suitable areas for coffee production will reduce by 50 per cent by 2050. This study maps the current locations of Arabica production using GBIF-mediated occurrences along with known locations of coffee farms, and then, using current climate data, models Arabica production onto so-called agro-ecological zones (AEZs). Combined with global climate models the researchers identify novel areas suitable for coffee production, and suggest alternative sites within AEZs that might be more robust in future climates. They also seek to inform coffee variety trials and to suggest providing farmers with guidelines on likely shift of AEZs from one type to another type in the future.

PLANNING CONSERVATION OF WILD RELATIVE SPECIES OF POTATO

This study assessed 73 wild relative species of potato in order to identify species and geographic areas in need of conservation efforts. Using 50,000 records including GBIF-mediated occurrences, it classifies 32 species as high priority and identifies Peru as having the highest count of such species.

A BRIGHT FUTURE FOR THE PEACH PALM?

This study examines the domestication and dispersal

ARABICA COFFEE (*COFFEA ARABICA*), CC BY 2011 MALCOLM MANNERS
https://flic.kr/p/ivaMdm

patterns of the peach palm (*Bactris gasipaes*). Using a combination of genetic analysis and distribution models based on GBIF-mediated occurrences, researchers provides new insights into the history of this important native staple. Their results suggest that the peach palm evolved from a wild species, with domestication taking place in southwestern Amazonia. Though models do predict an increase in suitable habitat for peach palm with very few losses, the authors do single out a number of priority areas for conservation of genetic and phenotypic diversity.

CONSERVATION TARGETS FOR CROP WILD RELATIVES OF SWEET POTATO

This study analysed 14 wild-relative species of sweet potato (*Ipomoea batatas*) in order to identify targets in need of conservation. Using 5,600 records provided through GBIF and other sources, they classify 11 of the species as high priority and point to a need for improving technologies for conserving germplasm.

COMMON BEANS (*PHASEOLUS VULGARIS*), CC BY 2013 ICIPE https://flic.kr/p/pDLe6J

DIVERSITY OF WILD YAMS

Magwé-Tindo J, Zapfack L & Sonké B (2015) Diversity of wild yams (*Dioscorea* spp., Dioscoreaceae) collected in continental Africa. *Biodiversity and Conservation* 25(1): 77-91. doi:10.1007/s10531-015-1031-4

Author country: Cameroon

Since crop wild relatives constitute critical genetic sources for breeding potentially useful properties like pest resistance and temperature tolerance into staple crops, this study sets out to describe the diversity of wild yams (*Dioscorea* spp.) in Africa. The wild species are under risk of extinction due to factors such as habitat destruction and climate change. Analysing 4,000 occurrences from GBIF and other sources, researchers identified 43 species, five subspecies, four varieties and seven morphospecies, locating the highest levels of yam diversity in a contiguous belt stretching across Africa from Sierra Leone to Tanzania. They also point to a number of potential sites for conserving wild yams in Africa.

BEANS ARE MOVING NORTH

Ramirez-Cabral NYZ, Kumar L & Taylor S (2015) Crop niche modeling projects major shifts in common bean growing areas. *Agricultural and Forest Meteorology* 218-219: 102-113. doi:10.1016/j.agrformet.2015.12.002

Author countries: Australia, Mexico
Research funding: Australian National Research Institute for Forestry, Agriculture and Livestock; University of New England (Australia); Australian Agency for International Development

The common bean (*Phaseolus vulgaris* L.) is the main source of protein and nutrients in both Africa and Latin America. This study focused on assessing the impact of climate change and how future climatic scenarios might intensify stress in the plant's development. Using mainly GBIF-mediated occurrences, researchers created an ecological niche model to describe current and future bean distributions. The model predicted that by 2100, the Southern Hemisphere might no longer be suitable for bean cultivation, whereas the Northern Hemisphere stands to increase its potential climatic suitability. These findings are essential to strategic planning, especially in developing countries now reliant on beans as a staple crop that are likely to lose the ability to grow it in the future.

food, fuel & fiber

Advancing biodiversity science

LEVIATHAN IMPACTS: THE ONCE—AND FUTURE?—PRESENCE OF THE ATLANTIC GRAY WHALE

Alter SE, Meyer M, Post K et al. (2015) Climate impacts on transocean dispersal and habitat in gray whales from the Pleistocene to 2100. *Molecular Ecology* 24(7): 1510-1522. doi:10.1111/mec.13121

Author countries: United States, Germany, Australia, United Kingdom, Netherlands

Research funding: Max Planck Society, Packard Foundation, European Research Council

GRAY WHALE (*ESCHRICHTIUS ROBUSTUS*) TAIL FIN, CC BY-NC-ND 2013 KAREN https://flic.kr/p/e42AYM

The extirpation of the gray whale (*Eschrichtius robustus*) from the Atlantic Ocean is often attributed to overharvesting by the early modern whaling industry. But this hypothesis fails to explain the lack of catch records while overlooking possible connections with the population that inhabits the Pacific today.

This study combines DNA analysis of present-day Pacific gray whales and fossils—including newly reported specimens from the North Sea—with predictive habitat models built on occurrence data that includes 162 GBIF-mediated records. The results indicate that three historic Atlantic lineages intermingled with Pacific populations as and when sea level and ice cover declined earlier in the (present) Holocene era to provide them with high-latitude feeding grounds—insights that suggest the usefulness of keeping watch for future climate-driven dispersals of this Arctic sentinel species.

