Science Review

2018

An annual compilation of research data uses enabled by

GBIF

Foreword

Compared to last year, 2017 saw a 60 per cent increase in number of scientific publications relying on GBIF-mediated data

As in previous years, this GBIF Science Review gives an exciting overview of the breadth and importance of research based on biodiversity data mobilized through the GBIF network. In the 2018 edition, which surveys literature published in 2017, we note a nearly 60 per cent growth in number of papers using GBIF-mediated data compared to 2016. With continued increases in data mobilization efforts across the GBIF network, more than 280 new publishers started sharing their data openly and freely, adding to the more than 250 million new species occurrences indexed by GBIF.org in 2017. This development has since allowed the community to pass a significant milestone, as the one billionth occurrence record was published in July 2018.

This document demonstrates why a community and infrastructure like GBIF is necessary. Countless people from all over the world played some part in making all of this research possible. Generations of scientists and naturalists provided the observations, collections, measurements and identifications now brought together in the GBIF data index. Much of this effort would be invisible without all the associated contributions by collection staff, database managers, software

engineers and frequently volunteers to transform all of this knowledge into standardized digital formats. And, of course, the publications summarized in this review are the results of research funding, the outputs of research institutions, and the work of researchers active in areas as diverse as taxonomy and ecology, medicine and food security, climate change and sustainability. GBIF sits at the heart of all this activity, a broker or catalyst that makes much of this possible and everywhere contributes to collaboration and reuse.

I particularly wish to acknowledge that this review would not exist without the efforts of many in the GBIF network to support researchers and to encourage good citation of data. Above all, our Science Communications Coordinator, Daniel Noesgaard has worked tirelessly through the year to monitor new publications and to produce the compact summaries that make up most of this document.

DONALD HOBERN
GBIF Executive Secretary
September 2018

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 and open access to data that the GBIF network of members and publishers make available.

We have labelled open-access scientific articles using the symbol ⓐ. We feel this step serves those interested in reading the research at a time of institutional journal subscriptions.

The comprehensive list of the year's uses remains decoupled from the printed version of the Science Review and is available exclusively through the online

literature index at https://www.gbif.org/resource/search?contentType=literature.

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.
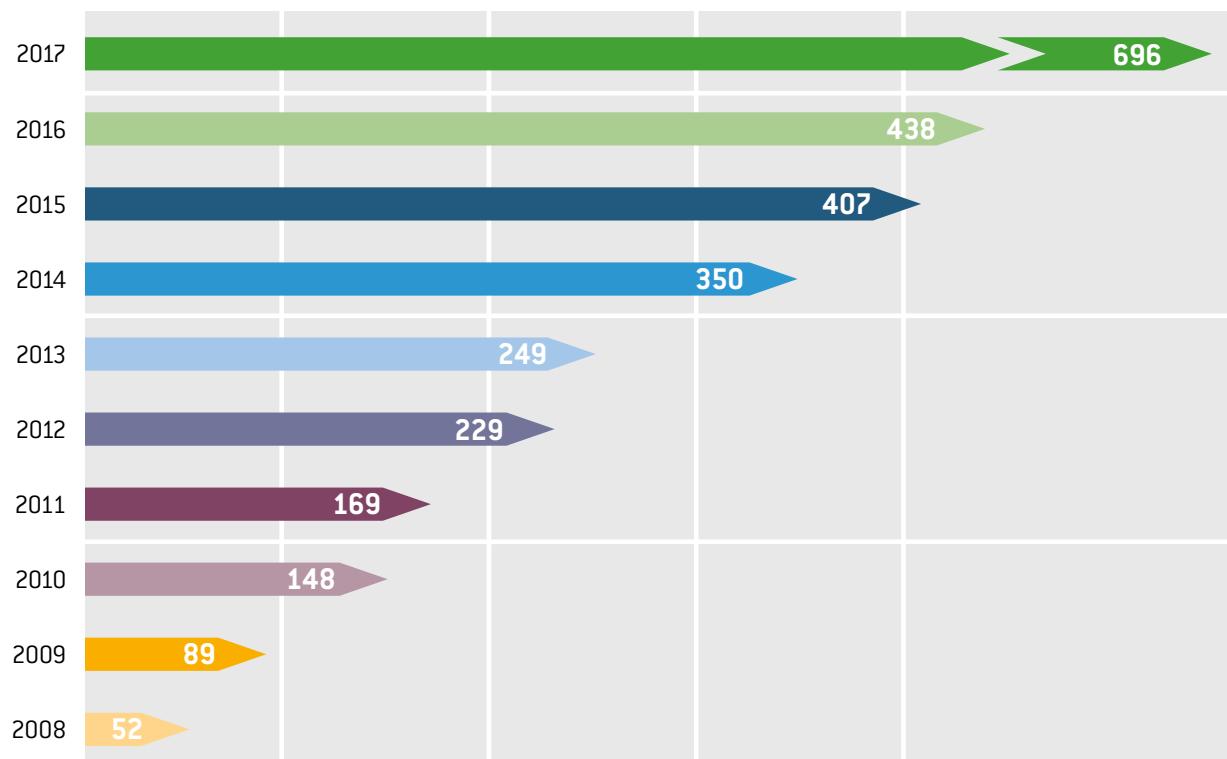
CONTENTS
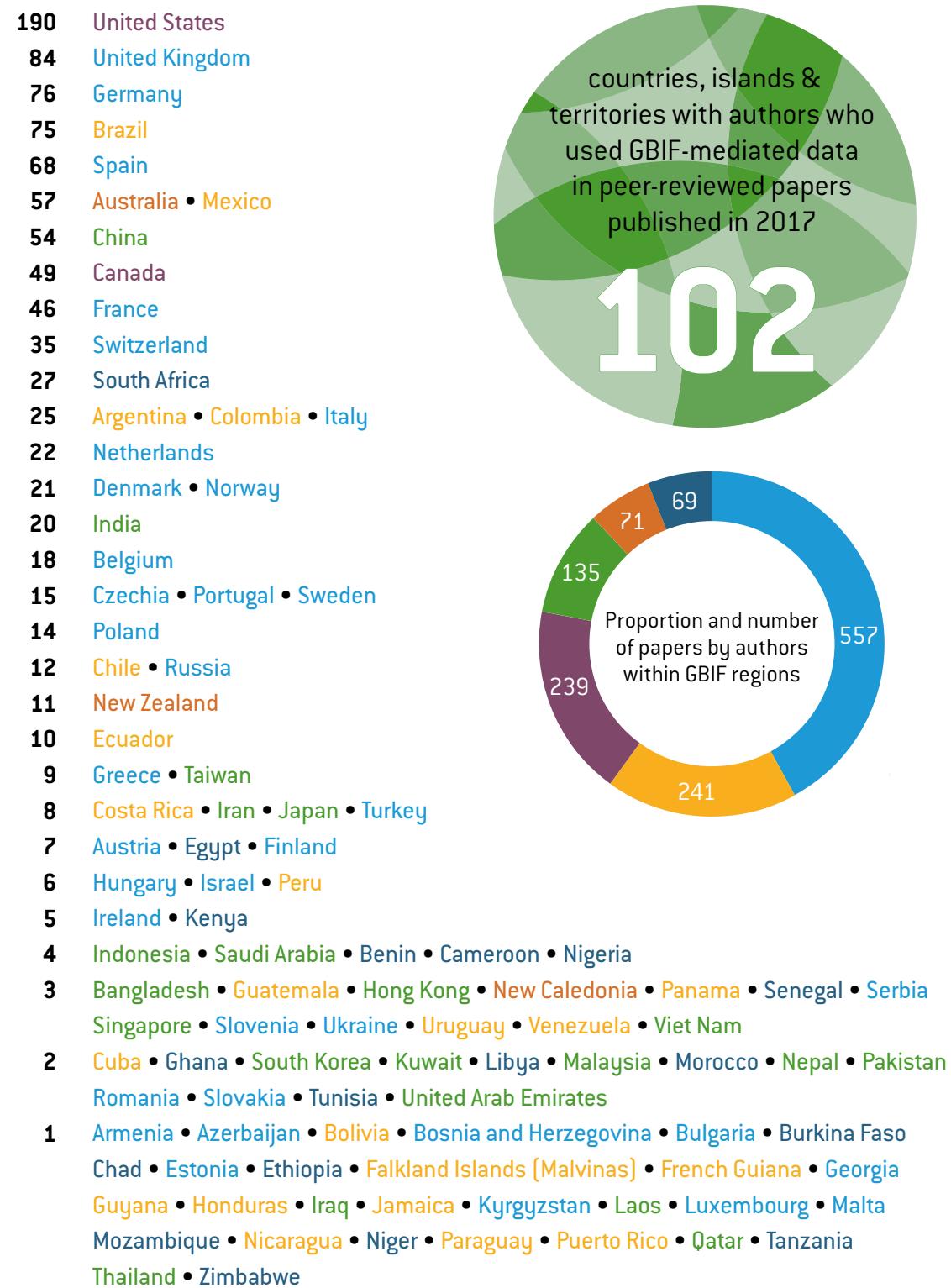
Uses and trends

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	Articles
2017	696
2016	438
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

190 United States
84 United Kingdom
76 Germany
75 Brazil
68 Spain
57 Australia • Mexico
54 China
49 Canada
46 France
35 Switzerland
27 South Africa
25 Argentina • Colombia • Italy
22 Netherlands
21 Denmark • Norway
20 India
18 Belgium
15 Czechia • Portugal • Sweden
14 Poland
12 Chile • Russia
11 New Zealand
10 Ecuador
9 Greece • Taiwan
8 Costa Rica • Iran • Japan • Turkey
7 Austria • Egypt • Finland
6 Hungary • Israel • Peru
5 Ireland • Kenya
4 Indonesia • Saudi Arabia • Benin • Cameroon • Nigeria
3 Bangladesh • Guatemala • Hong Kong • New Caledonia • Panama • Senegal • Serbia Singapore • Slovenia • Ukraine • Uruguay • Venezuela • Viet Nam
2 Cuba • Ghana • South Korea • Kuwait • Libya • Malaysia • Morocco • Nepal • Pakistan Romania • Slovakia • Tunisia • United Arab Emirates
1 Armenia • Azerbaijan • Bolivia • Bosnia and Herzegovina • Bulgaria • Burkina Faso Chad • Estonia • Ethiopia • Falkland Islands (Malvinas) • French Guiana • Georgia Guyana • Honduras • Iraq • Jamaica • Kyrgyzstan • Laos • Luxembourg • Malta Mozambique • Nicaragua • Niger • Paraguay • Puerto Rico • Qatar • Tanzania Thailand • Zimbabwe

countries, islands & territories with authors who used GBIF-mediated data in peer-reviewed papers published in 2017

102

Proportion and number of papers by authors within GBIF regions

69
71
135
239
557
241

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

Biodiversity and human health

ARTIBEUS JAMAICENSIS BY CHERYL HARLESTON https://www.gbif.org/occurrence/1291683823 CC BY-NC 4.0

BUILDING A NETWORK OF CHAGAS VECTORS AND HOSTS

DATA USED: 47,942 SPECIES OCCURRENCES

Rengifo-Correa L, Stephens CR, Morrone JJ, Téllez-Rendón JL and González-Salazar C (2017) Understanding transmissibility patterns of Chagas disease through complex vector–host networks. Parasitology. Cambridge University Press (CUP) 144(06): 760–772.

Author country/area: Mexico
Research funding: Consejo Nacional de Ciencia y Tecnología, Dirección General de Asuntos del Personal Académico, Fronteras de la Ciencia

Chagas disease is a parasitical infection caused by the protozoan *Trypanosoma cruzi* occurring in the American tropics. Typically transmitted through insect bites by so-called kissing bugs (subfamily Triatominae), Chagas is usually associated with mild symptoms, however, chronic infections can lead to cardiac, digestive or neurological alterations.

Little is known about the transmission patterns of the parasite, and in this study, researchers used GBIF-mediated occurrences of potential mammalian host species combined with records of Triatominae species to generate a complex interference network and predict interactions from co-occurrences.

A third of the mammals occur in sites where

Triatominae species are also present, and ten host species are potentially associated with three or more Triatominae bugs. Two species, *Baiomys musculus* and *Liomys pictus*, are highlighted as potentially associated with five Triatominae species.

The researchers test the predictive power of the network by confirming the presence of verified Chagas hosts. The additional co-occurrences provide testable hypotheses for new vector-host interactions to be addressed.

Link to paper: https://doi.org/10.1017/S0031182016002468

USING TRADITIONAL REMEDIES TO INSPIRE MODERN MEDICINES

DATA USED: 291 SPECIES

Odonne G, Houël E, Bourdy G and Stien D (2017) Treating leishmaniasis in Amazonia: A review of ethnomedicinal concepts and pharmaco-chemical analysis of traditional treatments to inspire modern phytotherapies. Journal of Ethnopharmacology. Elsevier BV 199: 211–230.

Author country/area: France
Research funding: Agence Nationale de la Recherche

Reviewing literature on traditional remedies for leishmaniasis in Amazonia, this study attempts to understand the mechanisms underlying plant

selection from a cultural perspective, while at the same time identifying plants with potential medicinal properties for pharmacological studies.

The researchers identify 34 different cultural groups each with their own local names and conceived etiologies of the disease. In one community, the glow of a lightning bug is believed to be the cause, while others point to the consumption of poisonous animals. Treatments vary but all relate to the local perception of the disease, which also affects the selection of plant remedies. In one group, remedies based on fast-growing plants are used when disease progression is quick, and vice versa.

Using GBIF-mediated occurrences, the researchers classify the identified plant species, and find that preferred traditional antileishmanials are native to Amazonia, but often wild. Through phytochemical and pharmacological review, the study surveys the medicinal properties of the species, providing candidates for potential therapeutic trials.

Link to paper: https://doi.org/10.1016/j.jep.2017.01.048

PREDICTING RISK OF ZIKA INFECTIONS THROUGH CO-OCCURRENCE OF VECTOR AND HOST

DATA USED: 37,297 SPECIES OCCURRENCES

González-Salazar C, Stephens CR and Sánchez-Cordero V (2017) Predicting the Potential Role of Non-human Hosts in Zika Virus Maintenance. EcoHealth. Springer Nature 14(1): 171–177.

Author country/area: Mexico
Research funding: Programa de Apoyo a Proyectos de Investigación e Innovación Tecnológica

Vector-borne public health threats such as Zika, Dengue and Chikungunya are caused by highly mutable arboviruses with potential for rapid adaptive changes in response to new hosts and host ranges. While mosquito vectors such as *Aedes aegypti* have been identified, understanding the role of mammalian reservoir hosts in the maintenance of arboviruses is crucial to limiting spread and emergence of these diseases.

In this study, researchers from Mexico used GBIF-mediated species occurrences to identify potential mammalian blood-meal sources for *Ae. aegypti* and as such, potential arbovirus hosts. These biotic interactions led to a ranked list of mammalian species, including seven bat species in the top 10, of which two species are already confirmed dengue hosts, and four species are hosts of protozoan parasites *Leishmania mexicana* and *Trypanosoma cruzi*.

Revealing a high correlation between significant mosquito-mammal interactions and confirmed human Zika infections, the study provides new material for future studies in Zika virus maintenance.

Link to paper: https://doi.org/10.1007/s10393-017-1206-4

THE FUTURE OF RAGWEED: MAKING MORE EUROPEANS SNEEZE

DATA USED: 10,539 SPECIES OCCURRENCES

Rasmussen K, Thyrring J, Muscarella R and Borchsenius F (2017) Climate-change-induced range shifts of three allergenic ragweeds (Ambrosia L.) in Europe and their potential impact on human health. PeerJ. PeerJ 5: e3104.

Author country/area: Denmark
Research funding: National Science Foundation

Ragweed (*Ambrosia* sp.) is considered to be among the most potent aeroallergens and the major cause of late summer hay fever. Medical costs exceed $18 billion per year in the US, and in Hungary, one in four people are allergic to ragweed, making this member of the sunflower family (Asteraceae) a major public health concern.

In the present study, researchers from Denmark used GBIF-mediated occurrences of three *Ambrosia* species (*A. artemisiifolia*, *A. psilostachya* and *A. trifida*) to create species distribution models for quantifying the allergy risk in Europe under future climates. Their results showed that areas of high risk are likely to double by the year 2100, leading to novel risk areas in Denmark, France, Germany, Russia and the Baltics.

AMBROSIA TRIFIDA BY JULIABOHEMIAN https://www.gbif.org/occurrence/1640119729 CC BY-NC 4.0

Understanding the future distributions of such allergenic plants is crucial to predicting the consequences for human health. The authors of this study conclude that unless strict management strategies are enforced, restricting dispersal and establishment of new colonies, Europe will face a substantial increase in areas affected by severe ragweed associated allergy problems.

Link to paper: https://doi.org/10.7717/peerj.3104

MAPPING MOSQUITOES TO IMPROVE PUBLIC HEALTH AND ENVIRONMENTAL MONITORING
DATA USED: 1,172 SPECIES OCCURRENCES
ⓐ Longbottom J, Browne AJ, Pigott DM, Sinka ME, Golding N, Hay SI, Moyes CL and Shearer FM (2017) Mapping the spatial distribution of the Japanese encephalitis vector, Culex tritaeniorhynchus Giles, 1901 (Diptera: Culicidae) within areas of Japanese encephalitis risk. Parasites & Vectors. Springer Nature 10(1).

Author countries/areas: Australia, United Kingdom, United States
Research funding: Wellcome Trust, Bill & Melinda Gates Foundation, University of Melbourne, University of Oxford

Culex tritaeniorhyncus, a mosquito native to northern Asia, is the primary vector of Japanese encephalitis virus (JEV). A relative of dengue, yellow fever and West Nile, this flavivirus infects nearly 68,000 humans each year, triggering incurable brain inflammation that causes death in up to 30 per cent of the cases and permanent neurological or psychiatric damage in another 30 to 50 per cent.

The World Health Organization estimates that more than 3 billion people in 24 countries in Southeast Asia and the Western Pacific risk exposure to JEV infection. But as with many arboviruses, the distribution of its arthropod vectors is poorly documented. Here the authors combined 225 *Cx. tritaeniorhyncus* records from GBIF.org along with data from VectorMap and 21st-century scientific literature, in hope of improving knowledge of where the species occurs and mapping environmentally suitable areas for incidence of JEV.

In addition to predicting high suitability in India, Nepal and China, the resulting models draw specific attention to highly suitable regions in northwest India, southeast Pakistan, northern Japan and southeast Russia where records of *Cx. tritaeniorhyncus* are lacking. While higher resolution occurrence data could improve the maps' ability to assess risks, this

research could help to target key monitoring sites, inform vector control measures and supplement education campaigns aimed at preventing the spread of JEV in environmentally suitable locales.

