

Science Review

2019



An annual compilation of
research data uses enabled by



GBIF

Foreword

Demonstrating the power of free and open biodiversity data for all

GBIF-mediated data is everyone's data. It represents the accumulation of efforts—from small university collections to large, globally recognized museum research institutions, from citizen scientist initiatives run on smartphone to the latest metagenomic studies. The power of these efforts is compounded when data is brought together to be free and open for all to use.

The GBIF 2019 *Science Review* demonstrates some of the power of a community working together. Take, for example, a research project by Watcharamongkoi et al. at the University of Sheffield in the United Kingdom and funded by the Thailand government studied C₄ photosynthesis evolution (p. 23). They used nearly 15 million occurrence records from the GBIF network to investigate potential geographic boundary limits for C₄ photosynthetic plants. The impressive aspect is that these records came from 1,453 individual datasets, not just from large European and North American herbaria, but also from institutions in Benin, Colombia, Brazil, Estonia, Australia and Japan (<https://doi.org/10.15468/dl.krwqzk>). Global studies of this kind would not be possible without a GBIF.

This year's *Review* also highlights several key studies with broad societal implications that relied on similar uses of data from thousands of sources. Possibly the most important link revealed through our literature tracking programme this year is the role that GBIF-mediated data played in the biodiversity-related assessments of the latest Intergovernmental Panel on Climate Change Special Report. The report rightfully received a lot of media publicity for its high-profile call to action, though few will have known at the time that the report relies heavily on work (Warren et al.—see p. 28) based directly on the analysis of 385 million occurrences from more than 5,400 datasets from the GBIF network.

These global analyses will become more common with increasing amounts of data available through GBIF. Through our work to improve the culture and practice of research data citation, we aim to give credit to the organizations that share data and the professionals who perform the work. We are deeply grateful for all that you do.

JOE MILLER

GBIF Executive Secretary
July 2019

Cover photo:

Cribaria purpurea available at <https://www.gbif.org/occurrence/2006052851>. Photo taken by Ricardo Arredondo T. and published through GBIF.org via iNaturalist Research-grade Observations. Licensed under a Creative Commons Attribution-NonCommercial 4.0 International (CC BY-NC 4.0) license.

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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 supported and enabled by free and open access to biodiversity data from the GBIF network.

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 changing institutional journal subscriptions.

The comprehensive list of this year's uses (as well as current and previous ones) is separate 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 may have escaped our attention can write to us at communication@gbif.org.

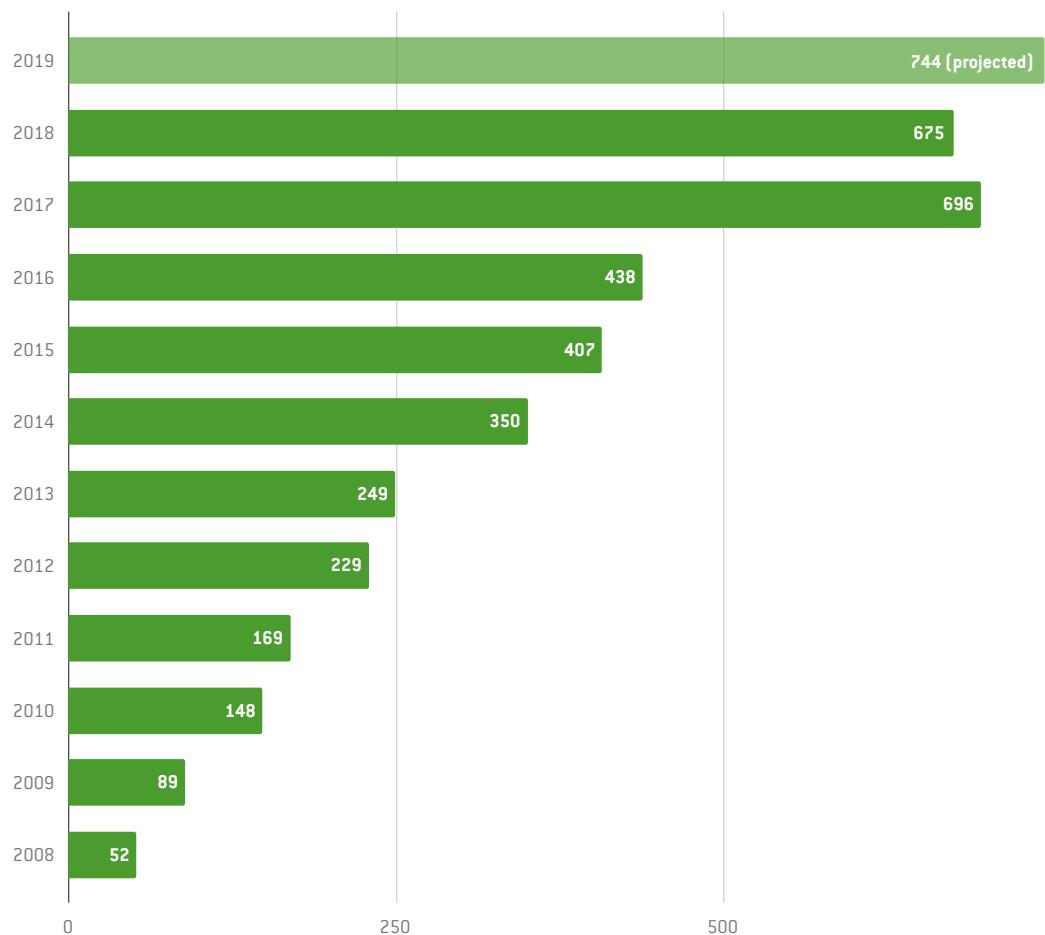
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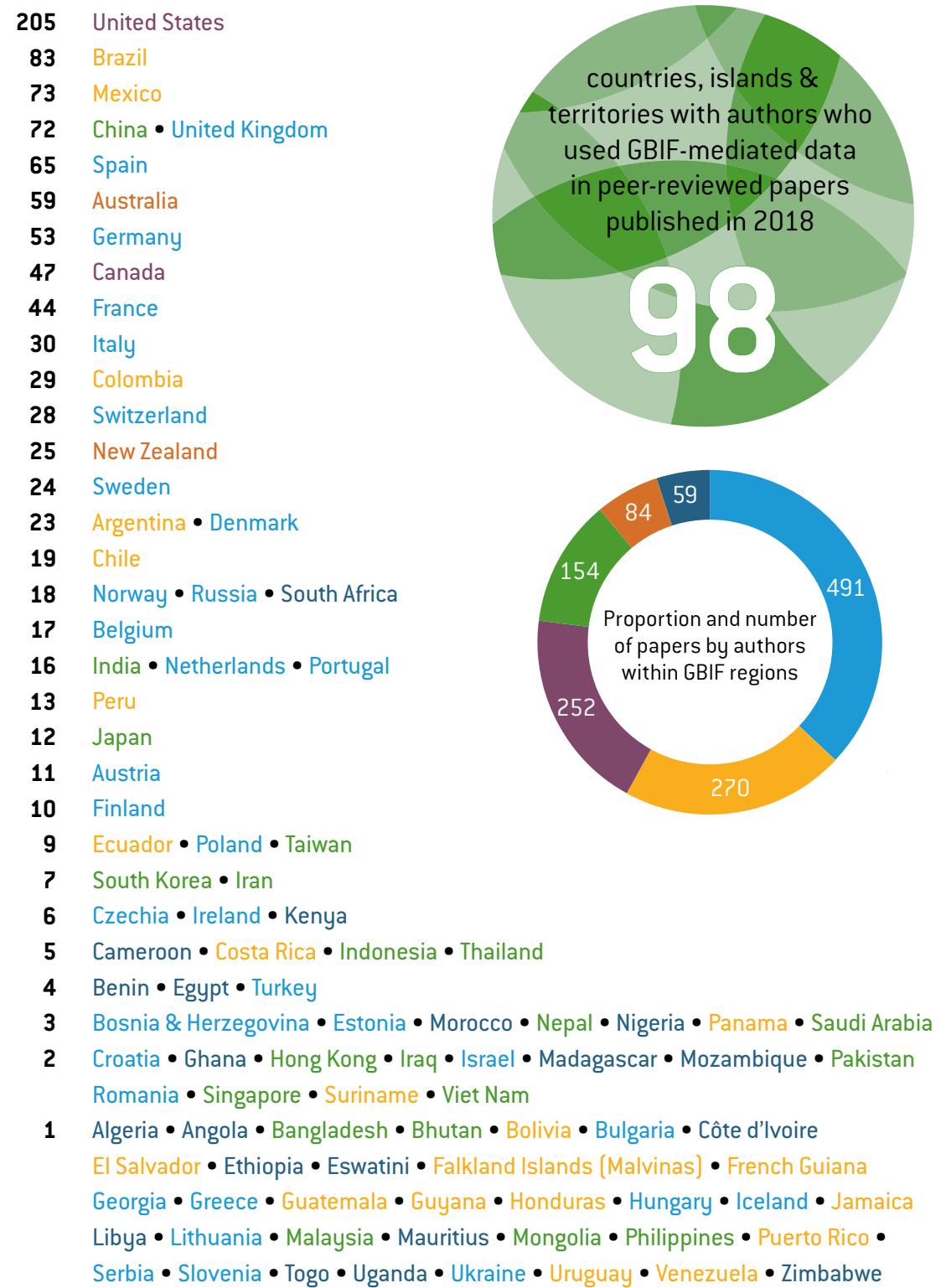
Uses and trends