AMERICA: "SPECIES PUMP" TO THE PLANT WORLD

ⓐ Antonelli A, Zizka A, Silvestro D et al. (2015) An engine for global plant diversity: highest evolutionary turnover and emigration in the American tropics. *Frontiers in Genetics* 6: 130. doi:10.3389/fgene.2015.00130

Author countries: Sweden, Switzerland, Belgium, Colombia

Research funding: Swedish Research Council; European Research Council; Carl Tryggers and Wennergren stiftelse; University of Liege

In this study, researchers used almost 25 million GBIF-mediated records alongside 9,000 fossil records and a single dated phylogenetic tree to provide insights into patterns of plant diversification and biogeography. The results shed light on differences in plant diversity between tropical and non-tropical regions, as well as between the tropical regions of Africa, Asia, and the Americas. Examining more than 27,500 species of flowering (angiosperm) plants in the last 60 million years, the authors found no difference in speciation and extinction rates between tropics and non-tropics, implying that another model might be needed to explain the so-called latitudinal diversity gradient. Their findings also noted significant differences between the world's three tropical regions, as a massive spike in emigration shifts out of America around 57 million years ago suggests that this region became a "species pump" for the rest of the world.

UNRAVELLING THE ORIGIN OF LEISLER'S BAT

Boston ESM, Ian Montgomery W, Hynes R et al. (2015) New insights on postglacial colonization in western Europe: the phylogeography of the Leisler's bat (*Nyctalus leisleri*). *Proceedings of the Royal Society B: Biological Sciences* 282(1804): 20142605. doi:10.1098/rspb.2014.2605

Author countries: United Kingdom

Research funding: U.K. Department of Education and Learning

This study uses a combination of DNA markers and paleoclimatic species distribution modelling (powered by GBIF-mediated data) to assess the origin and phylogeography of Leisler's bat (*Nyctalus leisleri*). The results suggest two distinct mitochondrial lineages and identify novel suitable habitats during the last glacial maximum 20,000 years ago that may also apply to other species.

STINGLESS BEES OF THE ATLANTIC FOREST

Carvalho AF & Del Lama MA (2015) Predicting priority areas for conservation from historical climate modelling: stingless bees from Atlantic Forest hotspot as a case study. *Journal of Insect Conservation* 19(3): 581-587. doi:10.1007/s10841-015-9780-7
Author countries: Brazil, United States
Research funding: Fundação de Amparo à Pesquisa do Estado de São Paulo

In this study, researchers used GBIF-mediated occurrences to model the potential distribution of 19 species of stingless bees during different periods of climatic extremes ranging from the Late Quaternary to the present. The results identify three climatically stable refuges that are important to the conservation of stingless bees in Brazil's Atlantic Forest.

REPEATED EVOLUTION OF ANT-PLANT MUTUALISMS

Chomicki G & Renner SS (2015) Phylogenetics and molecular clocks reveal the repeated evolution of ant-plants after the late Miocene in Africa and the early Miocene in Australasia and the Neotropics. *The New Phytologist* 207(2): 411-425. doi:10.1111/nph.13271
Author countries: Germany

This study compiled a comprehensive database of 681 known ant-associated plant species. A model relying on GBIF-mediated occurrences estimates the real number of species at 1,140. An analysis of one type of ant-plant mutualism, in which plants have structures that hosts ants (domatia), suggests it may have evolved repeatedly due to parasitic relationships with scale insects. This adaptation may have started as early as the Miocene epoch, later than previously thought. The data also suggest that ant-plant symbioses have no straightforward effect on diversification rates in the host plants.

WHAT TRAITS ARE ESSENTIAL FOR PLANTS TO BE SUCCESSFUL ON EARTH?

Díaz S, Kattge J, Cornelissen JHC et al. (2016) The global spectrum of plant form and function. *Nature* 529: 167-171. doi:10.1038/nature16489
Author countries: Argentina, Germany, Netherlands, Australia, France, Colombia, United Kingdom, United States, Panama, Russian Federation, French Guiana, Italy, Canada, Costa Rica
Research funding: Universidad Nacional de Córdoba; CONICET; FONCyT; and SECyT (Argentina); The Leverhulme Trust; Inter-American Institute for Global Change Research; U.S. National Science Foundation

The form and function of plants are immensely varied. But how constrained are traits when it comes to evolutionary viability and success? This massive study relies in part on GBIF-mediated data to examine plant trait variations at a global scale and draw a quantitative picture of functional diversity in 46,000 vascular plant species. Placing the plants into a six-dimensional trait matrix, the authors reveal how highly correlated and strongly constrained traits are, suggesting that a only small set of trait combinations are successful. Overall, the study presents a generalized backdrop for understanding plant biology and a global model for mapping the evolution of individual trait variations.

ASIAN BLACK BEAR *(URSUS THIBETANUS)*, CC BY 2014 MIKE PRINCE
https://flic.kr/p/nTcpUY

REFINING A NICHE MODEL FOR ASIATIC BLACK BEAR WITH NIGHTTIME LIGHTING IMAGERY

Escobar LE, Awan MN & Qiao H (2015) Anthropogenic disturbance and habitat loss for the red-listed Asiatic black bear (Ursus thibetanus): Using ecological niche modeling and nighttime light satellite imagery. *Biological Conservation* 191: 400-407. doi:10.1016/j.biocon.2015.06.040
Author countries: United States, Pakistan, China
Research funding: U.S. Armed Forces Health Surveillance Branch; National Natural Sciences Foundation of China

Despite its broad range across eastern Russia, northern India and northeastern China, the Asiatic black bear (*Ursus thibetanus*) is globally Red Listed as vulnerable, and its declining population faces rising conflict with humans over habitat and resources. A unique research team from the US, Pakistan and China modeled the bear's ecological niche—testing it against data accessed through GBIF, VertNet and other sources—and then looked to refine the resulting measures of long-term suitable habitat. Using data for artificial nighttime lighting as a proxy for human occupancy, the results account for human

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disturbance while highlighting more appropriate (and less disturbed) regions for long-term conservation and protected area planning.