Link to paper: https://doi.org/10.1186/s13071-017-2086-8

MORE HUMANS—MORE VIRAL SPILLOVER EVENTS
DATA USED: 7,126 SPECIES OCCURRENCES
ⓐ Walsh MG, Wiethoelter A and Haseeb MA (2017) The impact of human population pressure on flying fox niches and the potential consequences for Hendra virus spillover. Scientific Reports. Springer Nature 7(1).

Author countries/areas: Australia, United States
Research funding: None listed

When human activities lead to changed landscapes, new ecosystem configurations may entail, subsequently increasing potential for unprecedented contact between humans and wildlife, including species carrying human pathogens.

Bats are known reservoirs of Nipah, Ebola and Hendra viruses, the latter being the focus of a study examining how human migration in Australia has affected the range of fruit bats (*Pteropus* spp.)—also known as flying foxes—and whether these changes are associated with Hendra virus spillover events, i.e when a virus passes from a reservoir to a novel species.

Using GBIF-mediated occurrences, the authors modelled the distribution of four flying fox species in mainland Australia based on climate variables and human migration across three decades from 1980. The models showed that the niches of two species in particular have expanded southward along the eastern coast, following increases in human population, especially in the 1990s.

Finally, the authors showed how the changing geometry of flying fox habitat was strongly associated with Hendra virus spillovers, adding knowledge about epidemiology and infection ecology of this rare, but fatal zoonosis.

Link to paper: https://doi.org/10.1038/s41598-017-08065-z

Biodiversity data

SALIX CAPREA BY MARTIN GRIMM https://www.gbif.org/occurrence/1455569693 CC BY-NC 4.0

EXPANDING OBIS BEYOND SPECIES OCCURRENCES

ⓐ De Pooter D, Appeltans W, Bailly N, Bristol S, Deneudt K, Eliezer M, Fujioka E, Giorgetti A, Goldstein P, Lewis M, Lipizer M, Mackay K, Marin M, Moncoiffé G, Nikolopoulou S, Provoost P, Rauch S, Roubicek A, Torres C, van de Putte A, Vandepitte L, Vanhoorne B, Vinci M, Wambiji N, Watts D, Klein Salas E and Hernandez F (2017) Toward a new data standard for combined marine biological and environmental datasets - expanding OBIS beyond species occurrences. Biodiversity Data Journal. Pensoft Publishers 5: e10989.

Author countries/areas: Argentina, Australia, Belgium, Greece, Italy, Kenya, Mexico, New Zealand, United Kingdom, United States, Venezuela
Research funding: None listed

The Ocean Biogeographic Information System (OBIS) was established in 2000 to create an online, user-friendly system for absorbing, integrating and accessing data about life in the oceans. In 2005, OBIS adapted the Darwin Core (DwC) standard for biodiversity data, which supports publishing through GBIF.

Following the implementation of sampling event data in GBIF, OBIS established a pilot project to investigate best practices for storing and sharing combined datasets. This paper summarizes the findings of a

workshop in Oostende in 2015, at which members of the project consortium used pilot datasets to design DwC-based solutions to challenges of combined oceanic data.

The workshop explored several different combinations of DwC components and extensions, and decided that the most suitable solution would be based on the Event Core combined with an Occurrence extension and a revised MeasurementOrFact extension. The proposed standard will allow OBIS to move beyond just occurrence data and enable publishing of event-based datasets combining biological, physical and chemical measurements.

Link to paper: https://doi.org/10.3897/BDJ.5.e10989

THE GLOBAL POLLEN PROJECT: PROVIDING OPEN AND FREE ACCESS TO POLLEN IDENTIFICATION DATA
DATA USED: 1,500 SPECIES
ⓐ Martin AC and Harvey WJ (2017) The Global Pollen Project: a new tool for pollen identification and the dissemination of physical reference collections. Methods in Ecology and Evolution. Wiley-Blackwell 8(7): 892–897.

Author country/area: United Kingdom
Research funding: Natural Environment Research Council

Environmental changes affect vegetation dynamics and analyses of both fossil and modern pollen assemblages can be an important source of evidence. Taxonomic identification of pollen grains, however, can be a daunting task, as existing reference collections are kept private and inaccessible to researchers.

This paper presents a new online, open and peer-reviewed database of pollen data from across the world, allowing submission and identification of unknown grains through crowdsourcing, as well as a repository for digitization and sharing of existing reference collections. Connected to the GBIF.org database, The Global Pollen Project (GPP) tool provides direct and easy linkage from pollen grains to occurrences for more than 1,500 plant species.

Generating new opportunities for research, the GPP tool can be a valuable resource for automatic pollen identification through machine learning. As an alternative to physical slides that degrade over time, the tool has already proven useful in university teaching by being incorporated in lectures and lab exercises.

Link to paper: https://doi.org/10.1111/2041-210X.12752

BIG DATA PUTTING THE 'FUN' BACK IN FUNGAL RESEARCH

DATA USED: 245,382 SPECIES OCCURRENCES
Andrew C, Heegaard E, Kirk PM, Bässler C, Heilmann-Clausen J, Krisai-Greilhuber I, Kuyper TW, Senn-Irlet B, Büntgen U, Diez J, Egli S, Gange AC, Halvorsen R, Høiland K, Nordén J, Rustøen F, Boddy L and Kauserud H (2017) Big data integration: Pan-European fungal species observations' assembly for addressing contemporary questions in ecology and global change biology. Fungal Biology Reviews. Elsevier BV 31(2): 88–98.

Author countries/areas: Austria, Czechia, Denmark, Germany, Netherlands, Norway, Switzerland, United Kingdom, United States
Research funding: Research Council of Norway

Open access to biodiversity data presents an unparalleled potential for understanding many aspects of the ecology and biogeography of organisms. Many national initiatives have gathered species occurrence records from e.g. citizen science projects and museums, however, to answer global-scale questions, data needs to transcend national borders.

Striking in their absence from analyses of species' shifts in response to climate change, fungi are the focus of this study, in which researchers compile nine national datasets from Europe into one meta-dataset, called ClimFun. Through nomenclatural harmonization, formatting and filtering, the resulting dataset spans six million records of more than 10,000 species.

To demonstrate the value of the database, the researchers show simple examples of climate-related shifts in the fruiting dates for two species, *Amanita rubescens* and *Hypholoma fasciculare*. The patterns found rely on data spanning more than 15 degrees of latitude and altitudes from sea level to 1700 m, and are as such only achievable because of the continental scale of the data.

Link to paper: https://doi.org/10.1016/j.fbr.2017.01.001

DEVELOPING A COMMON STRUCTURAL FRAMEWORK FOR DATA PAPERS

Chen Y-N (2017) An analysis of characteristics and structures embedded in data papers: a preliminary study. Libellarium: journal for the research of writing, books, and cultural heritage institutions. University of Zadar 9(2).

Author country/area: Taiwan
Research funding: None listed

Many institutions, including GBIF, encourage sharing of research data through data papers that extend metadata in a way that mirrors the traditional scientific publication model. Dozens of journals now accept data papers, however, as highlighted by this study, they lack a common standard.

By reviewing submission templates and guidelines from 26 data journals, the authors describe a unifying framework consisting mainly of three distinct components: 1) basic information (e.g. title, abstract, author, etc.), 2) dataset descriptions (i.e. how was data collected, how it was formatted, what does it cover, etc.), and 3) relationships (i.e. links and references).

The authors use the proposed framework to highlight the successful case of mapping metadata directly derived from the GBIF Integrated Publishing Toolkit (IPT) onto a data paper template that can be edited and submitted to a journal for consideration.

As of September 2018, authors have contributed to more than 75 data papers describing datasets published in GBIF.

Link to paper: https://doi.org/10.15291/libellarium.v9i2.266

## TRACKING FREE-ROAMING CHEETAHS OUTSIDE PROTECTED AREAS OF SOUTH AFRICA

DATA PUBLISHED: 3,165 SPECIES OCCURRENCES
Marnewick K, Page-Nicholson S, Roxburgh L and Somers M (2017) Tracking data from nine free-roaming Cheetahs (Acinonyx jubatus) collared in the Thabazimbi area, Limpopo Province, South Africa. Biodiversity Data Journal. Pensoft Publishers 5: e11323.

Author country/area: South Africa
Research funding: GBIF

Two of South Africa's cheetah populations exist in protected areas, while a third roams free on privately owned ranchland outside protected areas.

ACINONYX JUBATUS BY WILLIAM WALLDEN https://www.gbif.org/occurrence/1315076539 CC BY-NC 4.0

Under continuous threat from illegal wildlife trade and retaliatory killings by ranch owners to protect livestock, this population is, however, the largest in South Africa.

During a tracking programme of nearly six years, researchers trapped nine free-roaming cheetahs, six males and three females, and fitted them with tracking collars. The cheetahs were then released and tracked for the remainder of their lives (or the life of the collar).

At the conclusion of the programme, four animals had been shot and one killed on the road, while one male, tracked for nearly six years had died of natural causes. The fate of the remaining three animals was unknown. The dataset, published in entirety to GBIF, revealed that ranges of free-roaming cheetahs covered on average 18 ranches, and that male cheetahs had slightly larger ranges than females.

Link to paper: https://doi.org/10.3897/bdj.5.e11323

TRACKING THE INVASION OF SOSNOWSKY'S HOGWEED IN THE KOMI REPUBLIC

DATA USED: 10,894 SPECIES OCCURRENCES
Chadin I, Dalke I, Zakhozhiy I, Malyshev R, Madi E, Kuzivanova O, Kirillov D and Elsakov V (2017) Distribution of the invasive plant species Heracleum sosnowskyi Manden. in the Komi Republic (Russia). PhytoKeys. Pensoft Publishers 77: 71–80.

Author country/area: Russia
Research funding: Russian Foundation for Basic Research, Government of Komi Republic

The autonomous Komi Republic located in the north-east of the Russian Plain constitutes an important biogeographic boundary between the European and Asian continents. Sosnowsky's hogweed (*Heracleum sosnowskyi*) was introduced as a forage crop in the second half of the 20th century, but now all populations in the region are invasive.

This data paper represents a study of the distribution of *H. sosnowskyi* in the Komi Republic recorded from moving vehicles mounted with video cameras synched with GPS trackers. Traveling at speeds of up to 90 km/h, the study vehicles collected data within a radius of 300 km around Syktyvkar, capital of Komi.

The researchers broke the recorded video feeds into frames and sorted the images based on *H. sosnowskyi* occurrences. The final dataset contains 10,894 occurrence records, all of which are available through GBIF.org.

Using the recorded occurrences combined with bioclimatic variables, the researchers modeled the potential distribution of the weed, and determined the northern range boundary to 67.2°.

Link to paper: https://doi.org/10.3897/phytokeys.77.11186

SSDM: A NEW SOFTWARE PACKAGE FOR CREATING STACKED SPECIES DISTRIBUTION MODELS

DATA USED: 6,641,610 SPECIES OCCURRENCES
Schmitt S, Pouteau R, Justeau D, de Boissieu F and Birnbaum P (2017) ssdm: An r package to predict distribution of species richness and composition based on stacked species distribution models. Methods in Ecology and Evolution. Wiley 8(12): 1795–1803.

Author country/area: New Caledonia
Research funding: Direction for Economic and Environmental Development (DDEE) of the North Province of New Caledonia

In this paper, researchers based in New Caledonia present a new user-friendly platform for stacking species distribution models (SSDM) implemented in

the popular **R** software environment. Free and open source, the "SSDM" package takes datasets of species presence/absence records and environmental variables, outputting maps of SSDMs based on a range of statistical methods. If absence records are required and not available, the package can generate pseudo-absences or use background data.

SSDM features a user-friendly graphical interface to accommodate loading of input data, modelling, and displaying the resulting model maps with an indication of the accurracy and performance.

To demonstrate the functionality and ease of use, the authors modelled the distributions of 100 of the world's worst invasive alien species using more than 6 million occurrences downloaded from GBIF.org combined with 19 WorldClim climate variables. Stacking the models, the output map provides a view of the worldwide vulnerability to these invasive species.

The SSDM package is available for download from CRAN or within the **R** environment.

Link to paper: https://doi.org/10.1111/2041-210X.12841

IS TAXONOMIC BIAS IN GBIF EXPLAINED BY RESEARCH FOCUS OR SOCIETAL PREFERENCES?

DATA ANALYSED: 649,767,741 SPECIES OCCURRENCES

ⓐ Troudet J, Grandcolas P, Blin A, Vignes-Lebbe R and Legendre F (2017) Taxonomic bias in biodiversity data and societal preferences. Scientific Reports. Springer Nature 7(1).

Author country/area: France
Research funding: Ministère de la Recherche

Describing and understanding taxonomic biases and their causes are undeniable priorities. Attempts to explain taxonomic bias include, apart from obvious, intrinsic reasons (such as species in remote locations), also extrinsic factors, such as research focus and societal pressures.

In this study, researchers quantify the relative impact of taxonomic research and societal preferences on taxonomic bias in data from GBIF, the world's largest open access biodiversity database.

Using a range of measures the researchers assessed both bias and precision across 626 million GBIF-mediated occurrences representing one million species in 24 taxonomic classes. They find that 94 per cent of occurrences are identified (at least) at species level. Highest precision is found among plants, fungi and birds, whereas classes Maxillopoda (crustaceans)

and Anthozoa (corals) lack species-level identification in a third of the occurrences. Within certain insect orders, however, taxonomic presicion is as low as 0.5 per cent.

Further comparing number of species with occurrences, with known species richness within each class, the researchers found birds and insects to be the most over- and under-represented classes, respectively. This bias is not new, but recent growth in data also shows that this gap is not becoming smaller.

Only in three classes (birds, amphibians and ray-finned fishes) did fewer than half the species have 20 occurrences. In comparison, less than nine per cent of arthropod species has a similar coverage.
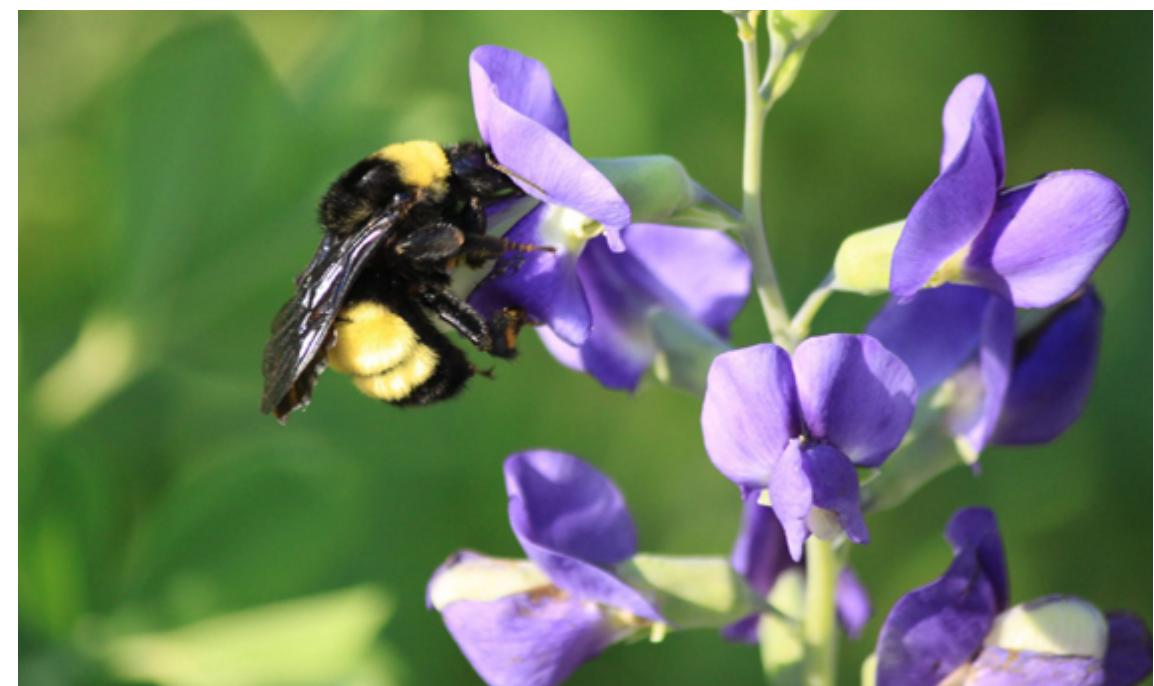
Relating these findings to number of web results for different species as a proxy for societal preferences, their model uncovered several significant correlations showing that a high societal preference is related to a high number of GBIF occurrences. This was, however, not the case for taxonomic research (proxied by number of research papers published), where the model revealed fewer correlations that in some cases were even negative. For instance, for the class Agaricomycetes having a large volume of research was related to a lower number of GBIF occurrences.

The authors conclude:

> Many international projects have been developed since the Convention on Biological Diversity, illustrating an increased awareness of the astonishing diversity of functions and services that biodiversity supports. Nevertheless, while biodiversity declines at an unprecedented rate, taxonomic bias is still a burden on biodiversity studies. It is urgent that we get rid of this burden and that we start embracing the whole of biodiversity. (CC BY 4.0)

Link to paper: https://doi.org/10.1038/s41598-017-09084-6

Crops and pollinators

BOMBUS PENSYLVANICUS BY KATHY RICHARDSON https://www.gbif.org/occurrence/1847522785 CC BY-NC 4.0

IDENTIFYING GAPS TO PRIORITIZE AREAS FOR CROP WILD RELATIVE CONSERVATION

DATA USED: 39,598 SPECIES OCCURRENCES

ⓐ García RM, Parra-Quijano M and Iriondo JM (2017) A Multispecies Collecting Strategy for Crop Wild Relatives Based on Complementary Areas with a High Density of Ecogeographical Gaps. Crop Science. Crop Science Society of America 57(3): 1059.

Author countries/areas: Colombia, Spain
Research funding: None listed

As climates change and the global human population keeps increasing, crop production and food security is under threat. Current cultivars lack adaptive mechanisms, so securing potential genetic diversity in crop wild relatives (CWR) is crucial.

In a study published in *Crop Science*, researchers present a new approach to prioritizing areas for collecting seeds. Based on a list of 88 mainly cereal and legume priority taxa from the Spanish National Inventory of CWR, the authors used occurrence data from GBIF to derive the most relevant bioclimatic, edaphic and geophysic variables for the taxa in question. Using the most important variables for each species, they generated land characterization maps to identify ecogeographic and spatial gaps, i.e. distance to location of available accessions.

When analysing the maps, the authors found that *Hordeum murinum* (CWR of barley) and *Vicia sativa* (CWR of fava beans) have the largest number of spatial gaps. They generate a ranked list of 10x10 km cells based on gap richness and find 523 populations in the top 10 areas across 58 taxa, of which 24 are not present in current germplasm collections.