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 geographic distribution of institutions hosting 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



NUMBER OF ARTICLES WITH AUTHORS BY COUNTRY/ISLAND/TERRITORY



Biodiversity and human health



PTEROPUS GIGANTEUS BY HEMANT KUMAR [HTTPS://WWW.GBIF.ORG/OCCURRENCE/1092888502](https://www.gbif.org/occurrence/1092888502) [CC BY-NC 4.0]

DATA STORY FLYING FOXES PREDICT NIPAH VIRUS TRANSMISSION RISK

DATA USED: 47,942 SPECIES OCCURRENCES

"We were in the process of submitting the final edits when the outbreak in Kerala took place. On the one hand, it's very exciting to see that you models can make accurate predictions, but knowing the consequences of these outbreaks puts an immediate dampener on your excitement."

—Mark Deka, CDC

In early May of 2018, Texas State University (TSU) alumnus Mark Deka submitted a study modelling Nipah virus (NiV) infection risk in South and Southeast Asia for publication in the journal *Tropical Medicine and Infectious Disease*. Part of his PhD, the paper had been in the works for nearly a year and a half.

Working in the area of medical geography, Mark—originally from Cleveland, Ohio—was interested in vector-borne diseases and the geospatial and geographic components of disease transmission.

"A lot of people don't realize the role of geography and spatial gradients in relation to distribution of

communicable diseases for hosts and susceptible populations", says Deka, who came to Texas in 2015 and started his career working on tick-borne diseases. It was during this time he started looking into using GBIF-mediated data for creating models for his research. This proved useful when he later turned to NiV research.

A relative of the Hendra virus that takes its name from the Malaysian village in which it was first isolated from pigs, the NiV causes encephalitis in infected organisms. Flying foxes (*Pteropus* sp.) are the presumed wildlife reservoir of NiV, and consumption of raw date palm (*Phoenix dactylifera*) sap contaminated with *Pteropus* urine or saliva is believed to be an important risk factor.

Mark's study combined biosurveillance data with GBIF-mediated *Pteropus* occurrences to create models mapping infection risk hot spots in South and Southeast Asia while identifying environmental features associated with increased risk.

"The data from GBIF.org played a huge role. While some people just build a single model to show human

transmission cases, we were interested in mapping the overlap between several models and also measuring it. The occurrence data for the flying foxes was very important, and there was a lot of it, too!"

The results of the study showed high risk of disease in a combined area of near 3 million sq. km, or 19 per cent of the total study area—including several risk hot spots in South India, in which no outbreak had previously occurred.

On 19 May 2018—within weeks of Mark and colleagues submitting their paper—the Indian Government's National Centre for Disease Control and the World Health Organization reported a NiV disease outbreak from Kozhikode district of Kerala, India—the first in South India. Within less than two weeks 18 people had contracted the disease and 17 were dead.

"We were in the process of submitting the final edits when the outbreak in Kerala took place. On the one hand, it's very exciting to see that your models can make accurate predictions, but knowing the consequences of these outbreaks puts an immediate dampener on your excitement."

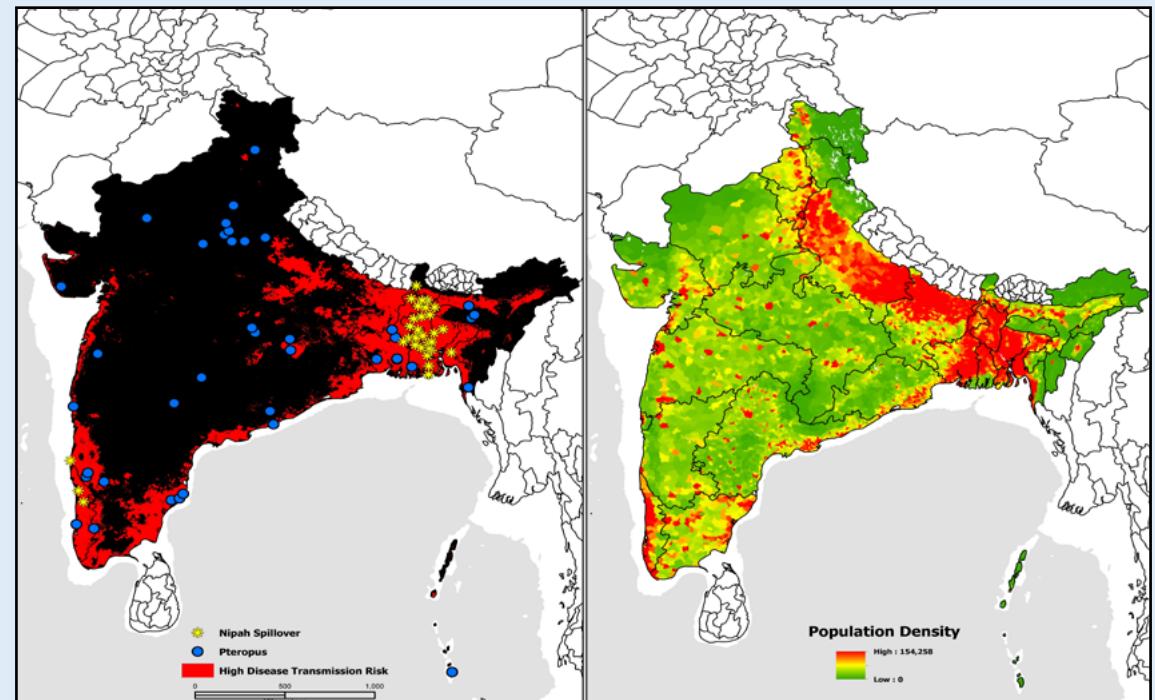
Since the study was published, Mark was approached by a vaccine consultant in Germany who wanted to understand if the results of the study could help them in their work.