A NETWORK OF TICKS

(a) Estrada-Peña A, de la Fuente J, Ostfeld RS & Cabezas-Cruz A (2015) Interactions between tick and transmitted pathogens evolved to minimise competition through nested and coherent networks. Scientific Reports 5: 10361. doi:10.1038/srep10361
Author countries: Spain, United States, France
Research funding: European Union

In this study, researchers used a network approach to systematically describe ecological relationships between ticks, their hosts, and the pathogens they carry. More than 3 million GBIF-mediated occurrences went into mapping habitats of 276 vertebrate hosts; combining these with phylogenetic trees and a systematic review of species interactions, the authors produced a clustered network of relationships. This novel application revealed a highly connected and robustly structured network and, in a noteworthy finding for parasitic ecology, shows that 70 per cent of ticks share hosts related only by environment, not genetics. The authors conclude that this framework is readily adaptable to similar scientific problems.

THE FATE OF MEDITERRANEAN SAWFISH

(a) Ferretti F, Verd GM, Seret B, Šprem JS & Micheli F (2015) Falling through the cracks: the fading history of a large iconic predator. Fish and Fisheries. doi:10.1111/faf.12108.
Author countries: United States, Spain, France, Croatia
Research funding: Lenfest Ocean Program

In this study, researchers compile a database of all available sawfish records, including GBIF-mediated occurrences and other historical records, to shed light on its waxing and waning presence—and possible

ILLUSTRATION OF COMMON SAWFISH (*PRISTIS PRISTIS*), CC BY 2012 BIODIVERSITY HERITAGE LIBRARY https://flic.kr/p/bQeTWg

extinction—in the Mediterranean. They describe 48 independent accounts of occurrences, including 24 documented catches, concluding that sawfish species most likely went extinct in the Mediterranean in the 1960s or '70s.

THE EVOLUTION OF THE COMMON MOLE

Feuda, R, Bannikova AA, Zemlemerova ED et al. (2015) Tracing the evolutionary history of the mole, *Talpa europaea*, through mitochondrial DNA phylogeography and species distribution modelling. Biological Journal of the Linnean Society, 114(3): 495-512. doi:10.1111/bij.12459
Author countries: Italy, United States, Russia, Germany
Research funding: Russian Foundation for Basic Research

The effect of climatic changes on subterranean mammals during the Pleistocene epoch is largely unknown. In this study, researchers examine the evolutionary history of the common mole (*Talpa europaea*) by combining molecular analysis with species distribution models using GBIF-mediated occurrences. Their results reveal three different lineages with specific ranges in Spain, Italy, and the rest of Europe, respectively. The phylogeographical structure of the latter two lines suggests a distinct break from the last Pleistocene glaciation. During phases when most of the current ranges were unsuitable, the mole appears to have been confined to refuges in southern Europe.

USING LEGACY LITERATURE FOR STUDIES OF BIODIVERSITY

(a) Groom Q (2015) Using legacy botanical literature as a source of phytogeographical data. Plant Ecology and Evolution 148(2): 256–266. doi:10.5091/plecevo.2015.1048
Author country: Belgium
Research funding: European Union

Although the GBIF network has mobilized hundreds of millions of occurrence records, a massive amount of data remains available only in undigitized form. By reviewing two data-mobilization case studies, the author explores how much information can be extracted from legacy literature and how useful it might be. And while the quantity of information retrieved from such documents can be considerable, records rarely have precise dates and are often not georeferenced. The study concludes with a testing effort to gather all existing records for stinking goosefoot (*Chenopodium vulvaria*), estimating that legacy literature contributes 20 per cent of all available observations.

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GAMBIAN EPAULETTED BATS (*EPOMOPHORUS GAMBIANUS*), CC BY-NC 2008 STEPHEN C SMITH https://flic.kr/p/aP1kZx

CRACLE: INFERRING CLIMATE FROM VEGETATION

Correlations between plant distributions and the climate and environmental conditions to which species have adapted are well known, and models can predict distributions accurately based on occurrences and climate. This study describes a novel approach for estimating climate from vegetation. Researchers created climate tolerance profiles for more than 4,300 species by pairing 3.75 million GBIF-mediated occurrences with climate data, then using the presence of the same plants in 165 survey sites to predict the local climate. The CRACLE method—'climate reconstruction analysis using coexistence likelihood estimation'—returned results with a strong linear correlation with actual climate and, when compared to other methods, yields lower error rates in estimating variables such as temperature and precipitation.

DISTRIBUTION AND DIVERSITY OF AFRICAN BATS

Bats' nocturnal habits and life on the wing limit our knowledge of the group's distribution and diversity. In this study, researchers create state-of-the-art distribution models of 250 African bat species using an unparalleled amount of occurrence data (including GBIF-mediated records). Stacking the models, they conclude that bat diversity generally increases towards the equator but varies substantially within the equatorial zone. They identify centres of endemism in areas characterized by substantial elevation ranges, and hotspots of species richness including an area on the Semliki River southwest of Lake Albert, home to no fewer than 84 bat species. The study's conclusion presents a very high-resolution view of mammalian biodiversity data that covers a vast geographic and taxonomic scope.