Link to paper: https://doi.org/10.2135/cropsci2016.10.0860

REFORESTATION THROUGH HOMEGARDEN-BASED NATURAL REGENERATION

DATA USED: 250 SPECIES

Rooduijn B, Bongers F and van der Wal H (2018) Wild native trees in tropical homegardens of Southeast Mexico: Fostered by fragmentation, mediated by management. Agriculture, Ecosystems & Environment. Elsevier BV 254: 149–161.

Author countries/areas: Mexico, Netherlands
Research funding: PROMEP CA SEP, CONACYT

Providing ecological, economic and socio-cultural values to local communities, tropical home gardens (THG) are diversified agroforestry systems also supporting important ecosystem services such as pollination and decomposition. THGs may also act as both sinks and sources of tropical biodiversity, however, quantitative evaluation of such dynamics

crops and pollinators

remain largely lacking.

In this study, authors examined abundance and diversity of wild native trees in THGs in the lowlands of Tabasco state in southeast Mexico—completely deforested in the 1950s and onwards—while assessing the role of tree cover fragmentation and socio-management. They inventoried a random selection of 59 THGs in 19 villages equally spread across the region, using GBIF to validate the origin of plant species observed.

Their analysis revealed that while tree cover fragmentation affects the level of self-established vs planted trees, socio-management—i.e. complex gardens with species-knowledgable owners—plays a bigger role also in terms of density of native trees and individual species' abundances.

Showing that THGs are important sinks for wild native trees, the study concludes that homegarden-based natural regeneration may be a key resource in reforestation.

Link to paper: https://doi.org/10.1016/j.agee.2017.10.015

THE DEMISE OF BUMBLEBEES: LINKING PESTICIDES AND PATHOGENS TO DECLINING POPULATIONS
DATA USED: 67,725 SPECIES OCCURRENCES

McArt SH, Urbanowicz C, McCoshum S, Irwin RE and Adler LS (2017) Landscape predictors of pathogen prevalence and range contractions in US bumblebees. Proceedings of the Royal Society B: Biological Sciences. The Royal Society 284(1867): 20172181.

Author country/area: United States
Research funding: National Institute of Food and Agriculture, NSF

Efficient pollinators of wild flowering plants and crops, bumblebees provide important ecosystem services, threatened by range contractions and declining populations. In the US, this has been linked to a variety of factors including urbanization, pesticides and pathogens.

In a study of bumblebees in the US, authors attempt to elucidate the relative importance of different stressors associated with range contractions. At 284 sites, they sampled and identified *Bombus* species, while screening for pathogens and quantifying landscape and pesticide usage.

Combining the field data with GBIF-mediated occurrences of eight target species, the authors used a machine learning model technique to show that the

usage of the fungicide chlorothalonil was the best predictor of prevalence of the bumblebee pathogen *Nosema bombi* in four declining species. They also found that total fungicide usage was correlated with range contractions in all declining species.

Adding to existing evidence, this study highlights fungicide exposure—linked to pathogen prevalence—as a critical factor affecting threatened and endangered bumblebees in the US.

Link to paper: https://doi.org/10.1098/rspb.2017.2181

Ecology, evolution, behaviour and systematics

HAKEA LAURINA BY LINGER https://www.gbif.org/occurrence/1099976883 CC BY-NC 4.0

ASSESSING ENDEMICITY OF JAPANESE FUNGI
DATA USED: 109 TAXA

剛細矢, 志穂美埋橋, 健太郎保坂, & 伸一工藤. (2016). An assessment of fungi endemic to Japan. 日本菌学会会報 [Japanese Journal of Mycology], 57(2), 77–84.

Author country/area: Japan
Research funding: None listed

Summary by Tsuyoshi Hosoya (GBIF Japan)

Fungi are one of the most important and highly diverse groups of organisms. Although some attention has been given to species with interest for conservation biology, such as endangered or invasive alien species, none of these have been examined systematically.

In the present paper, the authors seek to assess the endemicity of Japanese fungi using GBIF-mediated data. Endemic species are unique to a given geographic location, such as an island, country or other defined area. Categorizing a species as endemic should be limited to well-known species to avoid falsely classifying due to lack of data. Proving the endemicity of a species is difficult, if not impossible. Primary biodiversity data, however, makes it easy to confirm the occurrence of a species in an overseas location and thereby rule out endemicity.

By examining two volumes of *Colored Illustrations of Mushrooms of Japan (I and II)* (Imazeki and Hong 1987, 1989), a masterpiece on mycobiota information, researchers reviewed the comments of 3,928 mushrooms and found clear mention of endemicity for 182 taxa. These were selected and further assessed by referring to the GBIF-mediated records for occurrences in other countries.

Results revealed 109 taxa already known to occur outside Japan that should not be categorized as endemic. However, for 71 taxa endemicity could not be ruled out, and at present, these should be accepted as possible endemic mushrooms.

Link to paper: https://doi.org/10.18962/jjom.57.2_77

UNRAVELLING THE PLANT BIODIVERSITY HOTSPOTS OF MEDITERRANEAN-TYPE ECOSYSTEMS
DATA USED: 9,762 SPECIES OCCURRENCES

Skeels A and Cardillo M (2017) Environmental niche conservatism explains the accumulation of species richness in Mediterranean-hotspot plant genera. Evolution. Wiley-Blackwell 71(3): 582–594.

Author country/area: Australia
Research funding: None listed

Although much lower in productivity than tropical regions, some ecosystems with Mediterranean-like climates (MTE) are biological hotspots with species diversity comparable to that of the tropics. The evolutionary and ecological mechanisms behind this phenomenon are poorly understood.

In this study, researchers test the hypothesis that processes similar to those driving diversity in the tropics (known as the Tropical Niche Conservatism Hypothesis) could explain the MTE hotspots. Focusing on four large plant genera with most of their species found in two MTE hotspots - the floristic regions of 1) the Greater Cape in South Africa and 2) Southwest Australia - the researchers estimated the environmental niches of 136 species using occurrence data from GBIF combined with climate and soil data.

Using biogeographic modelling to infer ancestral areas, they designated species as being either hotspot or nonhotspot in origin, and compared the tempo and modes of niche evolution between the groups. Their results suggest that niche conservatism, too, is the underlying process in which plant diversity in MTEs results from longer time for speciation.

Link to paper: https://doi.org/10.1111/evo.13179

FIRE-RESISTANCE IN A HOTTER FUTURE

DATA USED: 578,071 SPECIES OCCURRENCES
Pellegrini AFA, Anderegg WRL, Paine CET, Hoffmann WA, Kartzinel T, Rabin SS, Sheil D, Franco AC and Pacala SW (2017) Convergence of bark investment according to fire and climate structures ecosystem vulnerability to future change. Ecology Letters. Wiley-Blackwell 20(3): 307–316.

Author countries/areas: Brazil, Norway, United Kingdom, United States
Research funding: National Science Foundation, National Oceanic and Atmospheric Administration, William Ebenstein Student Research Fund

Fires are common in drier regions of the world, and plants in such ecosystems have evolved traits to tolerate frequent burning and intense temperatures. The mechanisms involved in the evolution of fire-tolerance through e.g. thickened bark, however, are unknown.

In this study, researchers compiled a database of bark thickness for more than 500 woody plant species, and used GBIF-mediated occurrences combined with climate data to establish environmental niches for each species. By including a dataset on occurrences of fires, the researchers describe a strong, global

link between fire frequency and bark thickness. On average, species found in fire-frequent savannas have bark three times thicker than species in fire-infrequent forests.

The researchers further assessed the vulnerability of communities under future scenarios, and found that seasonal forests and savannas are robust, while tropical rainforests may be especially vulnerable, as wildfires are expected to increase in frequency in warmer climates.

Link to paper: https://doi.org/10.1111/ele.12725

SAMBUCUS NIGRA BY SARA RALL https://www.gbif.org/occurrence/1453533635 CC BY-NC 4.0

CONTINENTAL-SCALE DIFFERENCES IN LEAF UNFOLDING STRATEGIES

DATA USED: >1,411,996 SPECIES OCCURRENCES
Zohner CM, Benito BM, Fridley JD, Svenning J-C and Renner SS (2017) Spring predictability explains different leaf-out strategies in the woody floras of North America, Europe and East Asia. Ecology Letters. Wiley 20(4): 452–460.

Author countries/areas: Denmark, Germany, Norway, United States
Research funding: Bayerisches Staatsministerium für Umwelt und Gesundheit, European Research Council, Aarhus University

In temperate regions with unpredictable seasonal progression, plants rely on a combination of signals to guide when to unfold their leaves. Relying on temperature only and unfolding during an early warm spell means risks of frost damage, however, waiting too long means missing out on early carbon gain. Integrating additional signaling from day length and winter chilling, especially, provides a more robust strategy.

In this study, researchers investigate differences in leaf-out strategies among Northern Hemisphere

woody plants and how they relate to spring temperature predictability in East Asia, Europe, and North America. By combining experimental and monitoring data for a large representative set of species, they reveal continental-scale differences in leaf-out strategies, as plants from North America with high spring temperature variability have much higher winter chilling requirements than related species in East Asia with low spring temperature variability.

The differences in phenological strategies suggest that species' reactions to climate warming may vary depending on continent, highlighting the importance of considering regional climate histories in models of global change.

Link to paper: https://doi.org/10.1111/ele.12746

SPARKS OF CREATION: FIRE AS A PRIMARY DRIVER OF GLOBAL PLANT DIVERSITY

DATA USED: 109,140,607 GEOREFERENCED PLANT OCCURRENCES
Pausas JG and Ribeiro E (2017) Fire and plant diversity at the global scale. Global Ecology and Biogeography. Wiley 26(8): 889–897.

Author countries/areas: Netherlands, Spain
Research funding: Ministerio de Economía y Competitividad, Generalitat Valenciana, Spanish National Research Council

Why are there so many species? Ecologists persist in efforts to refine our understanding of how factors like climate, productivity and species interactions contribute to the boundless variety of life on earth. Disturbance receives its share of attention, at least in some forms, but here the authors call attention to one widespread disruptive force—namely, fire—that seems to have escaped in-depth study.

This first global assessment of fire regimes examines temporal and spatial patterns of speciation and plant diversity across 753 terrestrial ecoregions that account for 88 per cent of land surface. The authors combined thermal remote-sensing and climate data with species richness data in hope of unlocking relationships between ecoregional environmental variables and plant diversity. While relying on data from Kier et al. (2005) as their primary data source, the authors also test their results against more than 109 million GBIF-mediated plant occurrences.

Despite known limitations to the study's scale and data biases, clear patterns emerged from analyses of both data sources, suggesting that fire activity is one of the strongest indicators—perhaps the strongest indicator—of coarse-scale plant diversity.

Link to paper: https://doi.org/10.1111/geb.12596

IDENTIFYING AQUATIC INVERTEBRATES USING NEXT GENERATION SEQUENCING

DATA USED: 222 FAMILIES
Carew ME, Metzeling L, St Clair R and Hoffmann AA (2017) Detecting invertebrate species in archived collections using next-generation sequencing. Molecular Ecology Resources. Wiley-Blackwell.

Author country/area: Australia
Research funding: Australian Research Council, Melbourne Water Corporation, Victorian Government, EPA Victoria

In studies of aquatic invertebrate biodiversity, restraints on time and expenses often mean that communities are only identified to family levels. Archived samples stored in ethanol may, however, be identified more specifically at a later stage.

This study uses next-generation sequencing (NGS) of DNA barcodes to systematically identify species in archived macroinvertebrate samples from two sites in Australia, some of which had been stored up to 12 years at room temperature. Despite anticipated DNA degradation, the researchers were able to amplify partial DNA barcodes from most samples, and using these, identify the species often by more than one amplified sequence.

Not all families had identifiable species, however, when the researchers compared the number of identified species per family with estimated equivalents in GBIF, they revealed potential gaps in the barcode library that could explain the lack of identified species.

Link to paper: https://doi.org/10.1111/1755-0998.12644

NEW DATA ON BRYOZOANS IN THE SOUTH ATLANTIC OCEAN

DATA USED: 196 SPECIES OCCURRENCES
Figuerola B, Barnes DKA, Brickle P and Brewin PE (2017) Bryozoan diversity around the Falkland and South Georgia Islands: Overcoming Antarctic barriers. Marine Environmental Research. Elsevier BV 126: 81–94.

Author countries/areas: Falkland Islands (Malvinas), Spain, United Kingdom
Research funding: Shackleton Scholarship Fund

The cold, nutrient-rich waters of the South Atlantic Ocean are biodiversity hotspots due to the Antarctic Circumpolar Current, but also some of the fastest warming waters in the world. This study aimed to produce new species occurrence data on cheilostome

bryozoans from the waters of the Falkland (Malvinas) and South Georgia Islands, two clusters on each side of the Polar Front, to better understand spatial relationships within the region.

Through scuba sampling surveys, the study recovered 351 bryozoan samples including 18 and 23 potentially new genera and species, respectively. Combined with existing, mainly GBIF-mediated data, the findings expand the known ranges of 32 species. The surveys include the first reported occurrences of 43 species around the Falkland Islands (Malvinas) and ten species around the South Georgia Islands.

The study demonstrates that the islands of the South Atlantic are poorly explored, and the data uncovered suggests that the biogeographic barrier of the Polar Front is not as impermeable as previously thought.

Link to paper: https://doi.org/10.1016/j.marenvres.2017.02.005

SUPERSMART: A SELF-UPDATING SOFTWARE PLATFORM FOR INFERRING PHYLOGENETIC TREES

DATA USED: 724,002 SPECIES OCCURRENCES

ⓐ Antonelli A, Hettling H, Condamine FL, Vos K, Nilsson RH, Sanderson MJ, Sauquet H, Scharn R, Silvestro D, Töpel M, Bacon CD, Oxelman B and Vos RA (2016) Toward a Self-Updating Platform for Estimating Rates of Speciation and Migration, Ages, and Relationships of Taxa. Systematic Biology. Oxford University Press (OUP) syw066.

Author countries/areas: France, Netherlands, Sweden, Switzerland, United States
Research funding: Swedish Research Council, European Research Council, Wallenberg Academy, Carl Tryggers Stiftelse

Phylogenetic trees based on molecular and fossil data can be powerful tools for biogeographical analyses seeking to explain macroevolutionary processes such as migration, speciation, diversification and niche evolution.

In this paper, researchers present a new conceptual and bioinformatic approach to inferral of dated phylogenies called SUPERSMART (conveniently short for **S**elf-**U**pdating **P**latform for **E**stimating **R**ates of **S**peciation and **M**igration, **A**ges, and **R**elationships of **T**axa). The open source modular framework which relies on GenBank sequence data can be freely installed and run on Linux systems by anyone.

The authors demonstrate the functionality of SUPERSMART on two distinct clades: the very-well sequenced Primates order, and the much larger,

however, less studied family of Arecaceae (palms). They validate the latter tree through biogeographic analysis using GBIF-mediated occurrences by estimating ancestral ranges and calculating dispersal events, showing that SUPERSMART is a fully functional tool capable of dealing with vast amounts of data for producing time-calibrated species phylogenies.

Link to paper: https://doi.org/10.1093/sysbio/syw066

SEED DORMANCY DEPENDS ON SEED SIZE AND SEASONALITY

DATA USED: 216,600 SPECIES OCCURRENCES

Rubio de Casas R, Willis CG, Pearse WD, Baskin CC, Baskin JM and Cavender-Bares J (2017) Global biogeography of seed dormancy is determined by seasonality and seed size: a case study in the legumes. New Phytologist. Wiley 214(4): 1527–1536.

Author countries/areas: Canada, Spain, United States
Research funding: National Science Foundation, European Commission, Junta de Andalucia

In climates with unpredictable seasonal patterns, the ability of seeds to remain dormant provides ecological advantages by restricting germination to favourable growth periods. With aseasonal climates, however, this trait may be maladaptive.

In this study, researchers used a GBIF-mediated dataset of 216,600 legume (Fabaceae) family occurrences combined with data on climate, dormancy status and seed size to investigate the biogeography of seed dormancy and trait associations.

Plants exhibiting the trait are more prevalent in temperate zones, whereas seed size is inversely correlated with latitude. They propose a model in which the dormancy trait depends on seed size and seasonality, and this is supported the empirical results. Seed size alone, however, appears to be the better predictor of dormancy.

They suggest that the patterns uncovered will translate across ecological and phylogenetic scales- that aseasonal climates will be dominated by plants producing larger, nondormant seeds, while smaller, dormant seeds will predominate in seasonal habitats.

Link to paper: https://doi.org/10.1111/nph.14498

THE EVOLUTIONARY HISTORY OF AN ICONIC MULTISPECIES MUTUALISM

DATA USED: 23 SPECIES

Ward PS and Branstetter MG (2017) The acacia ants revisited: convergent evolution and biogeographic context in an iconic ant/plant mutualism. Proceedings of the Royal Society B: Biological Sciences. The Royal Society 284(1850): 20162569.

Author country/area: United States
Research funding: National Science Foundation

Certain species of ants nest inside specialized compartments of plants (domatia) and even receive food bodies from extra-floral nectaries of the host. In return, the ants aggressively patrol and protect the host plant against any and all intruders, including herbivores and competing plants.

In this study, researchers explore the evolutionary history of an iconic multispecies mutualism- between neotropical acacia ants (*Pseudomyrmex ferrugineus* group) and swollen-thorn acacias (*Vachellia* spp.). Using genetic sequencing and phylogenetic analysis of 18 different ant species of *Pseudomyrmex*, the researchers infer the phylogeny of the ant species and estimate their ancestral ranges. The group as a whole appears to have diverged 12-14 million years ago, and the domatium-nesting *P. ferrigeneus* subgroup is estimated to be about six million years old.

WELWITSCHIA MIRABILIS SUBSP. *MIRABILIS* BY LUIS QUERIDO https://www.gbif.org/occurrence/1668891775 CC BY-NC 4.0

The researchers also estimated the ancestral range of 23 *Vachellia* host species using GBIF-mediated occurrences. While the appearance of domatia in the host plant seems to have a single origin, the domatia-nesting trait unique to the *P. ferrigeneus* ants developed in two clades separately, about three million years apart.

Link to paper: https://doi.org/10.1098/rspb.2016.2569

EXPLORING PATTERNS AND GAPS IN PLANT DIVERSITY OF TROPICAL AFRICA

DATA USED: 70,220 SPECIES OCCURRENCES

ⓐ Sosef MSM, Dauby G, Blach-Overgaard A, van der Burgt X, Catarino L, Damen T, Deblauwe V, Dessein S, Dransfield J, Droissart V, Duarte MC, Engledow H, Fadeur G, Figueira R, Gereau RE, Hardy OJ, Harris DJ, de Heij J, Janssens S, Klomberg Y, Ley AC, Mackinder BA, Meerts P, van de Poel JL, Sonké B, Stévart T, Stoffelen P, Svenning J-C, Sepulchre P, Zaiss R, Wieringa JJ and Couvreur TLP (2017) Exploring the floristic diversity of tropical Africa. BMC Biology. Springer Nature 15(1).