"They're trying to develop a vaccine, figure out how many vaccines to develop and who to target. They were talking about vaccine stockpiles, but I had to explain that I am a geographer. I know nothing about vaccine stockpiles! I told them to target the people at highest risk—the people who work in date palm cultivation. If you're going to do a vaccine, target them first."

Having completed his PhD at TSU, Mark is now working for the Centers for Disease Control and Prevention (CDC) in Atlanta, Georgia, where he will be working on similar medical geography modelling with a focus on bacterial diseases.

a Deka M and Morshed N (2018) Mapping Disease Transmission Risk of Nipah Virus in South and Southeast Asia. *Tropical Medicine and Infectious Disease*. MDPI AG 3(2): 57. Available at: <https://doi.org/10.3390/tropicalmed3020057>

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



NIPAH VIRUS DISEASE TRANSMISSION RISK IN BANGLADESH AND INDIA WITH UPDATED HUMAN CASE LOCATIONS FROM MAY 2018.
FIGURE FROM DEKA M AND MORSHED N (2018) [HTTPS://DOI.ORG/10.3390/TROPICALMED3020057](https://doi.org/10.3390/TROPICALMED3020057) [CC BY 4.0]

MAPPING GLOBAL VULNERABILITY TO VENOMOUS SNAKEBITES

DATA USED: 51,952 SPECIES OCCURRENCES

ⓐ Longbottom J, Shearer FM, Devine M, Alcoba G, Chappuis F, Weiss DJ, Ray SE, Ray N, Warrell DA, Ruiz de Castañeda R, Williams DJ, Hay SI and Pigott DM (2018) Vulnerability to snakebite envenoming: a global mapping of hotspots. *The Lancet*. Elsevier BV 392[10148]: 673–684.

Available at:
[https://doi.org/10.1016/s0140-6736\(18\)31224-8](https://doi.org/10.1016/s0140-6736(18)31224-8)

Author countries/areas: Australia, Switzerland, United Kingdom, United States

Research funding: Bill and Melinda Gates Foundation

As many as 138,000 people die from venomous snakebites every year. Primarily affecting poor rural populations in Asia and sub-Saharan Africa, snakebite is an overlooked cause of mortality, also affecting livestock causing a burden on already impoverished communities.

Aiming to identify the most vulnerable populations at risk of snakebite, researchers mapped the distributions of 278 venomous snakes dangerous to humans, producing high resolution range maps for 179 species using GBIF-mediated occurrences. They further triangulated these data with metrics of antivenom availability, access to healthcare and efficacy of medical interventions.

While nearly seven billion people live within range of areas inhabited by snakes, the study identified 166 million living in areas with at least one venomous snake and more than 3 hours from urban centres with healthcare.

Within the lowest three deciles of healthcare quality, the authors highlight Angola, Pakistan, Indonesia, Ethiopia, and the Democratic Republic of the Congo as hotspots of vulnerable populations, with more than 92 million people at risk.

BITING AQUATIC INSECTS INVOLVED IN TRANSMISSION OF BURULI ULCER

ⓐ Cano J, Rodríguez A, Simpson H, Tabah EN, Gómez JF and Pullan RL (2018) Modelling the spatial distribution of aquatic insects [Order Hemiptera] potentially involved in the transmission of *Mycobacterium ulcerans* in Africa. *Parasites & Vectors*. Springer Nature 11[1]. Available at: <https://doi.org/10.1186/s13071-018-3066-3>

Author country/area: Cameroon, Spain, United Kingdom
Research funding: Bill and Melinda Gates Foundation

Rapidly emerging in West Africa, Buruli ulcer (BU), is the third most common mycobacteriosis in humans causing chronic debilitating disease, mainly affecting

the skin and sometimes bone.

Published in *Parasites & Vectors*, this study explores the distribution of biting aquatic insects, suggested as potential vectors of *Mycobacterium ulcerans*, the causative agent of the disease. Using GBIF-mediated occurrences of six hemipteran families combined with records from extensive literature searches, the authors produced ensemble consensus distributions mapping the potential ranges of the insect families.

By overlaying the predictive models and maps of BU-endemic communities, the study shows that all affected areas are suitable for at least one hemipteran family. In Cameroon, they show suitability for two families, whereas BU-areas in Ghana are suitable for all six investigated families.

Combined with existing pathophysiological knowledge, these findings strongly support considering the presence of biting aquatic insects as a risk factor in BU endemic areas.

REFINING TICK DISTRIBUTION MODELS USING HOST CONTACT RATES

DATA USED: 11,000,000 SPECIES OCCURRENCES

Estrada-Peña A, Adkin A, Bertolini S, Cook C, Crescio MI, Grosbois V, Horigan V, Ip S, Leger A, Mastrandio G, Maurella C, de Nardi M, Ru G, Simons R, Snary E, Staerk K, Taylor R and Smith GC (2018) Evaluating a mixed abiotic–biotic model for the distribution and host contact rates of an arthropod vector of pathogens: An example with *Ixodes ricinus* (Ixodidae). *Microbial Risk Analysis*. Elsevier BV. Available at: <https://doi.org/10.1016/j.mran.2018.12.001>

Author country/area: France, Italy, Spain, Switzerland, United Kingdom
Research funding: Ministry of Health (IT)

When modelling the distribution of a species of interest, covariates often include abiotic climatic measurements, such as temperature and precipitation. Interactions with other species, however, can also affect a species' distribution and should be considered.

One such interaction—between pathogen-carrying ticks and their vertebrate hosts—is the focus of this study in which researchers used remote-sensed environmental data combined with occurrence data sourced from GBIF and literature to assess the impact of host availability on the distribution of an arthropod vector—the castor bean tick (*Ixodes ricinus*), responsible for transmitting pathogens causing Lyme disease and tick-borne encephalitis.

Considering 29 rodents and 78 passerine birds the authors predict the highest contact rates between the tick and its hosts in large regions of Central Europe, UK and southern Scandinavia, while analysis of Artiodactyla (even-toed ungulates) revealed an even larger contact area, potentially suggesting a more important role as tick hosts.

MAPPING THE RISK OF SNAKEBITES IN ECUADOR

DATA USED: 9,111 SPECIES OCCURRENCES

ⓐ Yañez-Arenas C, Díaz-Gamboa L, Patrón-Rivero C, López-Reyes K and Chiappa-Carrara X (2018) Estimating geographic patterns of ophidism risk in Ecuador. *Neotropical Biodiversity*. Informa UK Limited 4[1]: 55–61. Available at:

<https://doi.org/10.1080/23766808.2018.1454762>

Author countries/areas: Mexico

Research funding: National Council of Science and Technology (MX)

Ophidism, the medical term for poisoning from snake venom, is a serious public health issue, especially in the tropics. While social and temporal aspects of snakebites have been studied, not much is known

about the geographic spread of snakebite risk.

With 39 venomous snakes, Ecuador's species richness is among the highest in the world. As assessments of actual bite rates are expensive at a large scale, this study takes a correlative approach, mapping the risk of snakebites by modelling GBIF-mediated occurrences of medically relevant species.

The models suggest a low risk in the central Andean region, while risk in the adjacent coastal and Amazonian regions is high, findings that confirm previous reports of snakebites. Applying these results to a map of local rural areas, the authors identified 187 densely populated communities with high risk of snakebites.

While the study doesn't use actual incidence data in the models, it represents significant progress in snakebite risk assessments. The authors call for the implementation of a national snakebite reporting system to improve understanding of the patterns of ophidism in Ecuador.