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VISUALIZING A COMPREHENSIVE VIEW OF LIFE PAST AND PRESENT

(a) Hinchliff CE, Smith SA, Allman JF et al. Synthesis of phylogeny and taxonomy into a comprehensive tree of life. *Proceedings of the National Academy of Sciences of the United States of America* 112(41): 201423041. doi:10.1073/pnas.1423041112
Author countries: United States
Research funding: U.S. National Science Foundation

This study represents the first automated process for assembling published phylogenies and taxonomic classifications into a single, complete tree of life. By merging the GBIF taxonomic backbone with numerous other taxonomic sources and phylogenies, researchers are able to produce a state-of-the-art, all-inclusive tree containing 2.3 million tips they dub the Open Tree of Life.

CLIMATE SECRETS FROM ANCIENT TASMANIAN PLANTS

Jordan GJ, Harrison PA, Worth JRP, Williamson GJ & Kirkpatrick JB (2015) Palaeoendemic plants provide evidence for persistence of open, well-watered vegetation since the Cretaceous. *Global Ecology and Biogeography*. doi:10.1111/geb.12389
Author countries: Australia, Japan
Research funding: Australian Research Council

This study identifies 51 paleoendemic plants in Tasmania, relying on occurrence data from both GBIF and the Atlas of Living Australia to find that these species tend to cluster in open areas with globally rare wet climates and lack extreme temperature variations. The results of the study suggest that the region has had open vegetation in moist areas with moderate temperatures since the Cretaceous period.

PREDICTING THE FUTURE FROM PREVIOUS CLIMATE-INDUCED CHANGES IN *PISTACIA*

Kozhoridze G, Orlovsky N, Orlovsky L, Blumberg DG & Golan-Goldhirsh A (2015) Geographic distribution and migration pathways of Pistacia - present, past and future. *Ecography* 38: 1-14. doi:10.1111/ecog.01496
Author country: Israel
Research funding: Albert Katz International School for Desert Studies; European Commission; U.S.-Israel Cooperative Development Research Program; Bureau for Economic Growth, Agriculture and Trade; U.S. Agency for International Development

MICROCACHRYS TETRAGONA IS PART OF A TASMANIAN CONIFER CLADE ESTIMATED TO BE 130 MILLION YEARS OLD. CC BY-NC-SA 2009 NATALIE TAPSON https://flic.kr/p/6UCB54

In hope of gaining a longer-term perspective of how diverse climatic conditions have previously affected species distributions, this study used the relatively genetically closely related species from the genus *Pistacia* as a case study. 125,000 GBIF-mediated records formed the basis for distribution models for ten *Pistacia* species combining it with climate, landscape and soil data to predict probable distributions from 121,000 years ago to 2100. Results suggest that deciduous species have greater tolerance to extreme temperatures than evergreens, and that the genus may have originated in boreal forests before migrating in response to climate change.

WHERE THE WILD OATS GROW

Loskutov IG, Melnikova SV & Bagmet LV (2015) Eco-geographical assessment of Avena L. wild species at the VIR herbarium and genebank collection. *Genetic Resources and Crop Evolution*. doi:10.1007/s10722-015-0344-1
Author country: Russian Federation
Research funding: Russian Scientific Foundation

This study analyses the habitats of wild oat species based on genetic records and herbarium records accessed through GBIF. The resulting distributions

show that most wild oat species prefer mountain soil conditions in moderately hot, semi-arid and dry climates.

ANDES UPLIFT AND ANURAN DIVERSITY

W RAINFROG (*PRISTIMANTIS W-NIGRUM*), CC BY-NC 2013 KOVASKA
HTTP://WWW.INATURALIST.ORG/PHOTOS/259592

The landscape of the American tropics has been continuously modified during the last 50 million years, and creation of barriers and connections has shaped the wildlife occupying the region. This study explores the role that the forming of the Andes played in the evolution and diversification of *Pristimantis* frogs. Using DNA sequencing and GBIF-mediated occurrences, researchers have produced a new phylogenetic tree and reconstructed ancestral ranges for the genus. Their results pinpoint the middle elevation band in the northwestern Andes as a hotspot for the origin and radiation of *Pristimantis*, and suggest that the paleogeological changes there acted as the main driver of speciation in the genus.

PRIORITIZING GAPS AND BIASES IN BIODIVERSITY DATA

The Convention on Biological Diversity's (CBD) Aichi Target 19 provides a specific mandate for developing and sharing an advanced biodiversity knowledge base. While the GBIF network has collected hundreds of millions of records, gaps and biases do remain. This study assessed nearly 200 million GBIF-mediated occurrences of terrestrial vertebrates to identify such gaps and biases. The results show that Asia, Africa, and South America have large areas with no records. By superimposing the occurrences on expert-curated maps, the researchers estimate the level of completeness and find that this is highly correlated with record density, except in very species-rich areas such as the American and African tropics. The strongest limiting factor of data completeness is related to digitization and mobilization rather than actual collection. National research funding and GBIF participation are consistently strong factors in determining completeness.

SEEKING THE ORIGINS OF TROPICAL PLANT DIVERSITY

Why are the tropics such a hotbed of plant diversity, and what mechanisms are most responsible for shaping these evolutionary patterns? This study sought to tackle 'one of the most intriguing questions in modern biogeography' by exploring the origins and spread of the genus *Begonia*. Pairing genetic analysis of around 1,600 Andean-centered Begonia species with a reconstruction of their ancestral ranges that relies on 22,374 GBIF-mediated records, the findings highlight *Begonia*'s numerous radiation events and the importance of chance in regional and continental-scale dispersals of species.