Author countries/areas: Belgium, Cameroon, Czechia, Denmark, France, Germany, Netherlands, Portugal, United Kingdom, United States
Research funding: French Foundation for Research on Biodiversity, Provence-Alpes-Côte d'Azur region

In this study, researchers used the RAINBIO database to investigate the main floristic patterns and gaps for tropical Africa. RAINBIO is a compilation of 13 datasets (two of which originated in GBIF), comprising more than 600,000 occurrences across 25,000 vascular plant species.

In their spatial analysis of the dataset they find only 21 half-degree units with more than 100 records. The average number of records per species in a unit is less than two, and more than 4,000 species are only found in a single sampling unit. This degree of endemism is highest in the central African forests with around 30 per cent of species being endemic.

Examining collection efforts through time, the researchers see clear patterns linked to political situations, both globally (e.g. the two world wars) and locally (e.g. Liberian civil wars). National Flora programmes also affect collection efforts. The best-explored countries according to the dataset are Cameroon and Benin, while the least explored countries include Angola and Somalia.

The authors point to citizen science as a possible means of aiding the filling of gaps in the knowledge of tropical African plant diversity.

Link to paper: https://doi.org/10.1186/s12915-017-0356-8

MATCHING SEED TO SITE
DATA USED: 82,920 SPECIES OCCURRENCES
Doherty KD, Butterfield BJ and Wood TE (2017) Matching seed to site by climate similarity: Techniques to prioritize plant materials development and use in restoration. Ecological Applications. Wiley 27(3): 1010–1023.

Author country/area: United States
Research funding: Bureau of Land Management

When land management agencies select plants to use in restoration, the first choice is often locally sourced native plants. However, propagules from such species may not be available, and commercial availability could end up being the deciding factor.

In this study, researchers use species distribution models (SDM) based on GBIF-mediated occurrences for charateristic grass and forb species of the cool deserts of the Colorado Plateau to demonstrate the utility of a climate similarity index developed to rank sites for collecting seeds to be transferred to a location being restored.

While the index is able to predict the relative performance of available accessions at the target location, it can also be used to guide seed-banking efforts. Adoption of the described methods is likely to increase efficiency and restoration success, and inform collection efforts for mitigating disturbances, such as climate change.

Link to paper: https://doi.org/10.1002/eap.1505

EXPLORING THE DIVERSIFICATION OF A NEOTROPICAL SONGBIRD
DATA USED: 12,209 SPECIES OCCURRENCES
Avendaño JE, Arbeláez-Cortés E and Cadena CD (2017) On the importance of geographic and taxonomic sampling in phylogeography: A reevaluation of diversification and species limits in a Neotropical thrush (Aves, Turdidae). Molecular Phylogenetics and Evolution. Elsevier BV 111: 87–97.

Author country/area: Colombia
Research funding: Universidad de los Andes, Instituto Alexander von Humboldt

Studies describing biogeographic patterns and evolutionary processes require thorough geographic and taxonomic sampling, especially if drawing conclusions that affect classification. In the Neotropical region, answers to the most interesting evolutionary questions involve taxa with wide distributions reaching far beyond existing political boundaries.

The present study explores diversification of a common and widely distributed songbird, the black-billed thrush (*Turdus ignobilis*), found in northwestern South America. The authors describe the distribution of the species using a combination of GBIF-mediated occurrences and recordings of vocalizations from xento-canto (https://www.xeno-canto.org), showing wider ranges than previously described across foothill and lowland areas east of the Andes.

Adding to the equation by combined mitochondrial and nuclear gene sequencing of 76 individual birds including all named *T. ignobilis* subspecies, they resconstruct a phylogeny revealing novel biogeographic interplay between populations.

Based on these observations, the authors suggest a new taxonomic treatment recognizing two distinct biological species in the group, highlighting the importance of cross-border collaboration to obtain the level of sampling neeeded for studies of Neotropical biogeography.

Link to paper: https://doi.org/10.1016/j.ympev.2017.03.020

TRACING THE MIGRATION OF FLOWERING PLANTS FROM CONTINENTS TO ISLANDS
DATA USED: 4,500,000 SPECIES OCCURRENCES
ⓐ **Liao C-C and Chen C-H (2017) Investigation of floristic similarities between Taiwan and terrestrial ecoregions in Asia using GBIF data. Botanical Studies. Springer Nature 58(1).**
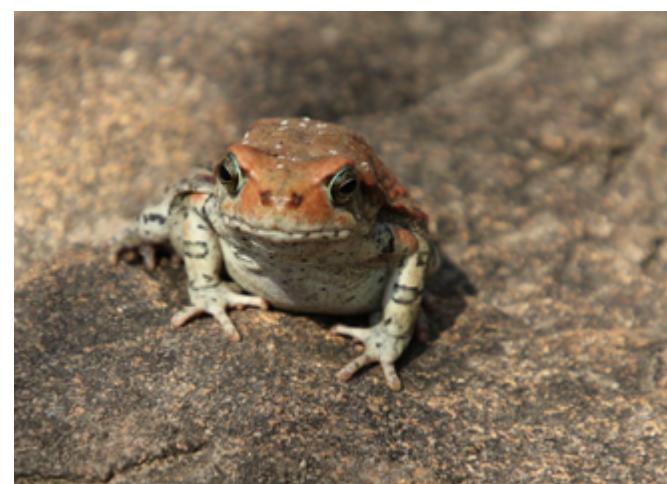
Author country/area: Taiwan
Research funding: None listed

Islands represent unique ecological niches as they are seperated from other land masses by water. Not all islands are the same, however, as the distance from an island to continents and neighbouring islands affects the level of endemism and relatedness with land masses in the vicinity.

Taiwan is a geologically active continental island formed 2-3 million years ago on a complex convergent boundary between four tectonic plates. In this study of Taiwanese flora, researchers used GBIF-mediated occurrences of all flowering plants in East and South Asia to categorize plants into either endemic or non-endemic, and to identify potential sources of the latter group.

Their work identified 847 endemic and 2,428 non-endemic angiosperm species. Analysis of the Asian

SCHISMADERMA CARENS BY FAYNE https://www.gbif.org/occurrence/1802758723 CC BY 4.0

distribution of non-endemics revealed 34 terrestrial ecoregions, of which those tropical and subtropical play the most important role as sources of species richness in Taiwan.

Surprisingly, closeness was not the only factor, as a higher number of angiosperm species in Taiwan are shared with Papua New Guinea than the Philippines, the closest tropical neighbour.

Link to paper: https://doi.org/10.1186/s40529-017-0171-0

IDENTIFYING AMAZONIAN FERNS USING A NEW ONLINE KEY

ⓐ **Zuquim G, Tuomisto H and Prado J (2017) A free-access online key to identify Amazonian ferns. PhytoKeys. Pensoft Publishers 78: 1–15.**

Author countries/areas: Brazil, Finland
Research funding: Academy of Finland, Brazilian National Council for Scientific and Technological Development

Being able to easily and accurately identify species is crucial to producing quality data on species distributions needed for improving conservation planning. Taxonomic identification based on printed floras may be difficult for the untrained eye, and with new species being described continuously, printed keys may become outdated quickly.

In this paper, researchers from Brazil and Finland present a new, free to use, online identification tool aimed at describing Amazonian fern species. Including data on more than 250 species, the Lucid-based tool offers the user the ability to differentiate species based on 54 morphological features, each described avoiding botanical jargon and accompanied by

exemplary illustrations and photos. While the user can select features in any order desired, they are ordered by the easiest to identify and most informative traits.

For possible species matches, the tool also provides direct links to maps of distributions based on GBIF-mediated occurrences that may help users confirm their identification.

The authors aim to continue developing the online key and invite colleagues to contribute to aid identification of these important indicators of enviromental conditions in Amazonia.

Link to paper: https://doi.org/10.3897/phytokeys.78.11370

EVOLUTION OF TERRESTRIAL BREEDING IN AFRICAN TOADS
DATA USED: 13,828 SPECIES OCCURRENCES
Liedtke HC, Müller H, Hafner J, Penner J, Gower DJ, Mazuch T, Rödel M-O and Loader SP (2017) Terrestrial reproduction as an adaptation to steep terrain in African toads. Proceedings of the Royal Society B: Biological Sciences. The Royal Society 284(1851): 20162598.

Author countries/areas: Czechia, Germany, Spain, Switzerland, United Kingdom
Research funding: None listed

Among terrestrial vertebrates, amphibians are the most reproductively diverse group, with more than 40 different reproductive strategies recognized in anurans, alone. In tropical climates especially, terrestrial breeding is common, but the factors driving the evolution of this strategy are unknown.

In this study, researchers reconstructed the most complete phylogeny of African toads (family Bufonidae) to date including 78 per cent of described species. Assigning reproductive strategies to species and examining environmental factors associated with GBIF-mediated occurrences, the authors found that the most likely factors contributing to the evolution of terrestrial reproduction were steep slopes and low water availability.

Based on the evolutionary timing of transitioning from the dry, flat and open habitats to steeper and wetter habitats, the authors note that the transition coincided with or preceded evolution of terrestrial breeding, suggesting an adaptive mode of evolution, rather than exaptation that made colonization of these new habitats possible.

Link to paper: https://doi.org/10.1098/rspb.2016.2598

NEON: 30 YEARS OF ECOLOGICAL MONITORING ACROSS THE UNITED STATES

DATA USED: 56,105 OCCURRENCE RECORDS

ⓐ Hoekman D, LeVan KE, Ball GE, Browne RA, Davidson RL, Erwin TL, Knisley CB, LaBonte JR, Lundgren J, Maddison DR, Moore W, Niemelä J, Ober KA, Pearson DL, Spence JR, Will K and Work T (2017) Design for ground beetle abundance and diversity sampling within the National Ecological Observatory Network. Ecosphere. Wiley 8(4): e01744.

Author countries/areas: Canada, Finland, United States
Research funding: National Science Foundation

Designed to improve understanding of the ecological effects of climate change, land-use change and invasive species, the National Ecological Observatory Network (NEON) is a continental-scale sampling platform of 47 sites across 20 ecoclimatic regions of the United States (including Alaska, Hawaii and Puerto Rico) that will enable researchers to collect and record samples and data for a period of 30 years.

In this paper, specialists describe efforts and rationale behind the NEON project dedicated to sampling abundance and diversity of ground beetles (Carabidae), an ideal sentinel taxon. Using a simple but effective pitfall trapping methodology, rigorously prototyped and tested to maximize efficiency and minimize vertebrate bycatch, the team will collect carabids from 40 traps per site every two weeks. The collected beetles will sorted and identified by experts to the species level.

Using initial project findings combined with existing GBIF-mediated data, the researchers show the potential usefulness in modelling how phenology might change with future climate alterations. All the data produced by the project will be freely available through the NEON data portal, and the team is also working towards publishing the data as sampling event datasets through GBIF.org.

Link to paper: https://doi.org/10.1002/ecs2.1744

SELF-FERTILIZING PLANTS ARE MORE COMMON ON ISLANDS

DATA USED: 11,473,392 SPECIES OCCURRENCES

Grossenbacher DL, Brandvain Y, Auld JR, Burd M, Cheptou P-O, Conner JK, Grant AG, Hovick SM, Pannell JR, Pauw A, Petanidou T, Randle AM, Rubio de Casas R, Vamosi J, Winn A, Igic B, Busch JW, Kalisz S and Goldberg EE (2017) Self-compatibility is over-represented on islands. New Phytologist. Wiley 215(1): 469–478.

Author countries/areas: Australia, Canada, France, Greece, South Africa, Spain, Switzerland, United States
Research funding: National Science Foundation

Plants that are able to self-fertilize may have an advantage when colonizing new habitats as they don't need to find a mate to reproduce. Baker's law describes this tendency and predicts an over-representation of self-compatible species among remote island colonizers. The hypothesis has been tested numerous times since it was put forward in 1955, however, the results have been very mixed.

Assessing 100+ such studies, researchers identified a number of weaknesses potentially responsible for the ambiguity. The majority of studies focused only on island species, disregarding mainland populations as a comparison, and the scope of most studies was also limited to a few species and islands.

To overcome this, the authors of this paper compared the worldwide frequency of breeding systems on mainland versus islands for three plant families of more than 1,500 species combined. Using GBIF-mediated occurrences combined with other sources to determine the distributions of each species, they found that 66 per cent of island species were self-compatible, whereas only 41 per cent of mainland species were able to self-fertilize.

This significant difference, consistent across all three families, provides strong support for Baker's hypothesis.

Link to paper: https://doi.org/10.1111/nph.14534

SYMBIOTIC TRAIT RESTRICTS ESTABLISHMENT OF LEGUMES OUTSIDE NATIVE RANGES

DATA USED: 7,800,446 SPECIES OCCURRENCES

ⓐ Simonsen AK, Dinnage R, Barrett LG, Prober SM and Thrall PH (2017) Symbiosis limits establishment of legumes outside their native range at a global scale. Nature Communications. Springer Nature 8: 14790.

Author country/area: Australia
Research funding: None listed

Many legumes (family Fabaceae) are dependent on symbiosis with nitrogen-fixing bacteria (rhizobia) for growth and reproduction, a trait evolved from a single origin almost 60 million years ago. The extent to which this microbial symbiosis either promotes or impeeds plant distribution is unknown.

In this study, researchers investigated and compared non-native establishment patterns of 3,500 species of symbiotic and non-symbiotic legumes. Relying on GBIF-mediated occurrences, the researchers verified legume range data from the International Legume Database and Information Service (ILDIS). By applying the nitrogen-fixation status of each species, their data revealed a significantly lower probability of symbiotic legumes occurring in non-native regions, suggesting symbiosis as a limiting factor. The authors point to lack of compatible bacterial species or inappropriate environmental conditions for nitrogen fixation as likely explanations.

While other factors (e.g latitude of origin, woodiness and human uses) also appeared important, their effects did not eliminate symbiosis as a key determinant of establishment in novel ranges. The study highlights the importance of mutualisms and other species interactions in predicting species invasiveness.

Link to paper: https://doi.org/10.1038/ncomms14790

ESTIMATING CHANGES IN SEASONAL SITE OCCUPANCY USING OPPORTUNISTIC OBSERVATIONS

DATA USED: 39,384 SPECIES OCCURRENCES

ⓐ Ruete A, Pärt T, Berg Å and Knape J (2017) Exploiting opportunistic observations to estimate changes in seasonal site use: An example with wetland birds. Ecology and Evolution. Wiley 7(15): 5632–5644.

Author country/area: Sweden
Research funding: Vetenskapsrådet

Species observations collected in a non-systematic manner e.g. through citizen science programs like iNaturalist, eBird, etc. make up a large proportion of occurrence data in GBIF. Providing wide coverage on spatial, temporal and taxonomic scales, opportunistic data, however, can be biased and often lacks information about absences of species.

Using occurrence data on 71 wetland bird species from GBIF publisher Artportalen, a study by Alejandro Ruete (1st prize winner of the 2016 Ebbe Nielsen Challenge) and colleagues introduces a novel dynamic occupancy model that attempts to cope with known sources of bias including lack of absence data and variation in sampling effort.

When applied to the real observations, the model estimates daily occupancy for a given species and site, and when summarized, provides a detailed picture of seasonal site use including within-season population dynamics.

Confirming the robustness of the model using simulated data, the authors conclude that modelling using opportunistic data with multiple replicates can provide more biologically relevant information than traditional annual occupancy models.

Link to paper: https://doi.org/10.1002/ece3.3100

EATING PLANTS—A RECIPE FOR EVOLUTIONARY SUCCESS

DATA USED: 490,319 SPECIES OCCURRENCES

Poore AGB, Ahyong ST, Lowry JK and Sotka EE (2017) Plant feeding promotes diversification in the Crustacea. Proceedings of the National Academy of Sciences. Proceedings of the National Academy of Sciences 114(33): 8829–8834.

Author countries/areas: Australia, United States
Research funding: None listed

Eating fruits and vegetables is second nature to humans, however, the ability to extract sufficient nutrients from plant material is a special adaptation. Once such an evolutionary hurdle is overcome, it may allow a lineage access to previously unexploited resources and thus lead the way to increased species richness, as shown in studies of insects, mammals and dinosaurs.

A new study published in PNAS examines the role of herbivory—eating plants—in the diversification of crustaceans, a diverse and important group of arthropods dominating aquatic environments. The authors carry out a phylogenetic analysis of the distribution of the trait followed by an examination of shifts in species richness within each lineage.

The authors identify 31 independent lineages of plant-feeding crustaceans and find that these have *21 times* more species than their nearest predatory or scavenging relatives. Using GBIF-mediated occurrences of all species, the authors showed that these findings were not likely confounded by distributional patterns, suggesting that the difficult evolutionary path of shifting diets to plants indeed promotes speciation among herbivorous crustaceans.

Link to paper: https://doi.org/10.1073/pnas.1706399114

LESS IS MORE: TRIMMING DISTRIBUTIONS USING NATURAL BARRIERS TO IMPROVE MODELS

DATA USED: 144,598 SPECIES OCCURRENCES
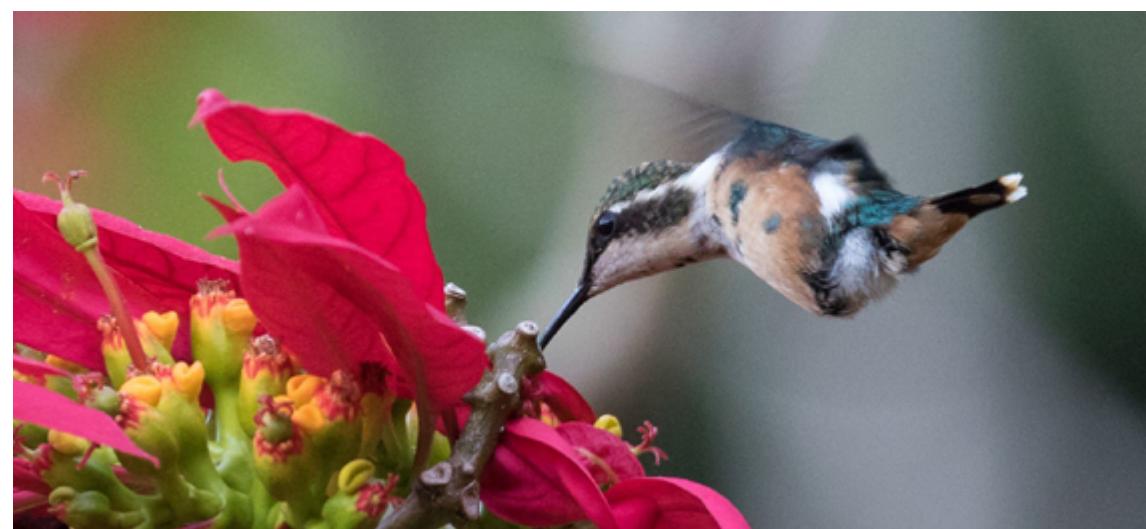
Cooper JC and Soberón J (2017) Creating individual accessible area hypotheses improves stacked species distribution model performance. Global Ecology and Biogeography. Wiley 27(1): 156–165.