TROPIDOLAEMUS SUBANNULATUS BY DANOLSEN [HTTPS://WWW.GBIF.ORG/OCURRENCE/1847602565](https://www.gbif.org/occurrence/1847602565) (CC BY-NC 4.0)

Biodiversity data



PENICHLERIS AFFINIS BY PINCETCZY [HTTPS://WWW.GBIF.ORG/OCURRENCE/1993735848](https://www.gbif.org/occurrence/1993735848) [CC BY-NC 4.0]

BIOTIME: A DATABASE OF BIODIVERSITY TIME SERIES FOR THE ANTHROPOCENE

DATA USED: 446,726 SPECIES OCCURRENCES

a Dornelas M et al (2018) BioTIME: A database of biodiversity time series for the Anthropocene. *Global Ecology and Biogeography*. Wiley 27(7): 760–786. Available at: <https://doi.org/10.1111/geb.12729>

Author countries/areas: Australia, Belgium, Brazil, Canada, Chile, Colombia, Czechia, Denmark, Faroe Islands, Finland, Germany, Hong Kong, India, Israel, Italy, Lithuania, New Zealand, Norway, Poland, Portugal, Russia, South Africa, Spain, Sweden, Switzerland, Taiwan, Netherlands, United Kingdom, United States, Viet Nam

Research funding: California Department of Fish and Game, German Academic Exchange Service, National Council for Scientific and Technological Development (BR), Norwegian Research Council, Russell Sage Foundation, Wellcome Trust, Vulcan, Foundation for Research Support of the State of São Paulo, Research Support Foundation for the State of Rio de Janeiro, Department of Conservation (NZ), Natural Environment Research Council (UK), National Science Foundation (US), ArcticNet, H2020 European Research Council

One of the major challenges of our time is to monitor and measure changes in biodiversity, especially with a warming climate and other human-induced changes

to the natural environment. With recent evidence of alarming biodiversity losses, high quality biodiversity data is crucial.

To facilitate research in the area, a group of 271 scientists from 35 countries in the BioTIME consortium spent almost eight years collecting data on species abundance records for assemblages sampled over time with consistent methodologies.

Compiling data from 361 studies carried out from 1874 to 2016—some sourced from GBIF.org—BioTIME consists of more than eight million records across more than 547,000 unique locations spanning 21 ecoregions and covering 44,440 taxa. The full database is freely available for download in several formats.

Providing instructions on how to download and re-use the BioTIME database, the authors aim to encourage other researchers to interact with the data, contribute to future releases and also promote an improved data citation culture.

NODDB: A GLOBAL DATABASE OF ROOT-SYMBIOTIC PLANTS

DATA USED: 156,200,298 SPECIES OCCURRENCES

Tedersoo L, Laanisto L, Rahimlou S, Toussaint A, Hallikma T and Pärtel M (2018) Global database of plants with root-symbiotic nitrogen fixation: NodDB. *Journal of Vegetation Science*. Wiley 29(3): 560–568. Available at: <https://doi.org/10.1111/jvs.12627>

Author countries/areas: Estonia

Research funding: Estonian Science Foundation, Estonian Ministry of Education and Research, European Union

In the battle for nutrients some plants have evolved symbiotic relationships with microorganisms, such as mychorrhizal fungi and nitrogen(N)-fixing bacteria that provide water and minerals in return for sugars. This type of association is found in the roots of most legume species and is common in nitrogen-limited ecosystems.

Despite playing an important role in agroforestry soil fertility, data on N-fixation in plants is scattered. In this paper, researchers from Estonia compile and curate a new database of root-symbiotic plants based on several metastudies and databases. For each genus, they provide details of the microorganism involved in the mutualism and how many species that have positive reports of N-fixation. The database, NodDB, named after bacteria-containing root nodules, includes data on 590 verified genera and also 234 likely candidates based on phylogenetic relationships.

Using GBIF-mediated occurrences the authors demonstrate the richness of N-fixing plants relative to all vascular plants globally, showing the highest richness in savanna and semi-desert biomes, not surprisingly where N supply is most limited.

KNOWBR: MAPPING GEOGRAPHICAL VARIATION OF BIODIVERSITY SURVEY EFFORT

DATA USED: 137,809 SPECIES OCCURRENCES

Lobo JM, Hortal J, Yela JL, Millán A, Sánchez-Fernández D, García-Roselló E, González-Dacosta J, Heine J, González-Vilas L and Guisande C (2018) KnowBR: An application to map the geographical variation of survey effort and identify well-surveyed areas from biodiversity databases. *Ecological Indicators*. Elsevier BV 91: 241–248. Available at: <https://doi.org/10.1016/j.ecolind.2018.03.077>

Author countries/areas: Spain

Research funding: Spanish Ministerio de Ciencia e Innovación, Consejería de Educación, Ciencia y Cultura, Junta de Comunidades de Castilla-La Mancha

The apparent lack of occurrence of a given species doesn't necessarily reflect its actual absence, but could also be explained by insufficient survey effort.

Such unknown bias can lead to unreliable results in downstream analyses, if unaddressed.

This paper by Spanish researchers in Ecological Indicators presents KnowBR—a novel software that assesses survey completeness across a territory of interest. Taking unfiltered georeferenced data from a source of primary biodiversity information, KnowBR calculates the completeness of a geographical unit—a cell or a polygon, as defined by the user—based on slopes of species accumulation curves. This curve describes the relationship between number of species and the total number of records (a surrogate survey effort).

To demonstrate the tool, the authors used a download of all bees (superfamily Apoidea) from GBIF.org to assess survey completeness at a one degree resolution. Their analysis revealed both general scarcity and bias of data, showing that only 18 per cent of terrestrial cells have georeferenced data for bees and that only nine per cent of species have more than 10 records. The accumulation curve slopes were below 0.01 (i.e. one species per 100 records) in less than one per cent cells. The tool identified the highest number of well-surveyed cells western North America, central and northern Europe, as well as Australia.

PREDICTING WILDLIFE POPULATION TRENDS USING CITIZEN SCIENCE DATA

DATA USED: 822,459 SPECIES OCCURRENCES

a Callcutt K, Croft S and Smith GC (2018) Predicting population trends using citizen science data: do subsampling methods produce reliable estimates for mammals? *European Journal of Wildlife Research*. Springer Science and Business Media LLC 64(3). Available at: <https://doi.org/10.1007/s10344-018-1189-7>

Author countries/areas: United Kingdom

Research funding: None listed

Population trends are an important tool in wildlife management and conservation. However, obtaining data can be impractical and expensive. Citizen science observations on the other hand are growing, but can they be used to quantify changes in wildlife populations accurately?

Focused on terrestrial mammals in the United Kingdom, this study used GBIF-mediated occurrences of 33 species from two periods in time to calculate changes in populations. With increasing surveying efforts over time, the author used subsamples to normalize the data from the two periods.

While the predicted trends for some species were in agreement with other studies, more than 80 per cent

were inconsistent with population trends in published literature. The authors point to spatial clustering due to an increase in smartphone wildlife tracking as a possible cause.

In order to use citizen science data for predicting population trends, the study concludes that such biases must be addressed. The authors suggest normalization against higher taxa observations, an approach also employed in the GBIF-developed relative observation trends tool (<https://www.gbif.org/tools/observation-trends>).