SEA STARS OF THE SOUTHERN OCEAN

Using more than 13,000 occurrences records aggregated from different sources including the GBIF network, the authors of this study propose an updated version of the checklist of Southern Ocean Asteroidea (sea stars) species. The finalized list has been provided as an update to the Register of Antarctic Marine Species and published through GBIF.org.

PARENCHYMA TISSUE COMPOSITION IN SEED PLANTS

Parenchyma is an important tissue in seed plants, consisting of cells of different types, but very little is known about the composition. This study used GBIF-mediated occurrences to present a global analysis of these cellular fractions, concluding that temperature and growth form are predictors of total parenchyma tissue composition.

TESTING ECOLOGICAL HYPOTHESES USING 'SYNTHETIC' DATASETS

Large data networks provide researchers with new means of addressing a large number of macroecological questions without having to collect new data. This study reviews common methods and principles, identifies bottlenecks and provides clear recommendations for using these approaches. The authors created a case study on a pine-marsh food-web structure based on interactions from a variety of database sources and species distribution models created using GBIF-mediated occurrences. They demonstrate that synthetic datasets like these can support large-scale qualitative predictions while identifying gaps in our knowledge of biological systems. The results describe methods that can aid in identifying high-priority areas for fieldwork.

RAFFLES' PITCHER PLANT (*NEPENTHES RAFFLESIANA*), CC BY-SA 2014 BERNARD DUPONT https://flic.kr/p/q2GUdF

ECOLOGICAL NICHE DIVERGENCE IN CARNIVOROUS PITCHER PLANTS

This study explores the relationship between genetic proximity and ecological niche divergence in carnivorous pitcher plants (*Nepenthes* genus) in the Malay Archipelago. Building from 735 GBIF-mediated records on 69 species, the results highlight distinct phylogenetic signals from highland and lowland species, suggesting that the groups reflect divergent evolutionary histories and may tolerate and respond differently to future climatic conditions.

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EULAEMA NIGRITA LEPELETIER ON A *PERIANDRA MEDITERRANEA* FLOWER. CC BY 2008 ALEX POPOVKIN HTTP://BIT.LY/2DZYZTJ

CLIMATE, NOT HOSTS, AFFECTS DISTRIBUTION OF NEST-STEALING BEES

Silva DP, Varela S, Nemésio A & De Marco P Jr (2015) Adding Biotic Interactions into Paleodistribution Models: A Host-Cleptoparasite Complex of Neotropical Orchid Bees. *PLoS ONE* 10(6): e0129890. doi:10.1371/journal.pone.0129890
Author countries: Brazil, Germany
Research funding: Conselho Nacional de Desenvolvimento Científico e Tecnológico

Orchid bees are colourful pollinators found exclusively in the Neotropics. Some species are cleptoparasites that hijack nests from host species. In this case, researchers evaluated the inclusion of a host bee species, *Eulema nigrita*, in modelling of distributions of the orchid bee *Aglae caerulea*. Using GBIF-mediated occurrences, researchers created distribution models for the parasite, combining them with historical climate data and the presence of *E. nigrita*. Surprisingly, the results showed that the host-parasite interaction complex did not improve the models. Instead, the ranges of *A. caerulea* appear mainly constrained by climatic factors, not the presence of the host.

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USING BIOGEOGRAPHICAL DATA TO EXPLORE THE PHYLOGENY OF RANGE AND NICHE

Spalink D, Drew BT, Pace MC et al. (2016) Evolution of geographical place and niche space Patterns of diversification in the North American sedge (Cyperaceae) flora. *Molecular Phylogenetics and Evolution* 95: 183-195. doi:10.1016/j.ympev.2015.09.028
Author countries: United States, China
Research funding: U.S. National Science Foundation; University of Wisconsin-Madison

To understand what role geography and ecological niches play in evolutionary processes of species, this research team downloaded and used 200,000 GBIF-mediated occurrences for a case study of Cyperaceae (sedges) species in North America. By constructing a quadrat map they identified six regions with exceptional species richness. When combined with more than 20,000 base pairs of genetic data, they found support for the hypothesis that diversification of the sedge flora is associated with the evolution of species distributions and climatic niches. The study offers a novel approach for making iterative improvements to the use of biogeographical data within a phylogenetic context.

WHAT CAUSED THE LATITUDINAL DIVERSITY GRADIENT?

Spano CA, Hernández CE & Rivadeneira MM (2015) Evolutionary dispersal drives the latitudinal diversity gradient of stony corals. *Ecography* 39(9): 836-843. doi:10.1111/ecog.01855
Author country: Chile
Research funding: FONDECYT; CONICYT

The 'latitudinal diversity gradient' is the name given to the upsurge in species richness from the poles to the equator. The evolutionary forces that drive the gradient are still poorly understood. This study examines stony corals (order Scleractinia), as they have one of the clearest and most exemplary gradients of all clades. Based on analyses of historical occurrences accessed through GBIF and other sources, the researchers concluded that the gradient demonstrated in stony corals is rather young, originating only after the end of the Cretaceous mass extinction. As a result, the evolutionary force behind the gradient pattern fails to meet the predictions of the so-called 'out of the tropics' (OTT) model, as it doesn't show an origin in the higher tropics, but instead demonstrates a far greater tendency for migration towards the tropics.

HUMAN IMPACT OUTPACES CLIMATE IN ABACO

Steadman DW, Albury NA, Kakuk B, et al. Vertebrate community on an ice-age Caribbean island. *Proceedings of the National Academy of Sciences of the United States of America* 112(44): E5963-E5971. doi:10.1073/pnas.1516490112
Author countries: United States, Bahamas
Research funding: U.S. National Science Foundation; National Geographic Society; University of Florida; American Museum of Natural History

This study presents the recovery of more than 5,000 fossils of 95 vertebrates in the flooded cave called Sawmill Sink on Abaco in the Bahamas. Aided by present-day models built on GBIF-mediated data, the analysis of this set of late Pleistocene fossils revealed that 17 species succumbed to climate changes between nine and 15 thousand years ago, but as many as 22 species have gone extinct as a direct result of the past 1,000 years of human presence.