Author country/area: United States
Research funding: National Science Foundation

Species distributions models (SDMs) are an important tool for predicting a species' distributional extent through use of e.g. climatic similarities. Stacking models of several taxa, moreover, can predict species richness and community composition, although the approach often leads to overpredictions.

Exploring a novel approach for improving stacked SDMs, this study suggests trimming the area used for calibration to a hypothesized accessible area, before the modelling is done. This involves visual inspection of the species occurrences and using natural breaks-e.g large rivers or mountain ranges—in habitats to limit theoretical distribution area.

The authors used GBIF-mediated occurrences of all hummingbird species (Aves: Trochilidae) to test the performance of stacked models—with or without constraining accessible area. By statistical comparison, the constrained model had significantly higher prediction success and also provided better estimates of richness and community composition.

In conclusion, limiting theoretical distribution area—effectively incorporating dispersal limitations—can improve efficacy of stacked species distributions models.

Link to paper: https://doi.org/10.1111/geb.12678

WASTE BASKET FUNGI: REVIEW OF HELOTIACEAE IN THE CANARY ISLANDS

DATA USED: 6,780 SPECIES OCCURRENCES

ⓐ **Quijada L, Ribes M, Negrín R and Beltrán-Tejera E (2017) Lignicolous species of Helotiales associated with major vegetation types in the Canary Islands. Willdenowia. Botanic Garden & Botanical Museum Berlin-Dahlem BGBM 47(3): 271–291.**

Author country/area: Spain
Research funding: Canarian Government, Autonomous Agency of National Parks (Government of Spain)

The subject of contention since the 19th century, Helotiaceae is family of fungi comprising 177 genera and 826 species (Kirk et al. 2008). Often placed as the last step of identification keys to members of the parent order Helotiales, Helotiaceae has become a "waste basket" family, only arrived at after discarding all other families.

In a study of Helotiaceae species in the Canary Islands, authors review nine genera and 12 species

of Helotiaceae present in the Spanish archipelago. Through field sampling and studies of literature and specimens available through GBIF.org, the researchers present detailed descriptions of species morphology (including images), distribution and ecology.

Adding a new report of *Cyathicula hysterioides* and three new genera (*Durella*, *Pseudohelotium*, *Velutarina*), each with one species, the Canary Island study also corrects a previous record of species occurrence (*Ascocoryne cylichnium*). Due to morphological characteristics, the latter, however, may represent a different species, and exact identification will require further molecular studies.

Link to paper: https://doi.org/10.3372/wi.47.47310

THE EVOLUTION OF FLOWERING PLANTS THROUGH POLLEN

DATA USED: 1,896,305 SPECIES OCCURRENCES

ⓐ **Kriebel R, Khabbazian M and Sytsma KJ (2017) A continuous morphological approach to study the evolution of pollen in a phylogenetic context: An example with the order Myrtales. PLOS ONE. Public Library of Science (PLoS) 12(12): e0187228.**

Author country/area: United States
Research funding: National Science Foundation

The study of flowering plant evolution through phylogeny has often included analyses of pollen. Mostly limited to traditional morphometric methods, pollen studies often bin traits and treat features like shape and size using discrete categories.

In this paper, authors present a novel approach to pollen evolution study based on quantitative size and shape variables. They used images of Myrtales pollen grains from two different angles to measure length and width of the grains, while analysing outlines of the shape and converting these into elliptic transformations used for comparisons.

They analysed pollen size and shape in a phylogenetic context and found significant differences among Myrtales families when comparing both shape and size. To test for linkages betwen pollen features and climate, the authors used GBIF-mediated occurrences and found that pollen shape was correlated with the mean latitude of a species' distribution.

The novel morphometric approaches presented in the study prove useful for taxonomic identification and phylogenetic placement of as yet unknown pollen fossils.

Link to paper: https://doi.org/10.1371/journal.pone.0187228

WALLACE: SPECIES DISTRIBUTION MODELLING MADE EASY

Kass JM, Vilela B, Aiello-Lammens ME, Muscarella R, Merow C and Anderson RP (2018) Wallace: A flexible platform for reproducible modeling of species niches and distributions built for community expansion. Methods in Ecology and Evolution. Wiley 9(4): 1151–1156.

Author countries/areas: Denmark, United States
Research funding: Global Biodiversity Information Facility, CUNY, U.S. National Science Foundation

Increased access to open data and a rise in computing power have enabled advanced modelling approaches in ecology. Researchers looking to model species distributions are often faced with either complicated command line interface (CLI) programming tools with high flexibility, but low user-friendliness, or fancy graphical user interfaces (GUI) that are easy to use, but lack reproducibility and flexibility.

This paper introduces WALLACE—a new web-browser based, flexible platform for species distribution modelling built in R. Modular in structure, WALLACE uses seperate components to guide the user through a series of simple steps—including obtaining species occurrences records, e.g. from GBIF, downloading relevant environmental layers, building the models, and finally visualizing the distributions.

The lead author of the paper originally presented the WALLACE concept as a finalist entry in the 2015 Ebbe Nielsen Challenge. Combining the strengths of CLI and GUI tools, the WALLACE platform provides an innovative approach to flexible and easy-to-use software for researchers in ecology and biodiversity sciences.

Link to paper: https://doi.org/10.1111/2041-210X.12945

Impacts of climate change

PORT STEPHENS, AUSTRALIA - A SEA HARE HAVEN?

DATA USED: 154 SPECIES OCCURRENCES
Nimbs MJ, Willan RC and Smith SDA (2016) Is Port Stephens, eastern Australia, a global hotspot for biodiversity of Aplysiidae (Gastropoda: Heterobranchia)? Molluscan Research. Informa UK Limited 37(1): 45–65.

Author country/area: Australia
Research funding: Southern Cross University, Linnean Society of NSW, Joyce W. Vickery Research Fund

Sea hares are heterobranch sea slugs of the Aplysiidae family with large ear-like rhinophores, responsible for the vernacular name of the group. Members of this globally distributed family usually only live up to one year, while producing up to 180 million eggs, and some species grow to a size of up to two kilograms.

In a recent study, researchers investigated and documented aplysiid diversity in Port Stephens, NSW, Australia, home to more species than anywhere else in the world. With the most diverse algal flora in the world, the waters of southern Australia provide the ideal living conditions for sea hares whose diets consist of marine plants- mostly algae.

While reviewing the taxonomy and nomenclature of the group, the authors describe the morphology

and distributions of 16 species found in the region, including the first observation of *Petalifera* sp. in Australian waters. Highlighting the global significance of Port Stephens for Aplysiidae and an obvious target for further sea hare studies, this study forms a baseline for detecting changes to aplysiid diversity in future, changing climates.

Link to paper: https://doi.org/10.1080/13235818.2016.1207280

PIONEERING BENIN FOREST RESTORATIONS UNDER FUTURE CLIMATE CONDITIONS

DATA USED: 2,732 SPECIES OCCURRENCES
ⓐ **Gbètoho AJ, Aoudji AKN, Roxburgh L, Ganglo JC (2017) Assessing the suitability of pioneer species for secondary forest restoration in Benin in the context of global climate change. Bois et Forêts des Tropiques. N° 332 (2), 43-55.**

Author countries/areas: Benin, South Africa
Research funding: JRS Biodiversity Foundation

Able to outcompete exotic weeds and attract important dispersers, fast-growing pioneer species are important for successful rehabilitation of degraded forests in areas such as West Africa. For long-term restoration projects, however, knowing the vulnerability of such species to future climates is key.

In a collaborative study from institutions in Benin and South Africa, researchers modelled the current and future distributions of two candidate species in Benin—*Lonchocarpus sericeus* and *Anogeissus leiocarpa*—using GBIF-mediated occurrences and environmental data from the WorldClim and AFRICLIM datasets.

Models for both species performed well with the most essential contributors being temperature seasonality for *L. sericeus* and annual precipitation for *A. leiocarpa*. The authors found suitable climate in 74 per cent of Benin for *L. sericeus* and in 88 per cent of the country for *A. leiocarpa*.

The authors found little, if any, reduction in potential distributions, suggesting that in terms of climate, both species could be considered good pioneer candidates for forest restorations now and in the future.

Link to paper: http://bft.cirad.fr/cd/BFT_332_43-55.pdf

WARMING CLIMATES AND THE RISK OF INVASIVE HYBRIDS

DATA USED: 5,928 SPECIES OCCURRENCES
ⓐ **Klonner G, Dullinger I, Wessely J, Bossdorf O, Carboni M, Dawson W, Essl F, Gattringer A, Haeuser E, van Kleunen M, Kreft H, Moser D, Pergl J, Pyšek P, Thuiller W, Weigelt P, Winter M and Dullinger S (2017) Will climate change increase hybridization risk between potential plant invaders and their congeners in Europe? Diversity and Distributions. Wiley 23(8): 934–943.**

Author countries/areas: Austria, China, Czechia, France, Germany, United Kingdom
Research funding: ERA-Net BiodivERsA, Austrian Science Fund, German Research Foundation, French National Research Agency, Czech Science Foundation, Czech Academy of Sciences

Certain plant traits are known to facilitate invasions, including early reproduction and rapid growth rate, while the general risk of invasion has been shown to increase with changing climates. Interspecies hybridization may also pose a threat, and as 16,000 plant species- many of which alien- are cultivated for ornamental purposes in Europe alone, knowing how future climates affect this risk is crucial.

By studying a large group of alien ornamentals not naturalized in Europe, but established outside their native range somewhere else in the world, researchers created species distribution models using GBIF-mediated occurrences for both non-native ornamentals and native/naturalized congeners (i.e. belonging to same genus). Projecting these into future climates, the authors compared the distributions of

alien ornamentals and their native congeners, finding that mean geographical overlap is likely to *decrease* under future climatic conditions.

These surprising results show that while warming climates may increase risk of naturalization of some alien ornamentals, hybridization between future invaders and resident species appears less likely to occur.

Link to paper: https://doi.org/10.1111/ddi.12578

LOSERS AND BIGGER LOSERS: IMPACT OF CLIMATE CHANGE ON EUROPEAN FOREST TREES

DATA USED: 1,848,587 SPECIES OCCURRENCES
Dyderski MK, Paz S, Frelich LE and Jagodzinski AM (2017) How much does climate change threaten European forest tree species distributions? Global Change Biology. Wiley 24(3): 1150–1163.

Author countries/areas: Poland, United States
Research funding: Polish Academy of Sciences

Not just about temperature and precipitation, the effects of climate change can also be catastrophic storms, fires and pest outbreaks. Among European trees, a new study suggests that warming climates will have varying effects, effectively making some species "winners" and other "losers".

Based on occurrence data from GBIF.org and other sources, researchers built species distribution models for 12 European forest tree species using bioclimatic variables now and in three future projections.

The species showed quite different responses to climate change, however, roughly dividing into two groups according to fraction of current distribution threatened under future climates: less than 50 per cent—mainly mid-to-late-successional species (e.g. beech, ash and oak)—and more than 50 per cent—

mainly pioneer and coniferous species (e.g. larch, silver birch and Norway spruce).

Faced with changing climate conditions, most studied species, however, are likely to experience significant net losses in suitable habitat, especially for the species with the northern-most distributions. In conclusion, the future for European forest trees appears to have no winners—only losers.

Link to paper: https://doi.org/10.1111/gcb.13925

COMPARING EFFECTS OF DEFORESTATION AND CLIMATE CHANGE ON NEOTROPICAL DRY FORESTS

DATA USED: 1,140 SPECIES OCCURRENCES

Ⓐ Manchego CE, Hildebrandt P, Cueva J, Espinosa CI, Stimm B and Günter S (2017) Climate change versus deforestation: Implications for tree species distribution in the dry forests of southern Ecuador. PLOS ONE. Public Library of Science (PLoS) 12(12): e0190092.

Author countries/areas: Ecuador, Germany
Research funding: Katholischer Akademischer Ausländer-Dienst
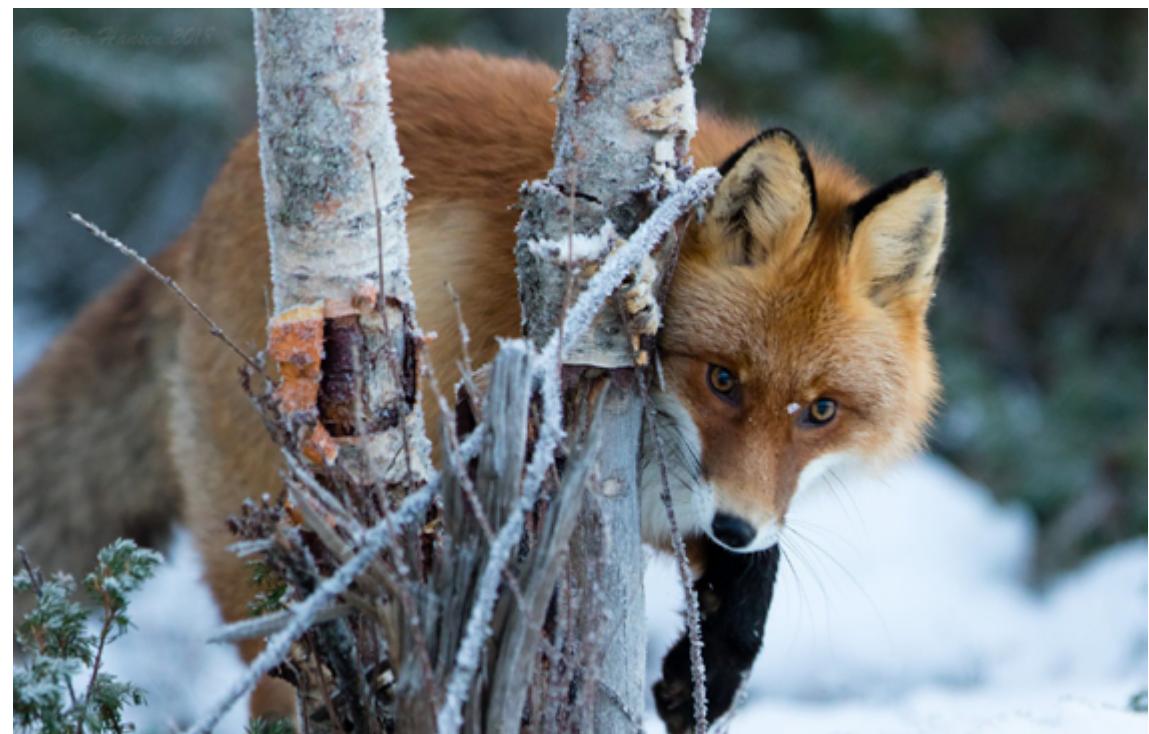
Affected by human activities as well as climate change, neotropical dry forests are the most threatened tropical forest ecosystem in the world. The effects of deforestation, land use change and warming climates all pose serious threats to these ecosystems, however, to prioritize conservation efforts a scientific frame for comparing threats is necessary.

In an attempt to identify the relative important of two evils, authors of this study examined the effects of climate change and deforestation on 17 tree species in southern Ecuador. Using GBIF-mediated species occurrences combined with WorldClim bioclimatic data, they modelled the distribution of all species and used governmental land-use data to estimate areas lost by deforestation.

Consistent for all but one species, the results of their analysis showed that losses in distribution area from deforestation were significantly greater than those resulting from climate change. While the effects of the latter were more severe for some species, the study clearly suggests that deforestation is the more imminent threat to neotropical dry forests.

Link to paper: https://doi.org/10.1371/journal.pone.0190092

Invasive alien species

VULPES VULPES BY PER HANSEN https://www.gbif.org/occurrence/1824044693 CC BY 4.0

PREDICTING ANTARCTIC SUITABILITY OF THE WORLD'S WORST TERRESTRIAL INVADERS

DATA USED: 2,329,509 SPECIES OCCURRENCES

Duffy GA, Coetzee BWT, Latombe G, Akerman AH, McGeoch MA and Chown SL (2017) Barriers to globally invasive species are weakening across the Antarctic. Diversity and Distributions. Wiley 23(9): 982–996.

Author country/area: Australia
Research funding: Australian Antarctic Division

Due to its geographic isolation and climate, the Antarctic region has been somewhat protected from biological invasions, however, with warming climates and increased human traffic, the protection afforded the region may be diminishing.

In a new study, researchers used species distribution modelling to assess the likelihood of establishment of the world's worst—according to IUCN—terrestrial invaders supplemented by cold-tolerant non-native species already known to occur in the Antarctic region.

Using ten different modelling methodologies, the authors created robust ensemble models based on GBIF-mediated occurrences and current climate data with projections for 2050 and 2100. They created a summed map from which they found the Antarctic continent unsuitable for all tested species under current conditions, however, within the next century the Antarctic peninsula may become suitable for six species.

While the continent may still be protected, the models showed that all but one of the Southern Ocean islands are currently suitable to multiple species. The islands of Auckland and Campbell, in particular, show suitability for a high number of species, but for all islands suitability is predicted to increase by 2100.

Link to paper: https://doi.org/10.1111/ddi.12593

MASSIVE DIVERSION PROJECT CREATES CONDUIT FOR POTABLE WATER—AND POSSIBLE INVADERS

DATA USED: 6,500 SPECIES OCCURRENCES

Liu D, Wang R, Gordon DR, Sun X, Chen L and Wang Y (2017) Predicting Plant Invasions Following China's Water Diversion Project. Environmental Science & Technology. American Chemical Society (ACS) 51(3): 1450–1457.

Author countries/areas: China, United States
Research funding: Shandong Science and Technology Program, China Water Project, National Nature Science Foundation of China, National Key Technology Research and Development Program of China

China's South to North Water Diversion (SNWD) aims to improve access to potable water for 110 million people by transferring water from the Yangtze River in the south to regions with groundwater deficits in the north. But despite best intentions, human-built infrastructure like the SNWD frequently provides highly efficient pathways for biological invasion. This study offers the first risk assessment of the world's largest and longest water diversion project's potential to spread invasive species.

Alligator weed (*Alternanthera philoxeroides*), water hyacinth (*Eichhornia crassipes*) and water lettuce (*Pistia stratiotes*) are aquatic plants whose ranges have strayed far beyond their South American origins to become notorious non-native aliens in China and elsewhere around the globe. Each produces dense mats of vegetation that have the potential to impair navigation and water flow, spawn floods, impact water quality and quantity, and imperil native and agricultural biodiversity.