BUSES AND HOTELS, NOT NATURAL WILDNESS, DRIVE WILDLIFE WATCHERS

DATA USED: 333,105 SPECIES OCCURRENCES

Mancini F, Coghill GM and Lusseau D (2018) Quantifying wildlife watchers' preferences to investigate the overlap between recreational and conservation value of natural areas. *Journal of Applied Ecology*. Wiley 56(2): 387–397. Available at: <https://doi.org/10.1111/1365-2664.13274>

Author countries/areas: United Kingdom
Research funding: University of Aberdeen

Offering physical and mental benefits to humans, recreation is a key cultural ecosystem service provided by nature. But what besides beauty and naturalness drives us to a specific destination for hiking and wildlife watching—and does conservation value translate into recreational value?

In this study, researchers from the University of Aberdeen used photographs posted to Flickr to quantify wildlife watching activities in Scotland. Combined with data on infrastructure, environment, protected areas, and species richness, as derived from GBIF-mediated occurrences, the authors analysed recreational activities at 10x10 km resolution to identify predicting variables.

Their results show that while wildlife watching is only slightly associated with the presence of a protected area, infrastructure, such as tourist accommodation and bus stations, plays a far larger role. In areas with good infrastructure, the most important predictor of wildlife watching is the number of species present.

The study shows that wildlife watchers in general prefer easily-accessible, highly transformed landscapes to wild ecosystems and protected areas.

AN UPDATED MAMMAL CHECKLIST OF ANGOLA

DATA USED: 15,782 SPECIES OCCURRENCES

Taylor PJ, Neef G, Keith M, Weier S, Monadjem A and Parker DM (2018) Tapping into technology and the biodiversity informatics revolution: updated terrestrial mammal list of Angola, with new records from the Okavango Basin. *ZooKeys*. Pensoft Publishers 779: 51–88. Available at: <https://doi.org/10.3897/zookeys.778.25964>

Author countries/areas: Eswatini, South Africa
Research funding: National Geographic Society

One of the most recent members of the GBIF network, Angola, has been largely overlooked in recent surveys of mammals. Researchers responsible for the ambitious African Mammal Project carried out in the 1960s and 70s by the Smithsonian Institution did not even go to Angola. Due to the late 20th century period of civil war, mammalian research in the country was also largely neglected.

To redress this, a new study compiles all available mammalian records in Angola from GBIF and published literature. In addition, the authors add records from two bat surveys and a camera-trapping survey of larger mammals—both carried out between 2013 and 2017 in the poorly surveyed Okavango River catchment area of the Angolan central highlands.

GBIF-mediated records covered 245 species while records from the literature and the field work added 30 species, totalling 275 mammals, an increase of 52 species since the latest exhaustive survey from 1941. New species added include rusty pipistrelle (*Pipistrellus rusticus*), lesser dwarf shrew (*Suncus varilla*), Setzer's mouse (*Mus setzeri*) and Woosnam's broad-faced mouse (*Zelotomys woosnami*).

ASSESSING THE COVERAGE AND QUALITY OF GLOBAL TREE OCCURRENCE DATA

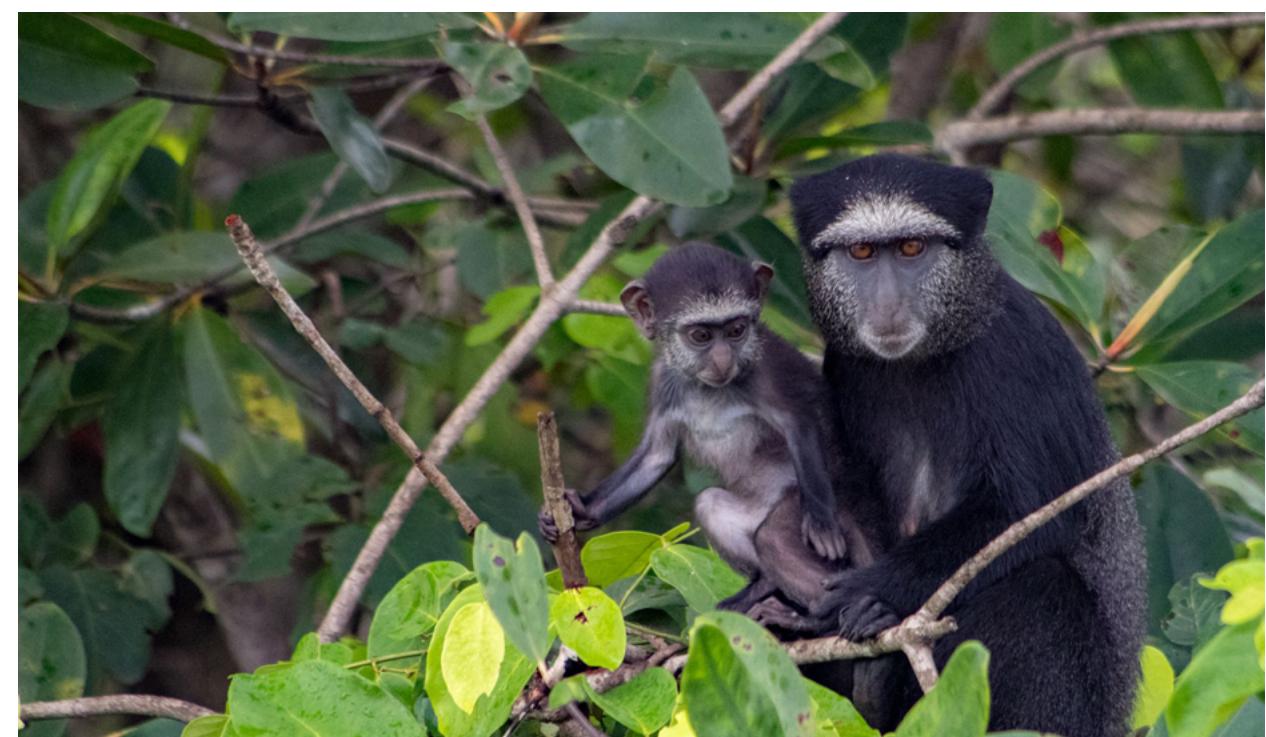
DATA USED: 36,000,000 SPECIES OCCURRENCES

a Serra-Diaz JM, Enquist BJ, Maitner B, Merow C and Svensson J-C (2017) Big data of tree species distributions: how big and how good? *Forest Ecosystems*. Springer Nature 4(1). Available at: <https://doi.org/10.1186/s40663-017-0120-0>

Author countries/areas: Denmark, United States
Research funding: Danish Council for Independent Research, US Division of Biological Infrastructure

Around 60,000 species of trees are known and thanks to researchers, museums, herbaria and citizen science programmes, a very large amount of primary biodiversity data exists on the world's tree populations.

This study sets out to assess the geographical coverage and quality of available tree occurrence



CERCOPITHECUS MITIS BY LUIS QUERIDO [HTTPS://WWW.GBIF.ORG/OCURRENCE/1831227285](https://www.gbif.org/occurrence/1831227285) [CC BY-NC 4.0]

data from five major aggregators, including GBIF. The authors develop a workflow to integrate and control data quality of species occurrences intended for species distribution modelling.

They identify 49,206 species in the data, representing almost 85 per cent of all known species. Among the 36 million occurrence records, 17 per cent are deemed high quality, however, only 15,140 species have enough high quality records to perform species distribution modelling. The majority of quality concerns among remaining records relate to duplicates and lacking coordinates.

The study finds that spatial coverage is high in Europe, North America and Australia, while large gaps still exist in key biodiverse regions such as South-East Asia and central Africa.