WITH TIME COMES DIVERSITY

Tanentzap AJ, Brandt A, Smissen R et al. (2015) When do plant radiations influence community assembly? The importance of historical contingency in the race for niche space. *The New Phytologist* 207(2): 468-79. doi:10.1111/nph.13362
Author countries: United Kingdom, New Zealand, United States
Research funding: Royal Society of New Zealand

This paper tests the mechanisms by which plant evolutionary radiations emerge and influence ecological dynamics with focus on 16 species-rich genera in the alpine zone of New Zealand. Occurrences from GBIF aided reconstruction of the niche space

MASKED CRIMSON TANAGER (*RAMPHOCELUS NIGROGULARIS*). CC BY-NC 2016 SAINTCHARLES HTTP://WWW.INATURALIST.ORG/PHOTOS/4396470

that each genus has occupied over the last 20 million years, along with ambitious steps like calculating sea-surface temperatures through the Cenozoic from isotopic measurements of foraminifera deposited in marine sediment cores, then using these to estimate past land temperatures. Their results suggest that genera that colonized New Zealand earlier encountered more 'vacant' environmental space, which promoted species diversification and further occupancy of the environment. Thus time not only explains why diversity arises, but how this diversity influences ecological dynamics.

DIVERSIFICATION OF THE TANAGERS

Title PO & Burns KJ (2015) Rates of climatic niche evolution are correlated with species richness in a large and ecologically diverse radiation of songbirds *Ecology Letters* 18(5): 433-440. doi:10.1111/ele.12422
Author countries: United States
Research funding: U.S. National Science Foundation

What causes certain groups of organisms to have more species than others? This study seeks an answer by examining the relationship between ecological niche evolution and diversification in the largest family of songbirds, the tanagers (Thraupidea). Researchers compiled distributions using GBIF-mediated data and other sources, then constructed niche models using 19 bioclimatic variables. Phylogenetic analysis divided the family into clades, scoring them according to climatic niche evolution. These scores correlate strongly with species richness, which correlate further with niche volume clade age and geographical area. The authors suggest that the study provides a replicable method for analysing niche evolution in large, widespread clades.

GALAXEA SP. OF THE STONY CORAL ORDER (SCLERACTINIA). CC BY-NC-SA 2014 PATRICK RANDALL https://flic.kr/p/mbc2ks

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SPECIES RICHNESS IS SHAPED BY CLIMATE

ⓐ Velasco JA, Martínez-Meyer E, Flores-Villela O et al. (2016) Climatic niche attributes and diversification in *Anolis* lizards. *Journal of Biogeography* 43(1): 134-144. doi:10.1111/jbi.12627
Author countries: Germany, Mexico, United Kingdom, Colombia
Research funding: U.S. National Science Foundation

In this study, researchers relied on 13,500 records mainly accessed through GBIF to test the link between climatic niche dynamics and species diversification in the species-rich genus of *Anolis* lizards. Having found significant association between niche position breadth and diversification, the findings provide evidence to suggest that climate plays a strong role in shaping species richness.

CLOSE BUT THOUSANDS OF YEARS APART

Wasof S, Lenoir J, Aarrestad PA et al. (2015) Disjunct populations of European vascular plant species keep the same climatic niches. *Global Ecology and Biogeography* 24(12): 1401-1412. doi:10.1111/geb.12375
Author countries: France, Norway, United States, United Kingdom, Sweden, Denmark, Germany, Austria, Switzerland, Iceland, Finland, Belgium, Estonia
Research funding: European Research Council; Swedish Research Council; Norwegian Research Council; Stockholm University

To assess whether species' climatic niches are constant in space and time, researchers used data from GBIF and other sources to examine two long-separated populations of 888 alpine plants that occur in both the Alps and Fennoscandia. The research used two approaches to quantify niche dynamics confirmed that climatic niches are in fact generally conserved between the two groups.

DYNAMICS OF SYMBIOTIC RELATIONSHIPS

ⓐ Werner GDA, Cornwell WK, Cornelissen JHC & Kiers ET (2015) Evolutionary signals of symbiotic persistence in the legume–rhizobia mutualism. *Proceedings of the National Academy of Sciences of the United States of America* 112(33): 201424030. doi:10.1073/pnas.1424030112
Author countries: Netherlands, Australia
Research funding: Netherlands Organisation for Scientific Research Grants; European Research Council; DIVERSITAS/Future Earth; German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig

Symbiotic relationships are an important driver of diversification of organisms. The connection between legumes and nitrogen-fixing bacteria, for example, is ancient—but why is this relationship sometimes lost,

when in other cases it plays a crucial role in evolution? In this study, researchers used more than three million GBIF-mediated legume occurrences in hope of shedding light on this mystery, testing whether certain traits or ecological factors might lead to persistence of symbiosis. The results showed that half the species analysed remain highly likely to maintain the symbiotic relationship over time, even if it isn't absolutely necessary. Such species tend to have high nitrogen and phosphorus leaf content and are located in climates with low mean annual temperatures.