Using occurrence data from each species' native and introduced ranges accessed via GBIF.org and other sources, the authors constructed ecological niche models underlining their suitability in nearly the entire diversion area. Alligator weed shows the greatest potential for expansion, having already reduced yields of sweet potato and rice by 63 and 45 per cent in the country's south. So as the northerly flow of water from the diversion increases, these models can help prioritize and direct management actions toward the most vulnerable areas where early detection and rapid response could mitigate or avoid the most costly impacts of any invasion.

Link to paper: https://doi.org/10.1021/acs.est.6b05577

TRACKING THE SPREAD OF THE FIRST INTRODUCED BIOLOGICAL AGENT IN EUROPE
DATA USED: 10,664 SPECIES OCCURRENCES
Stojanovic DV, Vajgand D, Radovic D, Curcic N, Curcic S (2017) Expansion of the range of the introduced moth Acontia candefacta in southeastern Europe. Bulletin of Insectology.

Author country/area: Serbia
Research funding: Ministry of Education, Science and Technological Development of the Republic of Serbia

A natural agent against the highly allergenic common ragweed (*Ambrosia artemisiifolia*), *Acontia candefacta* was the first insect species intentionally introduced to Europe for biological control of an invasive weed species. Released in 1969 in the Krasnodar and

PONOMETIA CANDEFACTA BY MARK D. READ https://www.gbif.org/occurrence/1586107230 CC BY-NC 4.0

Stavropol regions of the former USSR, the moth has since migrated and increased its range both in eastward and westward directions.

A recent study by researchers from Serbia investigates the expansion of *A. candefacta* in southeastern Europe. Since its introduction, it has been recorded in Ukraine, Bulgaria, and Romania, and reported for the first time in Serbia in 2009.

Through a combination of years of intense sampling by light trapping across all of Serbia and modelling of the host species using GBIF-mediated occurrences, the team present results indicating the moth is likely to spread to all areas where the weed is present.

As the radiation of ragweed is expanding with changing climates, so may the range of *A. candefacta*. Unfortunately, however, current populations appear incapable of controlling the spread of the harmful weed.

Link to paper: http://www.bulletinofinsectology.org/pdfarticles/vol70-2017-111-120stojanovic.pdf

CLIMATE CHANGE—A DOUBLE-EDGED SWORD FOR INVASIVE SPECIES?
DATA USED: 66,960 SPECIES OCCURRENCES
Merow C, Bois ST, Allen JM, Xie Y and Silander JA (2017) Climate change both facilitates and inhibits invasive plant ranges in New England. Proceedings of the National Academy of Sciences. Proceedings of the National Academy of Sciences 114(16): E3276–E3284.

Author country/area: United States
Research funding: National Science Foundation, United States Department of Agriculture

The interaction between climate change and biological invasions is complex. Several studies have shown that climate change may lead to increased

invasion, however, the opposite, in which invasions are mitigated by changing climates, is also plausible although harder to observe.

This study attacks the problem with a mechanistic case study of establishment risk for two invasive plants, *Alliaria petiolata* and *Berberis thunbergii*, in the northeastern United States compared with native analogue species.

By transplanting the invasive species into various locations across the region and thus environmental gradients, the authors created demographic models based on vitality in the given environment, and validated these by comparing the output with traditional ecological niche models based on GBIF-mediated occurrences.

For mid-century climate projections, the models predict increased suitability for *B. thunbergii* across the region. Surprisingly, however, future warming is likely to render the region unsuitable for *A. petiolata*. The study confirms how climate change may alter invasion patterns, but highlights that mechanistic studies are required to understand drivers and forecast potential invasions in novel environments.

Link to paper: https://doi.org/10.1073/pnas.1609633114

REFINING PREDICTIONS OF INVASIVE SPECIES USING REMOTE SENSING DATA
DATA USED: 2,011 SPECIES OCCURRENCES
Truong TTA, Hardy GESJ and Andrew ME (2017) Contemporary Remotely Sensed Data Products Refine Invasive Plants Risk Mapping in Data Poor Regions. Frontiers in Plant Science. Frontiers Media SA 8.

Author countries/areas: Australia, Viet Nam
Research funding: Department of Foreign Affairs and Trade

Given the potentially catastrophic consequences of invasive species, prediction, early detection and prevention are priorities in conservation policies. Relying primarily on climatic factors, species distribution models can aid in the prediction of invasiveness at a regional scale, but for finer scale models, biotic parameters and local abiotic conditions should be considered also.

In this study of invasive weeds in South East Asia, researchers used remote sensing (RS) data and climate data- separately and combined- to evaluate the potential distribution of 14 priority species based on occurrence data from GBIF.org. While the climate data included temperature and precipitation metrics, the RS data provided information on soil, elevation, land cover and productivity.

Overall, the combined models predicted substantially smaller risk areas than models based on either dataset alone. While RS-only models didn't perform well, the combined models showed that adding RS-based biotic and abiotic parameters to climate data, clearly refined the spatial patterns of predicted distributions.

The study identified shrub species as having the highest potential invasion risk in South East Asia, and also revealed that native invaders may pose as serious a threat as alien invasive species.

Link to paper: https://doi.org/10.3389/fpls.2017.00770

ASSESSING INVASIVE AQUATIC PLANTS OF SOUTH AMERICA
DATA USED: 10,735 SPECIES OCCURRENCES
Lozano V, Chapman D and Brundu G (2017) Native and non-native aquatic plants of South America: comparing and integrating GBIF records with literature data. Management of Biological Invasions. Regional Euro-Asian Biological Invasions Centre Oy (REABIC) 8(3): 443–454.

Author countries/areas: Italy, United Kingdom
Research funding: None listed

GBIF.org is a unique source of primary distribution data used in a multitude of studies worldwide. Derived from museums, herbaria, field researchers and citizen scientists, this data—as with any major source of biodiversity information—is prone to gaps and biases in taxonomic, geographical and temporal coverage.

In a study of invasions among South American aquatic plants, researchers assessed the state of data availability in GBIF and in literature. Based on a list of 40 native and 40 non-native species, the authors compile three datasets based on occurrences in GBIF.org, data manually extracted from literature, and the two combined, respectively. Initial comparisons showed significant differences between the two sources, and the combined dataset was deemed most reliable.

Based on this, the researchers generated maps of species distributions across 16 South American regions, finding the highest number of alien species in Argentina and Brazil. Adding a Human Influence Index layer, they further demonstrate that high risk species appear to cluster in areas of higher levels of anthropization, especially in coastal regions close to main ports.

Link to paper: https://doi.org/10.3391/mbi.2017.8.3.18

ILLEGAL ALIENS: PREDICTING RISK OF PET SNAKE INVASIONS IN BRAZIL

DATA USED: 2,723 SPECIES OCCURRENCES

ⓐ **Fonseca É, Solé M, Rödder D and de Marco P (2017) Pet snakes illegally marketed in Brazil: Climatic viability and establishment risk. PLOS ONE. Public Library of Science (PLoS) 12(8): e0183143.**

Author countries/areas: Brazil, Germany
Research funding: CAPES

The introduction of non-native species can be detrimental to both the environment and wildlife. Exotic pets living far away from their natural habitats may escape and cause havoc if allowed to naturalize. Prevention of alien invasion requires identifying potential invaders before it's too late.

Focusing on pet snakes in Brazil, a new study evaluates the invasion risk of five exotic species known to be traded illegally in the country—*Lampropeltis getula*, *Lampropeltis triangulum*, *Pantherophis guttatus*, *Python regius*, and *Python bivittatus*—all with records of being invasive in other countries.

Using GBIF-mediated occurrences and WorldClim environmental variables, authors modelled the potential distribution of each of the five species. From a generated consensus map, the authors identified the most suitable areas in Northern and Midwestern regions of Brazil—including the Cerrado and the Amazon—both areas important to Brazilian biodiversity.

Combining this with a herpetofaunal model scoring establishment risks and specific attributes required for successful invasion, the author point to *P. guttatus* and *P. bivittatus* as having the highest risk of establishment, concluding that these should the be focus of control and monitoring.

Link to paper: https://doi.org/10.1371/journal.pone.0183143

NOISY NEIGHBOURS: ACOUSTIC INTERFERENCE AMONG INVASIVE AMPHIBIANS

DATA USED: 33,901 SPECIES OCCURRENCES

ⓐ **Forti LR, Becker CG, Tacioli L, Pereira VR, Santos ACFA, Oliveira I, Haddad CFB and Toledo LF (2017) Perspectives on invasive amphibians in Brazil. PLOS ONE. Public Library of Science (PLoS) 12(9): e0184703.**

Author countries/areas: Brazil, United States
Research funding: Fundação de Amparo à Pesquisa do Estado de São Paulo, Conselho Nacional de Desenvolvimento Científico e Tecnológico, Coordenação de Aperfeiçoamento de Pessoal de Nível Superior

Alien invasive species can disrupt ecosystems directly by outcompeting native species for resources. Effects of invasions, however, can be also indirect and less predictable. Among animals that rely on sound for attracting mates, alien intruders may cause noise and reduce mating success.

In a study of invasive amphibians in Brazil, researchers used a combination of field studies, literature and GBIF-mediated species occurrences of six species with invasive populations to analyse current habitats and future distributions. The generated models revealed large increases in potential ranges for two species—*E. johnstonei* and *R. jimi*.

Through spectral analysis, the researchers compared vocalizations and found high overlaps between calls of invader *P. luteolus* and native *Ischnocnema* sp. For domestic invader *L. labyrinthicus*, they found spectral overlaps with locals *L. knudseni* and—even more pronounced—*L. pentadactylus*.

Determining whether these overlaps cause actual acoustic interference—or even mistaken recognition and potential hybridization— will require further studies, however, this paper highlights the potential effects of invasions, which, combined with projected range expansions, suggest a need for increased monitoring and control.

Link to paper: https://doi.org/10.1371/journal.pone.0184703

FROM CULTIVATION TO INVASION - NATURALIZATION OF GARDEN ORNAMENTALS

DATA USED: 1,124,139 SPECIES OCCURRENCES

Mayer K, Haeuser E, Dawson W, Essl F, Kreft H, Pergl J, Pyšek P, Weigelt P, Winter M, Lenzner B and van Kleunen M (2017) Naturalization of ornamental plant species in public green spaces and private gardens. Biological Invasions. Springer Nature 19(12): 3613–3627.

Author countries/areas: Austria, China, Czechia, Germany, South Africa, United Kingdom
Research funding: Landesanstalt für Umwelt, Messungen und Naturschutz, Baden-Württemberg, German Research Foundation, ERA-Net BiodivERsA, French National Research Agency, DFG, Austrian Science Fund, Czech Science Foundation, Ministry of Culture of the Czech Republic, Czech Academy of Sciences

Not only having important aesthetic value, private gardens and public parks also provide important ecosystem services in urban areas. Ornamental plants, however, are also the most important pathway for alien plant introductions worldwide.

A study from Germany investigated what factors might lead to a successful local naturalization of garden plants by surveying planted flora in 111 public and private gardens in the small city of Radolfzell in southern Germany. The researchers recorded species, abundance, lifeform and whether the plant was native or not. For alien plants, the authors also assessed the current naturalization status worldwide.

In total, the authors identified 1,268 species of which 75 per cent were alien. Using GBIF-mediated occurrences, the authors modelled the distribution of the alien species, not surprisingly finding that local naturalization success was linked to climatic suitability.

By projecting models into future climatic scenarios, they identified 45 species not currently naturalized in Germany but widely naturalized in other parts of the world—and thus likely to become naturalized in the future through increased climatic suitability.

Link to paper: https://doi.org/10.1007/s10530-017-1594-y

PHYLLODYTES LUTEOLUS BY OMAR ROJAS-PADILLA https://www.gbif.org/occurrence/1883498578 CC BY-NC 4.0

GLOBAL BANS ON BIRD TRADE NEEDED TO STOP INVASIONS

DATA USED: OCCURRENCES OF 14 BIRD SPECIES

ⓐ **Reino L, Figueira R, Beja P, Araújo MB, Capinha C and Strubbe D (2017) Networks of global bird invasion altered by regional trade ban. Science Advances. American Association for the Advancement of Science (AAAS) 3(11): e1700783.**

Author countries/areas: Belgium, Denmark, Germany, Portugal, Spain
Research funding: H2020 Marie Skłodowska-Curie Actions, Danmarks Grundforskningsfond, Fundação para a Ciência e a Tecnologia, Universidade do Porto

Wildlife trade can lead to species going extinct in their native ranges, but also to invasions in non-native habitats. Intended to protect endangered species, trade bans, however, may also limit the spread of invasive species, but the extent of this is unknown.

This study set out to assess how wildlife trade—and banning it—affects invasion risk globally. Using trade data from the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) database combined with avian invasion data including GBIF-mediated occurrences, researchers analysed the global trade network and how it relates to the establishment of non-native species.

Not surprisingly, their analysis showed that countries that import more birds are more likely to be invaded. In the global network, a high number of import sources and a more central position also correlated with a higher invasion risk.

In the European Union, the 2005 ban on importing wild birds reduced trade to about 10 per cent of pre-ban levels, and global avian invasion risk decreased— particularly in the EU. New trade routes, however, might overturn this development, suggesting a need for global bans.

Link to paper: https://doi.org/10.1126/sciadv.1700783

On the distribution of species

LAETIPORUS CINCINNATUS BY GREG LASLEY https://www.gbif.org/occurrence/1453398428 CC BY-NC 4.0

CLOUDY WITH A CHANCE OF FUNGI
DATA USED: 7,062 SPECIES OCCURRENCES
Del Olmo-Ruiz M, García-Sandoval R, Alcántara-Ayala O, Véliz M and Luna-Vega I (2017) Current knowledge of fungi from Neotropical montane cloud forests: distributional patterns and composition. Biodiversity and Conservation. Springer Nature 26(8): 1919–1942.

Author countries/areas: Guatemala, Mexico
Research funding: Dirección General de Asuntos del Personal Académico

Persistently immersed in clouds, neotropical montane cloud forests (NMCF) represent distinct biological communities, different from other tropical forests. Exhibiting an abundance of plants and usually high endemism, NMCF are unique sites of biodiversity. Despite ecological importance and ubiquity of fungi, very little is known about the NMCF distribution of this massive group of organisms.

In a comprehensive data mining exercise, researchers set out to describe in detail the distributional patterns and composition of microfungi, macrofungi and lichens in NMCF. Relying on published literature, GBIF-mediated occurrences as well as other online sources, the authors compile 6,349 records representing 2,962 fungal species. Based on a computed species

rarefaction curve, the authors estimate that doubling the sampling effort would increase number of species by 42 per cent.

Providing a thorough perpective on diversity and distribution of fungi in NMCF, the study concludes that Mesoamerica, particularly Mexico and Costa Rica, has the highest species richness, and compared to NMCF in the Caribbean and South America, the fungal assemblages are significantly different with very little overlap.

Link to paper: https://doi.org/10.1007/s10531-017-1337-5

USING SOCIAL MEDIA TO COMPLEMENT TRADITIONAL SOURCES OF BIODIVERSITY DATA
DATA USED: 25,905 SPECIES OCCURRENCES
ElQadi MM, Dorin A, Dyer A, Burd M, Bukovac Z and Shrestha M (2017) Mapping species distributions with social media geo-tagged images: Case studies of bees and flowering plants in Australia. Ecological Informatics. Elsevier BV 39: 23–31.

Author country/area: Australia
Research funding: Australian Research Council

While enthusiastic citizen scientists record great numbers of observations and photographic evidence of species in networks such as iNaturalist, their

numbers pale in comparison to the multitudes of images shared on generic social media platforms, like Flickr. Although the majority of such images have little relevance to biodiversity, being able to extract the few that do, could be a cheap and easy way of complementing existing biodiversity information.

Following this idea, researchers searched Flickr for geotagged images of two species of bees and flowering plants in Australia and used Google's reverse image search to validate the images and exclude false positives. The locations of the images were overlaid on a map with occurrences of the same species obtained via GBIF and the Atlas of Living Australia.

The produced maps showed a general overlap between Flickr-derived images and the range of the GBIF-mediated occurrences, and if used properly, this big-data methodology could provide an inexpensive and abundant source of occurrence data.

Link to paper: https://doi.org/10.1016/j.ecoinf.2017.02.006

STUDYING GLOBAL OLIVE DISTRIBUTION TO COMPARE ECOLOGICAL NICHE MODELS
DATA USED: 37,533 SPECIES OCCURRENCES
ⓐ **Ashraf U, Peterson AT, Chaudhry MN, Ashraf I, Saqib Z, Rashid Ahmad S and Ali H (2017) Ecological niche model comparison under different climate scenarios: a case study of Olea spp. in Asia. Ecosphere. Wiley 8(5): e01825.**

Author countries/areas: Pakistan, United States
Research funding: None listed

Modelling ecological niches and species distributions can be useful when predicting the potential spread of invasive species and species' response to changing climates. Numerous methods for modelling are used, but the choice of modelling approach depends on many factors, and no single method is likely to excel in all cases.

Relying on the near-global distribution of *Olea europea*, researchers used primarily GBIF-mediated occurrence data to compare performance of seven modelling approaches across a broad and varied landscape. First, the authors calibrated the models using global climate and occurrence data, and then narrowed in on a smaller study area in Asia to test the transferability of models into future climate scenarios.

The overall results of the comparative study showed very different predictions in future climates depending on the modelling approach. While six out of seven tested models yielded predictions significantly better than random, the authors concluded that models

based on Maxent and SVM (Support Vector Machines) were best at distinguishing between suitable and unsuitable distributional potential.

Link to paper: https://doi.org/10.1002/ecs2.1825

EXPLORING UNCERTAINTIES OF MARINE SPECIES MODELLING
DATA USED: 4,877 SPECIES OCCURRENCES
Chefaoui RM and Serrão EA (2017) Accounting for uncertainty in predictions of a marine species: Integrating population genetics to verify past distributions. Ecological Modelling. Elsevier BV 359: 229–239.

Author country/area: Portugal
Research funding: Fundação para a Ciência e a Tecnologia

An efficient approach to answering ecological and biogeographical questions, species distribution modelling depends on reliable occurrence data and suitable model algorithms. In models of terrestrial species, geographical bias can be ameliorated through filtering, however, less is known about the uncertainties affecting models of marine species, which are also influenced by a scarcity of predictor variables.

In a study of the common seagrass *Cymodocea nodosa*, researchers used GBIF-mediated occurrences to explore how a number of factors may affect the performance of models. First, researchers limited the number of predictors to only half of the available variables, which led to an expected and significant reduction in performance.