INTEGRATING KNOWLEDGE OF TERRESTRIAL MAMMALS OF MOZAMBIQUE

DATA USED: 6,607 SPECIES OCCURRENCES

a Neves IQ, Da Luz Mathias M and Bastos-Silveira C (2018) The terrestrial mammals of Mozambique: Integrating dispersed biodiversity data. *Bothalia*, 48(1). AOSIS. Available at: <https://doi.org/10.4102/abc.v48i1.2330>

Author countries/areas: Portugal
Research funding: None listed

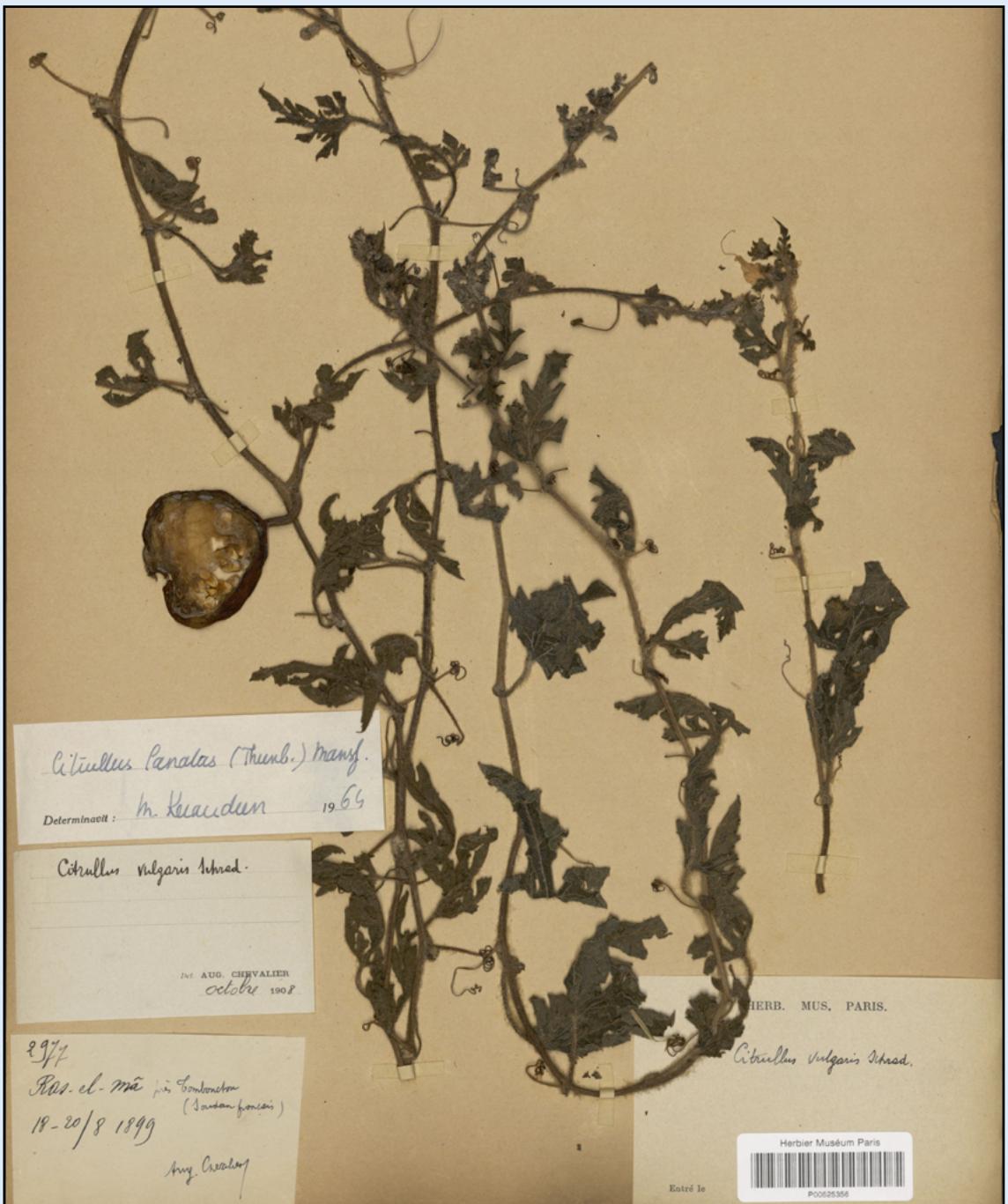
A comprehensive synopsis of mammals in Mozambique was published in 1976 listing 190 terrestrial species. Up-to-date knowledge of biodiversity is, however, important to conservation and management efforts, and political instability in the country during previous decades has made progress difficult.

Aimed at contributing to a more profound knowledge of Mozambican fauna, researchers compiled and curated more than 17,000 occurrence records from GBIF, national history museums, survey reports and literature to create an updated checklist of terrestrial mammalian species in the country.

They categorized species by number of observations and also collectors/observers to distinguish questionable occurrences. Their final list contains 217 species—from 14 orders, 39 families and 133 genera—accounting for 71 per cent of all species in southern African region.

While estimating total richness, the authors predict that their checklist is 93.5 per cent complete. When compared to neighbouring countries, however, they acknowledge that there might still be a considerable number of species unaccounted for, suggesting a need for further surveys, especially among lesser-known groups.

Biodiversity science



CITRULLUS LANATUS BY A.J.B. CHEVALIER [HTTPS://WWW.GBIF.ORG/OCURRENCE/436974457](https://www.gbif.org/occurrence/436974457) [CC BY 4.0]

DATA STORY LEARNING FROM—AND WITH—THE MACHINES: TAXON AND TRAIT RECOGNITION FROM HERBARIUM SCANS

DATA USED: 830,408 SPECIMEN IMAGES

"To our knowledge, this is the first study to deal with several traits in a large number of taxa, implying more abstraction in the concept of a trait and variability within a trait to be recognized."

—Younis et al. 2018

Advances in artificial intelligence (AI) are rapidly enabling new, innovative uses across the biodiversity informatics community. Examples of machine-learning technology used in the biodiversity observation network iNaturalist.org and other tools offer now-familiar examples of how computers can use image recognition to improve real-time species identification across wide-ranging taxonomic groups.

The application of deep learning on natural history collections represents an even more recent development, but a German-Saudi team led by Sohaib Younis of Senckenberg Research Institute has tied together numerous strands of investigation that highlight the potential for machine learning to increase our understanding of life on Earth.

The research taps one of the largest online collections of labelled species images: the GBIF species occurrence index, which contains more than 44 million records associated with at least one image (<https://www.gbif.org/occurrence/gallery>). While an increasing number of photos come from citizen scientists through automated species-recognition suggestions, about three quarters of them—more than 30 million—come from the world's natural history collections.

Younis and his co-authors focused on these herbarium scans as a first step in crafting this thoughtfully designed study. Recognizing that existing taxon recognition systems currently work best for the taxa of North America and Europe, they chose to concentrate on the plant taxa of Africa, downloading 830,408 images for the 1,000 most-scanned species. This element of the approach could bring the added benefit of improving taxon recognition for a region that needs additional taxonomic resources and expertise.

By capitalizing on rapid improvements in pattern-recognition algorithms, the authors sought to expand their deep-learning analysis to go beyond taxonomic recognition and explore a deep-learning system's ability to recognize morphological traits from herbarium scans. Extracting a subset of more than 150,000 images of 170 species for which trait data was available, this portion of the machine-based analysis settled on examining a limited set of 19 leaf traits (related to leaf arrangement, structure, form,

margin and venation) believed to be identifiable in herbarium scans.

As in other machine-learning analyses, systematic pre-processing plays a critical role in preparations. Cropping and reducing the downloaded images to a standard size—here, just 292 by 196 pixels—prepares them for image analysis and eliminates elements like colour bars, labels and handwritten annotations that only serve as background noise to the machines.