BUILDING THE LOCAL ECOLOGICAL FOOTPRINTING TOOL (LEFT)

Willis KJ, Seddon AWR, Long PR et al. (2015) Remote assessment of locally important ecological features across landscapes: how representative of reality? *Ecological Applications* 25(5): 1290-1302. doi:10.1890/14-1431.1
Author countries: United Kingdom, Norway
Research funding: Statoil; Operation Wallacea; Oxford University
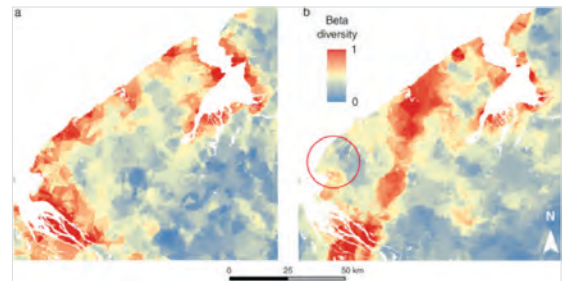
BETA-DIVERSITY MAPS FOR MAHAMAVO, MADAGASCAR, COMPUTED USING **LEFT** SOURCED WITH GLOBAL ONLINE DATABASES (A) AND COMPUTED USING LOCAL FIELD DATA (B).

In this project, researchers developed an automated web-service known as the Local Ecological Footprinting Tool or LEFT, to carry out environmental impact assessments quickly and easily with a minimum of user input. Based on measures of biodiversity, vulnerability, fragmentation, connectivity, and resilience, the service uses freely available data from GBIF and other sources to output a map and report of ecological features and risks. To test the performance of the tool, the researchers compared results from an automated report with biological field study data for a number of validation sites and found that the tool provides very robust results. However, regional gaps in biological occurrence data can have the effect of adding to the results' uncertainty.

Data management

THE FUTURE OF BIOLOGICAL RECORDING IS HERE

August T, Harvey M, Lightfoot P et al. (2015) Emerging technologies for biological recording. *Biological Journal of the Linnean Society* 115(3): 731-749. doi:10.1111/bij.12534
Author country: United Kingdom
Research funding: Joint Nature Conservation Committee; Natural Environment Research Council

Rapid technological changes have always had an impact on the biological sciences from the invention of the microscope to the use of smartphone apps in research today. This paper systematically reviews past, present and potential future technologies for biological data recording, concluding that despite the challenges that adopting these technologies present to some, they will lead to better, more open and reliable scientific data.

RETHINKING GEOSPATIAL PROCESSING

Authmann C, Beilschmidt C, Drönner J, Mattig M & Seeger B. VAT: A system for visualizing, analyzing and transforming spatial data in science. *Datenbank-Spektrum* 15(3): 175-184. doi:10.1007/s13222-015-0197-y
Author country: Germany
Research funding: Deutsche Forschungsgemeinschaft; Bundesministerium für Bildung und Forschung

In this study, researchers propose a general system for visualization, analysis and transformation (VAT) of spatial data in research. They validated their system using GBIF-mediated occurrences and concluded that VAT outperforms other systems on speed and graphical performance.

HOW OPEN IS OPEN DATA?

Campbell J (2014) Access to scientific data in the 21st century: Rationale and illustrative usage rights review. *Data Science Journal* 13: 203-230. doi:10.2481/dsj.14-043
Author country: United States

Numerous online data repositories claim to provide open access to scientific data, but specific usage conditions often apply, and no consensus exists on what "open" exactly means. This paper lists and reviews 49 scientific data repositories and their usage rights, concluding that in order to make data truly open, repositories should apply recognized and standardized data licences like those provided through Creative Commons.

SURVEY OF DATA JOURNALS

Candela L, Castelli D, Manghi P & Tani A (2015) Data journals: A survey. *Journal of the Association for Information Science and Technology* 66(9): 1747-1762. doi:10.1002/asi.23358
Author country: Italy
Research funding: OpenAIREplus; iMarine

This overview of more 100 journals that accept data papers describes various approaches for handling and preparing peer-reviewed metadata. Automated manuscript preparation, a functionality that GBIF's Integrated Publishing Toolkit (IPT) provides, is included in the survey.

TAXONOMIC CATALOGS FOR THE FUTURE

ⓐ Dikow T & Agosti D (2015) Utilizing online resources for taxonomy: a cybercatalog of Afrotropical apiocerid flies (Insecta: Diptera: Apioceridae). *Biodiversity Data Journal* 3: e5707 doi:10.3897/BDJ.3.e5707
Author countries: United States, Switzerland
Research funding: Encyclopedia of Life; Field Museum of Natural History; U.S. National Science Foundation

This paper describes the creation of a taxonomic cybercatalog of Afrotropical apiocerid flies. Although small in scope, this catalog relies on open-access online repositories like GBIF.org, and demonstrates the potential of using linked data to develop other online resources.

INTEGRATING FRESHWATER DATA TO ANALYSE SPECIES RICHNESS

González Vilas L, Guisande C, Vari RP et al. (2015) Geospatial data of freshwater habitats for macroecological studies: an example with freshwater fishes. *International Journal of Geographical Information Science* 30(1): 126-141. doi:10.1080/13658816.2015.1072629
Author countries: Spain, United States, Colombia

This study demonstrates the use of the ModestR package to bring together a massive freshwater habitat dataset that includes GBIF-mediated occurrences of freshwater fishes. While focused on an assessment of species richness in different habitat types, the study also underlines the impact of continental-scale data biases for freshwater.