To alleviate effects of observed sampling bias, the authors constructed a weighted filter taking into account general marine sampling efforts, national GBIF-publishing activity and level of country development. Surprisingly, however, the filters did not improve the performance of any model.

The authors finally verified the models by confirming hindcasted predictions of so-called glacial refugia with regions where the highest genetic diversity of *C. nodosa* is found today.

Link to paper: https://doi.org/10.1016/j.ecolmodel.2017.06.006

distribution of species

RAFINESQUIA NEOMEXICANA BY DFONG16 https://www.gbif.org/occurrence/1880487003 CC BY 4.0

IMPORTANCE OF POSITIVE INTERACTIONS ON SPECIES DISTRIBUTION MODELS

DATA USED: 4,269 SPECIES OCCURRENCES

Filazzola A, Sotomayor DA and Lortie CJ (2017) Modelling the niche space of desert annuals needs to include positive interactions. Oikos. Wiley 127(2): 264–273.

Author country/area: Canada
Research funding: York University, Government of Canada

Facilitation through positive interactions between species can affect the range of a beneficiary by changing the microclimate to match its fundamental niche in an otherwise unsuitable and high-stress environment such as a desert. When modelling ecological niches, these interactions may affect models.

In an attempt to quantify the effects of such microclimate ameliorations, authors used GBIF-mediated occurrences to model the distribution of 20 annual plant species—10 known beneficiaries and 10 unreported—in the Mojave Desert while examining the results of including benefactor shrub species.

For known beneficiary species, the performance of models improved significantly when taking shrub co-occurrences into consideration, but they were not different for unreported species. These results highlight the importance of positive interactions and other biotic interactions in modelling, and suggest that co-occurrence of benefactor species can be used as a proxy for facilitation.

Link to paper: https://doi.org/10.1111/oik.04688

NOT JUST A NUMBERS GAME: SMALL COLLECTIONS WITH BIG IMPACT

DATA USED: 15,967 SPECIES OCCURRENCES

Glon HE, Heumann BW, Carter JR, Bartek JM and Monfils AK (2017) The contribution of small collections to species distribution modelling: A case study from Fuireneae (Cyperaceae). Ecological Informatics. Elsevier BV 42: 67–78.

Author country/area: United States
Research funding: None listed

Natural history collections of many sizes contribute data to GBIF.org—used extensively to model the distribution of species for a variety of purposes. Every record counts, however, small collections may be more regional in scope with a specific taxomic or ecological focus compared to larger collections.

To quantify the impact of small collections, authors of this study built distribution models of five test case species relying on GBIF-mediated data partitioned by size of source collection. Despite having fewer records, the dataset based on small collections contributed unique information that when combined with the data from the large collections led to more refined and robust predictions of habitat suitability— compared to the large collections alone—across all test species.

While using high numbers of species occurrences as input for distribution models can improve performance and reliability, the present study suggests that the nature of data source can be important too. This potentional of small, regional collections should be considered when planning digitization and data publication efforts.

Link to paper: https://doi.org/10.1016/j.ecoinf.2017.09.009

ASSESSING COVERAGE OF FRESHWATER FISH DATA IN THE UNITED STATES

DATA USED: 557,680 SPECIES OCCURRENCES

Troia MJ and McManamay RA (2017) Completeness and coverage of open-access freshwater fish distribution data in the United States. Diversity and Distributions. Wiley 23(12): 1482–1498.

Author country/area: United States
Research funding: Oak Ridge National Laboratory

The work of researchers testing ecological and evolutionary hypotheses using primary biodiversity data, like species occurrences in GBIF.org, depend on the even distribution of ecological surveys in both space and time. The ecological coverage of freshwater

habitats having a disproportionately high number of species, is largely unexplored and thus in urgent need of assessment.

Through compilation of all available freshwater fish records from GBIF, the Multi-State Aquatic Resources Information Facility (MARIS) and federally administered fish survey (FFS), authors of this paper set out to assess the completeness of freshwater fish data in the contiguous United States.

Having standardized taxonomic nomenclature across the entire dataset of 1.5 million occurrences of 21 million individuals across 892 species, their analysis revealed spatial and temporal differences between the three sources. FFS data was sparse but widespread, whereas GBIF data was dense in coastal regions, however, spanned more years than FFS or MARIS data.

Overall, more than 95 per cent of data originated from flowing waters such as springs and rivers, suggesting that while data on freshwater fish is plentiful, future surveys should focus on still waters—like lakes and reservoirs—to improve completeness.

Link to paper: https://doi.org/10.1111/ddi.12637

ARE SPECIES MOST ABUNDANT IN THE CENTRE OF THEIR CLIMATIC NICHES?

DATA USED: 20,210,035 SPECIES OCCURRENCES

Dallas T, Decker RR and Hastings A (2017) Species are not most abundant in the centre of their geographic range or climatic niche. Ecology Letters. Wiley 20(12): 1526–1533.

Author country/area: United States
Research funding: National Science Foundation

The *abundant centre hypothesis* represents the phenomenon that a species is most abundant at the centre of its geographical range or climatic niche. However intuitive this may sound, the empirical support for this claim is rather weak.

In a large data analysis, researchers from UC Davis tested the hypothesis by examining the relationships between abundance and distance to centre of range or niche for more than 1,600 species of birds, mammals, fish and trees. Relying on GBIF-mediated species occurrences to define the range and niche centroids, the authors' analyses found only slight correlations for some species—both positive and negative—while the majority of tested species showed no relationship at all.

Contrasting previous findings, the results of the study, however, have since been questioned by other researchers, arguing that a number of methodological

problems in fact hinders a robust conclusion. While the original paper represents the largest-scale analysis of species spatial abundance patterns, the jury on abundant centres still appears hung.

Link to paper: https://doi.org/10.1111/ele.12860

DISTRIBUTION AND DIVERSITY OF AMPHIBIANS IN ALBANIA

DATA USED: 8 SPECIES OCCURRENCES

Szabolcs M, Mizsei E, Jablonski D, Vági B, Mester B, Végvári Z and Lengyel S (2017) Distribution and diversity of amphibians in Albania: new data and foundations of a comprehensive database. Amphibia-Reptilia. Brill Academic Publishers 38(4): 435–448.

Author countries/areas: Hungary, Slovakia
Research funding: None listed

Due to long political isolation, Albania and its biodiversity—part of the Mediterranean hotspot— is poorly explored and little is known about the amphibian fauna of the country.

A new study aimed to describe the distribution of Albanian amphibians by combining GBIF-mediated occurrences with data from field studies of remote and less known areas. Pooling a total of 1,097 records of 16 species, the authors analysed the amphibian richness patterns and found 1.8 species per 10 square km cell. Almost 70 per cent of all cells had at least one species present.

Modelling the distribution of known species revealed that land cover and precipitation were the most important predictors of diversity. The authors identified amphibian hotspots in several regions, including the Prokletije, Grammos, Çikës and Korab Mountains, near lakes Ohrid and Prespa, and the coastal regions near Vlorë.

While representing the largest study of amphibian diversity in Albania so far, the authors acknowledge that sampling is scarce and uneven. To evaluate efficiency of protected areas, they call for increased sampling and a detailed assessment of amphibian diversity in Albania.

Link to paper: https://doi.org/10.1163/15685381-00003126

MOTHS OF FACEBOOK: ENHANCING PROFESSIONAL COLLECTIONS WITH OPTIMIZED CITIZEN SCIENCE DATA

DATA USED: 393 SPECIES OCCURRENCES

ⓐ Lin Y-P, Lin W-C, Lien W-Y, Anthony J and Petway J (2017) Identifying Reliable Opportunistic Data for Species Distribution Modeling: A Benchmark Data Optimization Approach. Environments. MDPI AG 4(4): 81.

Author country/area: Taiwan
Research funding: None listed

Preferred for species distribution modelling, occurrence data derived from well-defined, controlled surveys is expensive and as a consequence, often in short supply compared to the vast amounts of opportunistic data gathered by citizen science initiatives. Although the latter may be more prone to misidentification and biases, citizen science data—used correctly—can be a good supplement to professional surveys.

In a new study, researchers in Taiwan used GBIF-mediated occurrences from professionally curated datasets to test a novel optimization procedure for opportunistic data from a citizen science project on Facebook called EnjoyMoths. Using four different approaches, the authors modelled the distributions of nine moth species based on GBIF and EnjoyMoths datasets—both raw and optimized, separate and combined—while comparing the performance of the generated models.

Their results showed that the optimization procedure significantly improved the performance of models based on opportunistic data. Furthermore, the highest performing models were found among those based on GBIF data in combination with optimized opportunistic data. These findings suggest that the optimization approach is able to increase quality of such data, and highlights the value and potential of citizen science in biodiversity.

Link to paper: https://doi.org/10.3390/environments4040081

RAIN OR SHINE: RELATIVE IMPORTANCE OF ABIOTIC FACTORS ON SPECIES DISTRIBUTIONS

DATA USED: 1,045,514 SPECIES OCCURRENCES

ⓐ Manjarrés-Hernández AM, Guisande C, García-Roselló E, Pelayo-Villamil P, González-Dacosta J, Heine J, González Vilas L, Granado-Lorencio C, Duque SR and Lobo JM (2017) A procedure to assess the spatial variability in the importance of abiotic factors affecting distributions: the case of world freshwater fishes. Current Zoology. Oxford University Press (OUP).

Author countries/areas: Colombia, Spain
Research funding: None listed

The distribution of a species is controlled by a number of biotic and abiotic factors—but also access to suitable areas for dispersal and/or evolutionary ability to adapt to new conditions. The relative contribution of these vary by species, but their importance may be related to geography.

To be able to assess the spatial variability of abiotic factors, researchers studied the distribution of the world's freshwater fishes, using a novel approach—an instability index—to examine and visualize the varying importance of different predictors. Using GBIF-mediated occurrences combined with several bioclimatic and topograhic variables, the authors modelled the distribution of each species in three progressively widening extents.

In their results, they find temperature and altitude to be the most important predictors at the river basin level. Expanding to the regional level, altitude is replaced by precipitation, which finally becomes the single most important predictor at the global level.

Suggesting that predictors depend on geographical scope, this study presents an important implication to be considered in species distribution modelling.

Link to paper: https://doi.org/10.1093/cz/zox063

ATLAS OF THE REPTILES OF LIBYA

DATA USED: 3,350 SPECIES OCCURRENCES
Bauer AM, DeBoer JC and Taylor DJ (2017) Atlas of the Reptiles of Libya. Proceedings of the California Academy of Sciences. Series 4, volume 64, no. 8, pp. 155-318.

Author country/area: United States
Research funding: National Science Foundation

Limited by authoritarian restrictions and civil war, access to Libya has been hindered and herpetological research curbed since World War II. This combined with a perceived low reptilian diversity means that very little is known about reptiles in Libya.

Originally intended to survey and collect reptiles in Libya, this study was impeded by the events of the "Arab Spring" in 2011, and as a result continued as a museum-based programme. Entitled "Atlas of the Reptiles of Libya", the study gathers all available data from museums records via GBIF, scientific publications and other publicly available sources.

The produced atlas contains records from 2061 occurrences of 66 reptile species in 683 localities, many of which unfortunately, are too imprecise to

AGAMA AGAMA BY DAVID GUNN VIA WIKIMEDIA COMMONS (PUBLIC DOMAIN)

georeference. Describing three marine turtles, three terrestrial chelonians, 39 lizards and 21 snakes, the atlas provides full taxonomic details, descriptions and images of each species with information on known distributions including maps of occurrences in Libya.

Link to paper: http://bit.ly/2NhWhzg

THE SPECIES RICHNESS OF THE SOUTHERN SEAS OF IRAN

DATA USED: 30,423 SPECIES OCCURRENCEES
Maghsoudlou A, Momtazi F, Nasiri K, Pazooki S, Molavi-Arabshahi M, Sepahvand V, Hekmatara M and Khaledi H (2017) A review on the state of the biodiversity knowledge on Iran's southern seas: introducing a methodology to evaluate the validity of the reported cases. Marine Biodiversity. Springer Nature.

Author country/area: Iran
Research funding: Iranian National Institute for Oceanography and Atmospheric Science

Scattered, sparse and often only available on dusty library shelves, information about biodiversity in Iran—especially on marine taxa—is challenging to discover and access. With very high maritime traffic in the Persian Gulf and Gulf of Oman, standardized and easy to access data about marine diversity in these waters is needed.

Compiling all available biodiversity data records from books, academic dissertations, research articles and open databases—OBIS and GBIF—authors from Tehran review the current knowledge of marine taxa in Iranian southern seas. They extract a total of almost 60,000 records, which after rigorous quality control turn out to cover more than 3,300 species—ranging from phytoplankton to whales—more than twice previously predicted. More than 60 per cent of the records belong to Animalia, while Chromista and Plantae are also well-represented. Fungi, Protozoa and Bacteria together, represent less than one per cent.

Concluding that long-term availability of data is important for conservation, the authors call for increased training in marine research and for the establishment of a national marine biodiversity facility with international partnerships.

Link to paper: https://doi.org/10.1007/s12526-017-0835-8

distribution of species

distribution of species

Species conservation and protected areas

TRACHEMYS SCRIPTA SUBSP. *ELEGANS* BY AMALIBRAHIM https://www.gbif.org/occurrence/1269537010 CC BY-NC 4.0

ASSESSMENT OF THE GLOBAL DISTRIBUTION OF REPTILES

DATA USED: 14,680 SPECIES OCCURRENCES

Roll U, Feldman A, Novosolov M, Allison A, Bauer AM, Bernard R, Böhm M, Castro-Herrera F, Chirio L, Collen B, Colli GR, Dabool L, Das I, Doan TM, Grismer LL, Hoogmoed M, Itescu Y, Kraus F, LeBreton M, Lewin A, Martins M, Maza E, Meirte D, Nagy ZT, de C. Nogueira C, Pauwels OSG, Pincheira-Donoso D, Powney GD, Sindaco R, Tallowin OJS, Torres-Carvajal O, Trape J-F, Vidan E, Uetz P, Wagner P, Wang Y, Orme CDL, Grenyer R and Meiri S (2017) The global distribution of tetrapods reveals a need for targeted reptile conservation. Nature Ecology & Evolution. Springer Nature 1(11): 1677–1682.

Author countries/areas: Belgium, Brazil, Cameroon, China, Colombia, Ecuador, Germany, Israel, Italy, Malaysia, Senegal, United Kingdom, United States
Research funding: Gerald M. Lemole, CAPES, CNPq, FAPDF, Niche Research Grant Scheme, FAPESP, SENESCYT, University of Oxford, BSF

Comprising about one third of terrestrial vertebrate species, reptiles—including lizards, snakes and crocodiles—are surprisingly poorly described in terms of global distributions, and present knowledge is scattered, at best. This gap prevents proper incorporation into conservation planning, and as a result, reptiles may be underrepresented.

Consisting of researchers from 13 countries, the Global Assesment of Reptile Distributions group published a large study analysing 10,000 reptile species, thus updating the knowledge on global patterns. Based on literature, field studies and online databases including GBIF.org, the authors produced distribution maps of all species, and from those derived important knowledge on reptile species richness.

Their results revealed that reptile richness patterns—largely dominated by snakes—correspond well to those of other tetrapod vertebrates, with lizards and turtles being less congruent. The same is evident for hotspots of richness. Analysing coverage of protected areas, the authors show that only 3.5 per cent of reptile species ranges are protected.

The paper shows that reptile conservation as a whole falls behind that of other vertebrates and identifies novel reptilian hotspots, such as the Arabian peninsula, Lake Chad and the Brazilian Caatinga, as future priorities for conservation efforts.

Link to paper: https://doi.org/10.1038/s41559-017-0332-2

STRATEGY FOR CONSERVATION OF CROP WILD RELATIVES

DATA USED: 86 SPECIES OCCURRENCES

Taylor NG, Kell SP, Holubec V, Parra-Quijano M, Chobot K and Maxted N (2017) A systematic conservation strategy for crop wild relatives in the Czech Republic. Diversity and Distributions. Wiley-Blackwell 23(4): 448–462.

Author countries/areas: Czechia, Italy, United Kingdom
Research funding: European Union, Crop Research Institute

Ensuring increasing crop yields is a priority as climates change and the world's population continues to grow. This be achieved by using crop wild relatives (CWR) as the source of new material to the genetic base of current crop cultivars. But as CWRs face the same threats as other wild plants, targeted strategies for conservation are needed.

In this study, researchers used a checklist of CWRs in Czechia to identify priority species based on criteria related to vulnerability and relation to crops of high socioeconomic importance. The shortlist contained 204 species for which the researchers did *in situ* conservation analyses revealing that all but one species occurs in at least one protected area. One hundred and sixty species occur in five or more protected areas.

However, the study also identifed eight species occurring in only one PA in which they are endemic, making them particularly vulnerable. In addition, *ex situ* analyses found huge gaps, pointing to a need for targeted collection of germplasm for gene banks.

Link to paper: https://doi.org/10.1111/ddi.12539

MODELLING TAXON DISTRIBUTIONS TO PROTECT LONG-HORNED BEETLES IN FIJI ISLANDS

DATA USED: 24 SPECIES OCCURRENCES

ⓐ **Aguilar GD, Waqa-Sakiti H, W. L. (2017). Using predicted locations and an ensemble approach to address sparse data sets forspecies distribution modelling: Long-horned beetles (Cerambycidae) of the Fiji islands.**

Author country/area: New Zealand
Research funding: None listed

In biodiversity conservation, species distribution modelling can provide initial guidance on the potential distribution of a taxon of interest and help identify areas worth prioritizing. A low number of species occurrences, however, may result in inconsistent predictions for some modelling algorithms.

In this study, researchers set out to inform conservation planning to protect rare insect species in Fiji. Using GBIF-mediated occurences and five environmental variables for the region, the

researchers employed an ensemble-based approach to predict the distribution of long-horned beetles (the Cerambycidae family) in the Fiji islands.

Despite an inherent scarcity of Cerambycidae occurrence records, the researchers were able to produce a predictive map based on an ensemble model of the best-performing modelling algorithms, including machine learning-based SVM, randomForest and MaxEnt.

The resulting distribution map pointed to highest taxon suitability on the middle slopes of the central mountains of the islands Viti Levu, Vanua Levu and Taveuni.

Link to paper: http://bit.ly/2NkIE3I

MODELLING SPECIES DISTRIBUTIONS TO PROTECT BIODIVERSITY HOTSPOTS IN SOUTHEAST ASIA

DATA USED: 300,000 SPECIES OCCURRENCES

Hughes AC (2017) Mapping priorities for conservation in Southeast Asia. Biological Conservation. Elsevier BV 209: 395–405.

Author country/area: China
Research funding: None listed

Southeast Asia is a global biodiversity super-hub, home to four of the world's biodiversity hotspots. Unfortunately, the region is also a hotspot of threat due to hunting and deforestation, and a lack of baseline data makes assessing efficacy of protected areas highly challenging.