In results the authors deem 'promising', taxon recognition from herbarium specimens proved 'very efficient', with 96.3 percent accuracy based on the analysis's top five predictions. While the approach 'on average also performed well for traits,' there's room for further study. For example, sample size fails to explain why the machines find it more difficult to identify generalized traits than taxon-specific patterns—something that's directly opposed to humans, who can recognize an individual trait much more easily than they can correctly identify a species.

This last finding highlights the fact that unanticipated gaps remain between human and machine forms of understanding. Automating species and trait recognition from diverse collections offers an auspicious method for supporting and enriching the ongoing work of collections digitization, but cultural norms and practices tend to trail behind the capabilities of the latest technological advances. How we can best integrate them with their respective shortcomings?

The 2018 Montreal Declaration for a Responsible Development of Artificial Intelligence (<https://www.montrealdeclaration-responsibleai.com/the-declaration>) notes that "numbers cannot determine what has moral value, nor what is socially desirable." Like this study's research team, the biodiversity informatics community can expect to face choices about how best to design and engage deep-learning tools while striving toward ethically responsible and socially desirable outcomes.

Younis S, Weiland C, Hoehndorf R, Dressler S, Hickler T, Seeger B and Schmidt M (2018) Taxon and trait recognition from digitized herbarium specimens using deep convolutional neural networks. *Botany Letters*. Informa UK Limited 165(3–4): 377–383. Available at: <https://doi.org/10.1080/23818107.2018.1446357>

Author country/area: Germany, Saudi Arabia

Research funding: German Research Foundation, National Multiple Sclerosis Society (Michigan Chapter)

PRIMARY BIODIVERSITY INFORMATION: THE SHIFT FROM SPECIMENS TO OBSERVATIONS

DATA USED: 649,767,741 SPECIES OCCURRENCES

Troudet J, Vignes-Lebbe R, Grandcolas P and Legendre F (2018) The Increasing Disconnection of Primary Biodiversity Data from Specimens: How Does It Happen and How to Handle It? *Systematic Biology*. Oxford University Press [OUP] 67(6): 1110–1119.

Available at: <https://doi.org/10.1093/sysbio/syy044>

Author country/area: France

Research funding: Ministère de la Recherche

The majority of species occurrences available from GBIF.org represent either a physical specimen or sample, typically stored in a museum or herbarium, or an observation, often by citizen scientists accompanied by an image, sound or video recording. While the first records to be published in GBIF came from museums, observations now make up more than 80 per cent of all species occurrences in GBIF.

Examining the consequences of this shift in recording biodiversity data, Troudet and colleagues downloaded all occurrences from GBIF.org available in June 2016 and analysed developments across 24 taxonomic classes. As expected, the shift from predominantly specimen-based to observation-based reflects an exponential growth in species observation data recently and relatively low growth in specimen-based records.

The shift, however, doesn't imply a lack of quality, as records with low spatial precision decreased from 50 per cent in 1900 to 0.6 per cent in 2014, while species-level identification increased from 86 to 99 per cent over the same period.

The authors argue that the increase in general availability of primary biodiversity data is on one hand good, but unless recording practice is expanded to include more data and physical evidence, its potential use will be limited to ecological studies, preventing deeper insights into systematics and evolution.

CLASSIFYING CRICKETS' CHIRPS: ACOUSTIC PROFILING IN ORTHOPTERA

DATA USED: 16,900 SPECIES OCCURRENCES

Riede K (2018) Acoustic profiling of Orthoptera: present state and future needs. *Journal of Orthoptera Research*. Pensoft Publishers 27(2): 203–215.

Available at: <https://doi.org/10.3897/jor.27.23700>

Author country/area: Germany

Research funding: None listed

Allowing for non-invasive and cheap detection of elusive species, identifying animals through

sound, especially birds and frogs, is becoming increasingly popular, particularly in habitats where visual observation is difficult or even impossible. In December 2018, the addition of Xeno-canto—a long-term collaborative bird song project—doubled the number of audio-enabled records in GBIF.

In a new article, a researcher from Germany reviews the current state of acoustic profiling of another group of singers: Orthoptera, known for the sounds produced by rubbing wings and/or legs together. While this insect order of grasshoppers, locusts and crickets has many species with specific songs reliable for classification, availability and accessibility of Orthoptera song recordings in general is extremely limited.

In GBIF, Orthoptera occurrence records with associated audio derive mainly from the Zoological Research Museum Alexander König—in particular DORSA (Digitized Orthoptera Specimens Access)—but also the Borror Lab of Bioacoustics (BLB) at Ohio State University. While Orthoptera records with sound are scarce compared to vertebrates, the number of available records has increased by more than 50 per cent since the publication of the article.

The author points to passive acoustic monitoring as a potential means of increasing sound data available, but this will require a data warehouse for bioacoustic data. Automatic classification and identification of records may necessitate novel acoustic profiling algorithms, or existing methods already employed in human speech recognition may be the way forward.

REFINED ECOLOGICAL NICHE MODELS FOR MEXICAN PRIMATES

Calixto-Pérez E, Alarcón-Guerrero J, Ramos-Fernández G, Dias PAD, Rangel-Negrín A, Améndola-Pimenta M, Domingo C, Arroyo-Rodríguez V, Pozo-Montuy G, Pinacho-Guendulain B, Urquiza-Haas T, Koleff P and Martínez-Meyer E (2018) Integrating expert knowledge and ecological niche models to estimate Mexican primates' distribution. *Primates*. Springer Nature 59(5): 451–467.

Available at: <https://doi.org/10.1007/s10329-018-0673-8>

Author country/area: Mexico, Spain

Research funding: National Council of Science and Technology (MX), National Polytechnic Institute (MX)

Ecological niche modelling can predict the potential area in which a species is likely to occur, however, as these derive mainly from climatic and topographic features, they may overestimate the distribution of a species.

To improve otherwise controversial knowledge on the distribution of primates in Mexico, authors of this study combined ecological niche models—using GBIF-mediated data—with specific expert ecological and historical knowledge of the three relevant taxa: *Ateles geoffroyi*, *Alouatta pigra*, and *Alouatta palliata* subsp. *mexicana*. Integrating expert knowledge at different steps of the modelling procedure, they produce new, refined distribution maps, while assessing the performance of the models both with and without expert contribution.

Not surprisingly, the non-expert modeled distribution areas were much larger than those refined by expert knowledge. While the resulting maps are important resources for prioritizing conservation efforts, the transparency of the underlying methodology can help avoid experiences of bias involved with including expert knowledge in ecological niche modelling everywhere.

ON THE EVOLUTION OF FOOD CUSTOMS

van Erp M, Wevers M and Huurdeeman H (2018) Constructing a Recipe Web from Historical Newspapers. *Lecture Notes in Computer Science*. Springer International Publishing, 217–232. Available at: https://doi.org/10.1007/978-3-030-00671-6_13

Author country/area: Germany
Research funding: None listed

The way we eat and think about food is a part of our culture and a product of our time. Today, you can find even the most obscure recipe simply by going online. Before the internet, newspapers and magazines were an important source of culinary inspiration, and by going back in time these can provide valuable insights into the evolution of food customs.

In this paper, researchers from Amsterdam extract and structure recipes found in Dutch newspapers published between 1945 and 1995. Relying on digitized and OCR'd (Optical Character Recognition) text from the National Library of the Netherlands, they use machine learning methods to construct a historical database of more than 27,000 recipes. To enrich the data, their workflow separates and tags



OECANTHUS NIGRICORNIS BY EDGARALLENHOOPOE [HTTPS://WWW.GBIF.ORG/OCURRENCE/1668809618](https://www.gbif.org/occurrence/1668809618) [CC BY-NC 4.0]

quantities, units and ingredients. Using GBIF-mediated data, they even match naturally sourced ingredients against scientific names and determine their origin.