INTEROPERABILITY RUNS ON GLOBALLY UNIQUE IDENTIFIERS

Guralnick RP, Cellinese N, Deck J, et al. (2015) Community next steps for making globally unique identifiers work for biocollections data. *ZooKeys* 494: 133-54. doi:10.3897/zookeys.494.9352
Author countries: United States, Bulgaria, Germany, Switzerland
Research funding: U.S. National Science Foundation, Genomic Standards Consortium, European Union

The generation and preservation of Internet links (such as DOIs used in GBIF) are crucial to assembling, tracking and linking large online biological datasets. This review recaps the results of a workshop of informatics experts and stakeholders held in Stockholm, Sweden in October 2014, and summarizes the consensus views of the participants.
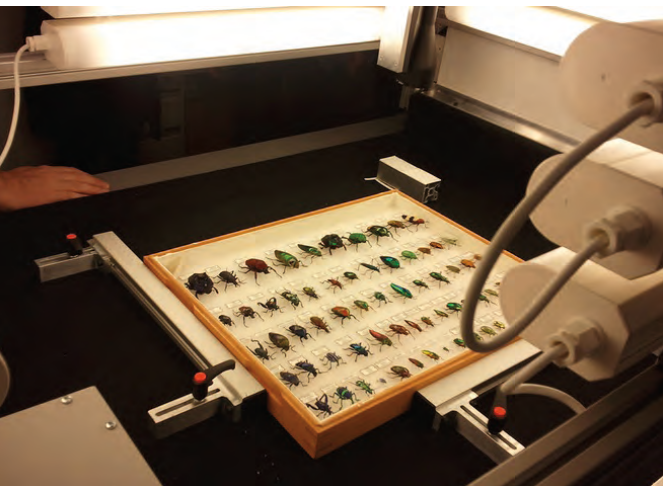
NATURALIS' DIGITIZATION PROCESSES ARE DESIGNED TO PROVIDE MAXIMUM EFFICIENCY FOR EACH TYPE OF COLLECTION OBJECT.

INDUSTRIAL-STRENGTH DIGITIZATION OF MUSEUM SPECIMENS

Heerlien M, Van Leusen J, Schnörr S et al. (2015) The Natural History Production Line. *Journal on Computing and Cultural Heritage* 8(1). doi:10.1145/2644822
Author country: Netherlands
Research funding: Dutch Fund for Economic Structure

This paper provides an overview of digitization at the Netherlands' Naturalis Biodiversity Center, one of the world's five largest natural history collections. The authors describe decision-making processes and methods for maximizing the impact of a €13 million grant, which funds a project aimed at making 7 of their 37 million specimens digitally available through GBIF.org among other sources.

TO UNDERSTAND BIAS IS TO KNOW IT

Isaac NJB & Pocock MJO, (2015) Bias and information in biological records. *Biological Journal of the Linnean Society* 115(3): 522-531. doi:10.1111/bij.12532
Author country: United Kingdom
Research funding: Joint Nature Conservation Committee; U.K. Natural Environment Research Council

This study describes some of the biases potentially present in biological recording datasets. While stressing how critical it is to understand the sources of biases when using data, the authors also specifically highlight the value that species checklists from citizen-science projects and targeted surveys would have when records are shared with the UK National Biodiversity Network Gateway and GBIF.

WEB-BASED COLLECTING AND CLEANING OF GBIF-MEDIATED DATA

Kong X, Huang M & Duan R (2015) SDMdata: A Web-Based Software Tool for Collecting Species Occurrence Records. *PLoS ONE* 10(6): e0128295. doi:10.1371/journal.pone.0128295
Author country: China
Research funding: National Natural Science Foundation of China; China Postdoctoral Science Foundation

High-quality occurrence data is key to creating robust species distribution models. In this paper, the authors present a simple yet robust web app that uses the GBIF API to help researchers verify species names, collect occurrences and automatically cross-checking the data for errors. After processing, users can download a cleaned set of occurrences for their research purposes.
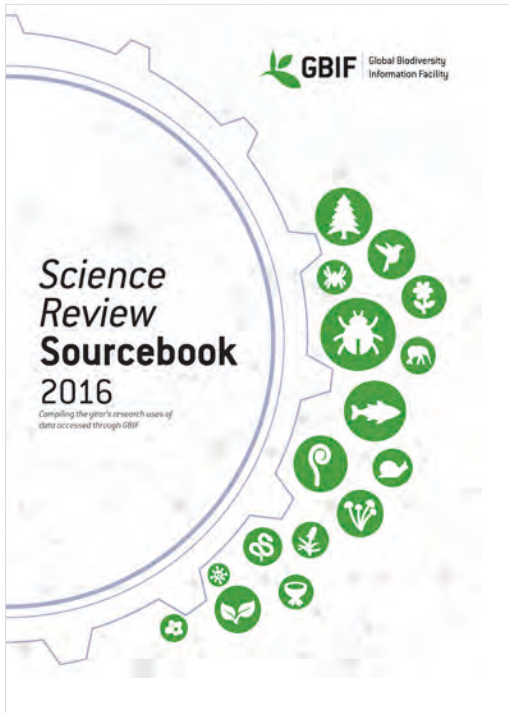
WORKFLOWS FOR USE IN LARGE DIGITIZATION PROJECTS

Nelson G, Sweeney P, Wallace LE et al. (2015) Digitization Workflows for Flat Sheets and Packets of Plants, Algae, and Fungi. *Applications in Plant Sciences* 3(9): 1500065. doi:10.3732/apps.1500065
Author countries: United States
Research funding: U.S. National Science Foundation

The authors present a comprehensive view of the workflows currently employed by more than 30 U.S. herbaria to digitize flat sheets and packets. The community-vetted workflows cover all steps from pre-digitization to curation and publication, and the free-to-download modules are fully customizable for the needs and practices of local institutions elsewhere.

data management

What's next

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