In this study, a researcher from the Xishuangbanna Tropical Botanical Garden uses GBIF-mediated occurrences of birds, mammals, reptiles and amphibians in mainland Southeast Asia combined with environmental data to create distribution models of all species. Based on the models, the author shows that about half of the most diverse areas for mammals and amphibians fall within existing protected areas. For birds, however, the number is around only 20 per cent, and for reptiles even lower, about 10 per cent.

Comparing the models to expert-drawn IUCN range maps, the author find large disparities, as the models predict areas of maximum richness that are only a fraction of those indicated by the IUCN maps, suggesting that including modelling approaches could improve effectiveness of conservation planning.

Link to paper: https://doi.org/10.1016/j.biocon.2017.03.007

Species conservation

PICKING THE BEST SPOT FOR RELEASING REHABILITATED PRIMATES

DATA USED: 427 SPECIES OCCURRENCES

Stone OML and Guy AJ (2017) Predicting Optimal Release Sites for Rehabilitated Monkeys: a Vervet Monkey (Chlorocebus aethiops) Case Study. International Journal of Primatology. Springer Nature 38(3): 485–499.

Author country/area: Australia
Research funding: None listed

When primate rescue centres take in injured or orphaned animals of unthreatened species, the motivation is animal welfare and the goal is successful rehabilitation and eventual release into the wild. Choosing appropriate sites for releasing rehabilitated animals can be highly challenging due to limited resources.

In this study, focused on finding optimum release sites for rehabilitated vervet monkeys (*Chlorocebus aethiops*) in KwaZulu-Natal, South Africa, researchers create an environmental model based on own sightings, literature, and GBIF-mediated occurrences of wild monkeys. They refine the output by excluding urban areas and roads, while ensuring proximity to fresh water sources, considered to be the most important factor for successful release.

Initially, the authors identify 80 per cent of KwaZulu-Natal to be suitable habitat, but applying refinements reduce this to 298 areas of a combined 6,225 km², equivalent to about six per cent of the total area. Unfortunately, a large proportion of these areas are found within protected land with non-release policies.

While using modelling for choosing release sites doesn't guarantee success, the approach identifies the best candidate sites for pre-release surveys, a critical aspect of successful rehabilitation in the wild.

Link to paper: https://doi.org/10.1007/s10764-017-9956-y

PROTECTING THE HERB-SHRUB FLORA OF THE CERRADO

DATA USED: ~1 MILLION SPECIES OCCURRENCES

Amaral AG, Munhoz CBR, Walter BMT, Aguirre-Gutiérrez J and Raes N (2017) Richness pattern and phytogeography of the Cerrado herb-shrub flora and implications for conservation. Journal of Vegetation Science. Wiley 28(4): 848–858.

Author countries/areas: Brazil, Netherlands
Research funding: National Council for Scientific and Technological Development, Coordination for the Improvement of Higher Education Personnel

Covering nearly a quarter of Brazil, the Cerrado is the largest neotropical savanna in the world, home to more than 12,000 plant species including a large herb-shrub flora widely neglected in scientific studies and conservation policy.

In a recent study published in the Journal of Vegetation Science, researchers used nearly a million primarily GBIF-mediated occurrences combined with bioclimatic predictors and soil variables to model distributions of more than 5,000 herb-shrub species. By stacking the predicted distributions, the authors derived a species richness map of the Cerrado, revealing the highest levels of richness in the central-south and western parts of the region. The study also identifies two floristically distinct clusters of phytogeographic regions.

Plotting protected areas over the species richness map indicated that only 18 per cent of areas with predicted high species richness are found in priority areas, showing that current Cerrado conservation plans do not reflect the actual biological importance of herb-shrub flora.

Link to paper: https://doi.org/10.1111/jvs.12541

CHLOROCEBUS PYGERYTHRUS BY BERNARD DUPONT
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PANTHERA ONCA BY JONATHAN CAMPBELL https://www.gbif.org/occurrence/1880558846 CC BY-NC 4.0

USING PHYLOGENETIC DIVERSITY TO ASSESS EFFICACY OF PROTECTIVE AREAS

DATA USED: 1,695,781 SPECIES OCCURRENCES

Quan Q, Che X, Wu Y, Wu Y, Zhang Q, Zhang M and Zou F (2018) Effectiveness of protected areas for vertebrates based on taxonomic and phylogenetic diversity. Conservation Biology. Wiley 32(2): 355–365.

Author countries/areas: China, United States
Research funding: National Nature Science Foundation of China, Environment Construction & Capacity Building of GDAS, Nanling Wildlife Survey and Monitoring Program, Fasheng Zou, National Natural Science Foundation of China

Shielded from serious human disturbances, protected areas play a key role in preventing irreversible biodiversity loss in a world of increased rates of environmental disruption. Often based on taxonomic diversity, the locations of protected areas seldom consider the unique evolutionary status and functional traits of species although phylogenetic diversity may be crucial for sustaining an ecosystem.

To assess the current conservation efficacy of protected areas in China, the authors of this paper used IUCN range maps supplemented by GBIF-mediated occurrences of terrestrial vertebrates combined with previously published phylogenies of clades to estimate and identify hotspots of phylogenetic diversity and evolutionary distinctiveness. Mapping these against existing protected areas, the authors were able to reveal gaps in coverage.

Based on their analysis, the paper concludes that the current network of protected areas targeting species richness appears to protect phylogenetic diversity fairly well. However, highlighting the lack of protection of severely threatened birds in the coastal areas of eastern China, the authors suggest room for improvement in the distribution of protected areas.

Link to paper: https://doi.org/10.1111/cobi.12986

ASSESSING GAPS IN PROTECTED AREAS OF BRAZIL

DATA USED: 659,062 SPECIES OCCURRENCES

ⓐ **Oliveira U, Soares-Filho BS, Paglia AP, Brescovit AD, de Carvalho CJB, Silva DP, Rezende DT, Leite FSF, Batista JAN, Barbosa JPPP, Stehmann JR, Ascher JS, de Vasconcelos MF, De Marco P, Löwenberg-Neto P, Ferro VG and Santos AJ (2017) Biodiversity conservation gaps in the Brazilian protected areas. Scientific Reports. Springer Nature 7(1).**

Author countries/areas: Argentina, Brazil, Singapore
Research funding: Climate and Land Use Alliance, Conselho Nacional de Desenvolvimento Científico e Tecnológico, Fundação de Amparo à Pesquisa do Estado de Minas Gerais, Humboldt Foundation, CNPq, FAPEMIG, Instituto Nacional de Ciência e Tecnologia dos Hymenoptera Parasitóides da Região Sudeste Brasileira, FAPESP

Brazil is among the countries that hold the largest share of Earth's species: the megadiverse countries. Protecting ecosystems is a priority and the country has invested significantly in expanding its network of protected areas. However, the extent to which these areas help protect biodiversity is unknown.

In a study of gaps in protected areas in Brazil, researchers built a database of vertebrate, arthropod and angiosperm species occurrences mainly from GBIF.org, mapping these against protected areas to

quantity sampling effort. They also reconstructed phylogenetic trees of Brazilian taxa in order to identify patterns of evolutionary lineages.

The study found that fewer than one per cent of protected areas are well sampled, and as many as 50 per cent are not sampled at all. For Brazilian biodiversity, more than 50 per cent of species and 40 per cent of evolutionary lineages are found outside protected areas. Modelling distributions showed that less than 40 per cent of median species distributions overlap with protected areas.

These findings combined suggest a need for increased sampling and protection priorities based on inventories and biodiversity analyses.

Link to paper: https://doi.org/10.1038/s41598-017-08707-2

AMPHIBIAN REFUGIA IN THE COASTAL FORESTS OF EASTERN AFRICA

DATA USED: 30,000 SPECIES OCCURRENCES
Barratt CD, Bwong BA, Onstein RE, Rosauer DF, Menegon M, Doggart N, Nagel P, Kissling WD and Loader SP (2017) Environmental correlates of phylogenetic endemism in amphibians and the conservation of refugia in the Coastal Forests of Eastern Africa. Diversity and Distributions. Wiley 23(8): 875–887.

Author countries/areas: Australia, Italy, Kenya, Netherlands, Switzerland, United Kingdom
Research funding: Humer Foundation, Stipendienkommission für Nachwuchskräfte, Freiwilligen Akademischen Gesellschaft Basel
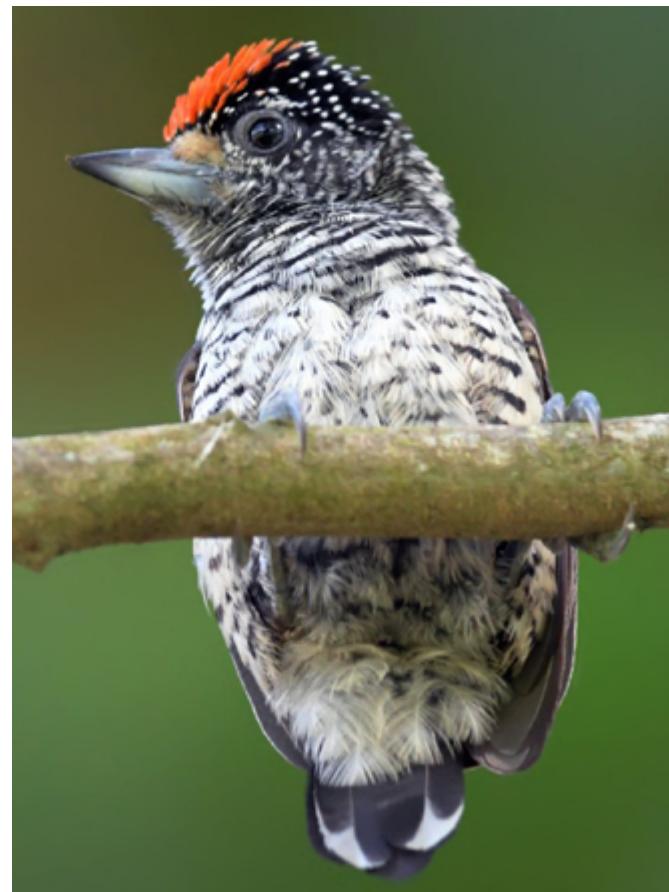
Africa is home to more than a quarter of the world's biodiversity hotspots, yet knowledge and understanding of the factors leading to such biological richness—key to prioritizing conservation efforts—is still mostly lacking.

Working with molecular data combined with spatial occurrence data from GBIF.org, researchers studied the entire amphibian assemblage in a focus area containing parts of the Coastal Forests of Eastern Africa hotspot and the Eastern Afromontane region. Deriving a phylogeny of the assemblage and modelling the distribution of each species, the authors created a map of phylogenetic endemism from which they identified environmental correlates to predict potential refugia.

The study confirmed known centres of amphibian endemism, but also identified new potential refugia. In total, conservation analyses showed ten hotpots accounting for more than 25 per cent of phylogenetic endemism in the region. As only a very small fraction

of these overlapped with areas currently protected, the study highlights a need to consolidate protection within centres of endemism.

Link to paper: https://doi.org/10.1111/ddi.12582

PICUMNUS SPILOGASTER BY JOSH_VANDERMEULEN
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TRANSLATING INTERNATIONAL CONSERVATION COMMITMENTS INTO NATIONAL PLANNING ACTION

DATA USED: 6,402 SPECIES OCCURRENCES
ⓐ **Bicknell JE, Collins MB, Pickles RSA, McCann NP, Bernard CR, Fernandes DJ, Miller MGR, James SM, Williams AU, Struebig MJ, Davies ZG and Smith RJ (2017) Designing protected area networks that translate international conservation commitments into national action. Biological Conservation. Elsevier BV 214: 168–175.**

Author countries/areas: Australia, Canada, Guyana, United Kingdom
Research funding: NERC

Through Aichi Target 11, signatories to the Convention on Biological Convention (CBD) have committed to protection of 17 per cent of terrestrial areas by 2020, but in 2017 less than 15 per cent was protected—a shortfall of more than 3 million square km. For

countries falling behind targets, plans for expansions based on biodiversity and conservation science are needed.

This study present an example of a systematic national-scale conservation planning process in Guyana, in which only 8.5 per cent of the land area is currently protected. Using published range maps and GBIF-mediated occurrences for species distribution models, the study focuses on 329 vertebrate species as well as 17 vegetation types.

In the current Guyanan network of protected areas, their results showed that only 48 per cent of vertebrates and 29 per cent of vegetation types are represented, and among threatened species eight are completely absent. To meet all targets, the authors identify new priority areas for conservation, bringing the combined protected area up to 22.5 per cent, however, 17 per cent coverage could be reached by focusing effort on just two areas—the protection of which would mean complete representation.

Link to paper: https://doi.org/10.1016/j.biocon.2017.08.024

CULTURAL HERITAGE AND TRADITIONS THREATENED BY LAND USE CHANGES

DATA USED: 161 SPECIES OCCURRENCES
Semotiuk AJ, Colunga-GarcíaMarín P, Valenzuela Maldonado D and Ezcurra E (2017) Pillar of strength: Columnar cactus as a key factor in Yoreme heritage and wildland preservation. Ambio. Springer Nature 47(1): 86–96.

Author countries/areas: Mexico, United States
Research funding: University of California Institute for Mexico and the United States

Often connected with local flora and fauna, cultures and traditions of indigenous peoples are affected by land use changes associated with rapidly altering globalized societies. In Sonora and Sinaloa, Mexico—ancestral territory of the Yoreme people—mechanized, large-scale farming co-exists with traditional practices and knowledge, exemplified by the organ pipe cactus—also known as the pitaya (*Stenocereus thurberi*).

In this paper, authors carried out interviews with harvesters and sellers of pitaya products, showing usage in a variety of goods from marmalade and dried fruit rolls to flavoured water and sorbet, providing economic benefits to community members while preserving Yoreme heritage.

Unfortunately, based on vegetation surveys and GBIF-mediated occurrences, the authors showed that the distribution of pitaya—particularly in the Yoreme territory—converged with the the highest rates of

land conversion to modern agriculture, effectively leading to wildland loss of more than two and a half per cent per year. If allowed to continue at current rates, pitaya habitat shrinking presents a major threat to the cultural practices and livelihoods of the Yoreme.

Link to paper: https://doi.org/10.1007/s13280-017-0940-8

CONSERVATION OF PLANT DIVERSITY BY BOTANIC GARDENS WORLDWIDE

DATA USED: 8,246,424 SPECIES OCCURRENCES
Mounce R, Smith P and Brockington S (2017) Ex situ conservation of plant diversity in the world's botanic gardens. Nature Plants. Springer Nature 3(10): 795–802.

Author country/area: United Kingdom
Research funding: Cambridge University Botanic Garden, National Environmental Research Council

Plants are the foundation for life on the planet and botanic gardens serve an important purpose in conserving plant diversity and preventing species extinction. Widely distributed worldwide, these gardens harbour thousands of species, but combined knowledge of their content and coverage is unclear.

In an analysis of world's botanic gardens, UK researchers identified 3,269 collections in 180 countries with known holdings of more than 105,000 plant species combined—corresponding to about 30 per cent of accepted species in The Plant List covering 93 per cent of all vascular plant families.

Based on GBIF-mediated occurrences, the authors determined the latitudinal ranges of held species and found a remarkable bias towards temperate species, counter to the natural gradient where most diversity is found in the tropics. Mapping combined collections against a phylogenetic tree of all accepted land plant genera revealed another striking bias as non-vascular lineages are almost completely undocumented.

These findings combined suggest a remarkable degree of worldwide coverage, but also points to gaps to be addressed for conservation in botanic garden collections.

Link to paper: https://doi.org/10.1038/s41477-017-0019-3

PROTECTING ENDEMIC PALMS OF THE AMAZON

DATA USED: 17,310 SPECIES OCCURRENCES

Alvez-Valles CM, Balslev H, Carvalho FA, Garcia-Villacorta R, Grandez C and Menini Neto L (2017) Endemism and conservation of Amazon palms. Biodiversity and Conservation. Springer Nature 27(3): 765–784.

Author countries/areas: Brazil, Denmark, Peru, United States
Research funding: PGECOL/UFJF, CAPES, OEA, GCUB

Widespread and abundant in the tropics and nearly absent in temperate regions, palms play important ecological roles as a food source, but also in supporting local communities with cultural and economic significance. The Amazon region is home to more than 120 endemic palm species, and recognizing the areas of palm endemism is important for conservation planning.

By plotting GBIF-mediated occurrences of palm species in the Amazon region, authors of a new study identified one and three-degree squares containing at least two distinct species—defining these as endemic areas—based on two different analytic approaches.

The highest level of palm endemicity appeared in the Peruvian Amazon with seven species, followed by the Andean sub-region with six species. Combining the results of the two analyses revealed two main endemic areas—a large one in Western Amazon and a smaller one in the Andean sub-region.

Among the species supporting the identified endemic areas, five species are endangered according to IUCN, however, the known distributions of these all fall outside current protected areas in the region.

Link to paper: https://doi.org/10.1007/s10531-017-1463-0

CONR: LARGE-SCALE, MULTISPECIES CONSERVATION ASSESSMENTS USING SPECIES OCCURRENCE DATA

DATA USED: 74,352 SPECIES OCCURRENCES

ⓐ **Dauby G, Stévart T, Droissart V, Cosiaux A, Deblauwe V, Simo-Droissart M, Sosef MSM, Lowry PP, Schatz GE, Gereau RE and Couvreur TLP (2017) ConR: An R package to assist large-scale multispecies preliminary conservation assessments using distribution data. Ecology and Evolution. Wiley 7(24): 11292–11303.**

Author countries/areas: Belgium, Cameroon, France, United States
Research funding: Fondation pour la Recherche sur la Biodiversite, Agropolis Fondation, Agence Nationale de la Recherche, Fonds De La Recherche Scientifique - FNRS

The IUCN Red List provides an authorative and comprehensive methodology for assessing the conservation status of a species. As yet, only a tiny fraction of known species have been assessed according to the Red List criteria, and tools for accelerating preliminary assessments are needed.

This paper introduces a new R package—ConR—for conducting large-scale, preliminary multispecies conservation assessments based on sets of species distribution data from e.g. GBIF. Using four functions operating on datasets of species occurrences, ConR returns estimates for extent of occurence (EOO), area of occupancy (AOO), number of locations—all main parameters of Red List criterion B—as well as a preliminary threat category with details of the subcriteria this is based on. If desired, ConR will return images visualizing the results graphically, useful for including in a formal submission to the IUCN.

Providing means of carrying out preliminary Red List assessments simulatanously for hundreds or even thousands of spieces, ConR is novel, timely tool for conservation communities.

Link to paper: https://doi.org/10.1002/ece3.3704

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