Combining language processing, machine learning and semantic structuring, this work provides a valuable source of data on food culture. One example of a changing concept is how some vegetarian recipes often contained animal products (e.g. chicken broth and fermented shrimp). The authors, however, leave the actual interpretation of the results to humanities researchers, as the code and resulting database are available for anyone to use, browse and analyse.

SHORTLISTING PLANT TAXA FOR IDENTIFICATION USING NEARBY OCCURRENCE RECORDS

DATA USED: 27,969,662 SPECIES OCCURRENCES

ⓐ Wittich HC, Seeland M, Wäldchen J, Rzanny M and Mäder P [2018] Recommending plant taxa for supporting on-site species identification. *BMC Bioinformatics*. Springer Science and Business Media LLC 19(1).

Available at: <https://doi.org/10.1186/s12859-018-2201-7>

Author country/area: Germany

Research funding: Federal Ministry of Education and Research (DE), Federal Ministry for the Environment, Nature Conservation, Building and Nuclear Safety (DE)

Being able to accurately identify a species is the basis of numerous disciplines within biodiversity science, and increasingly also for citizen scientists using their smartphones for observing and recording occurrences in nature.

This study by bioinformatics researchers in Germany evaluates the feasibility of generating ranked shortlists of plants likely to be encountered by an observer at a given location—based on already reported observations through GBIF and national range maps of ~2,700 taxa. The idea being: the fewer potential candidates, the simpler the identification.

The authors test the methodology on a set of 28,000 plant photos from Flickr, each tagged with the name of the taxa in question and coordinates of where the photo was taken. By combining the range maps and occurrence data, they were able to include the correct species in a shortlist in 86 per cent of the photos.

Overall, the approach proved successful in significantly reducing the number of species to be considered when making an identification. The performance of such methods will only improve as more species occurrences are added to GBIF.

TRACKING INSECT MIGRATIONS USING POLLEN METABARCODING

Suchan T, Talavera G, Sáez L, Ronkier M and Vila R [2018] Pollen metabarcoding as a tool for tracking long-distance insect migrations. *Molecular Ecology Resources*. Wiley 19(1): 149–162.
Available at: <https://doi.org/10.1111/1755-0998.12948>

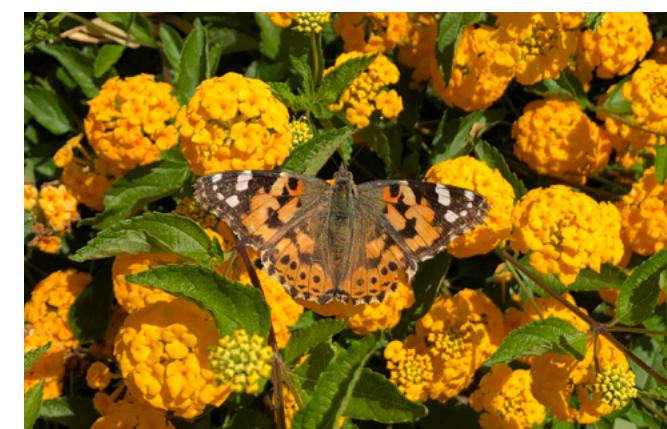
Author country/area: Poland, Spain, United States
Research funding: Ministry of Economy and Competitiveness (ES), British Ecological Society, Polish Academy of Sciences, European Commission Seventh Framework Programme, National Geographic Society

Migration with changing seasons is a well-known and studied phenomenon in birds, but little is known about insect migrations as small organism movements are significantly more difficult to track.

Feeding on flowers, insects can carry pollen deposited on their bodies across long distances. This study proposes a novel approach to studying insect migrations by pollen metabarcoding. By capturing painted lady butterflies (*Vanessa cardui*) landing on the Mediterranean coast of Spain, researchers obtained pollen carried by the insects and sequenced the DNA, targeting a specific ribosomal sequence.

Using GBIF-mediated occurrences the authors determined the geographic distributions of all detected plants, highlighting the species not apparently overlapping with the sampling sites. They found DNA of 40 plants not known to occur where the butterflies were caught.

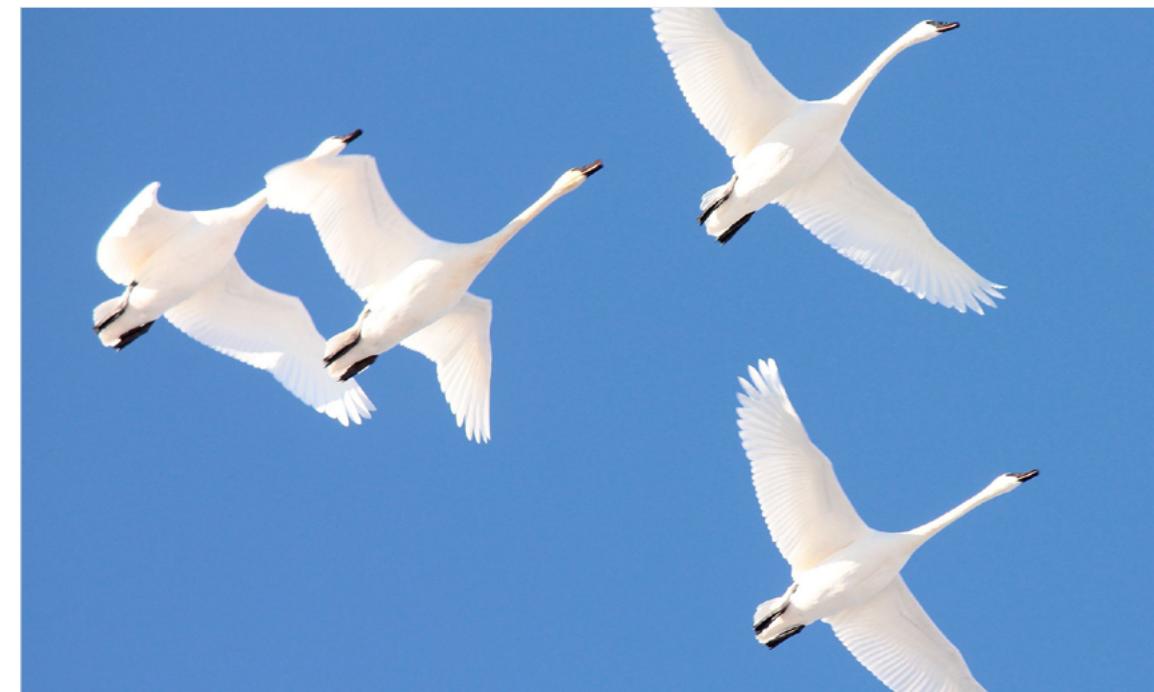
By mapping extent of all alien plant distributions combined with recent wind trajectories in the area, the researchers predict migration routes from Africa originating in a much larger range than previously believed.



VANESSA CARDUI BY SHD1998
[HTTPS://WWW.GBIF.ORG/OCURRENCE/2269313136](https://www.gbif.org/occurrence/2269313136) (CC BY-NC 4.0)

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DO YOU BELIEVE IN OPEN BIODIVERSITY DATA?



CYGNUS BUCCINATOR BY KARRIN [HTTPS://WWW.GBIF.ORG/OCURRENCE/1315046432](https://www.gbif.org/occurrence/1315046432) (CC BY-NC 4.0)

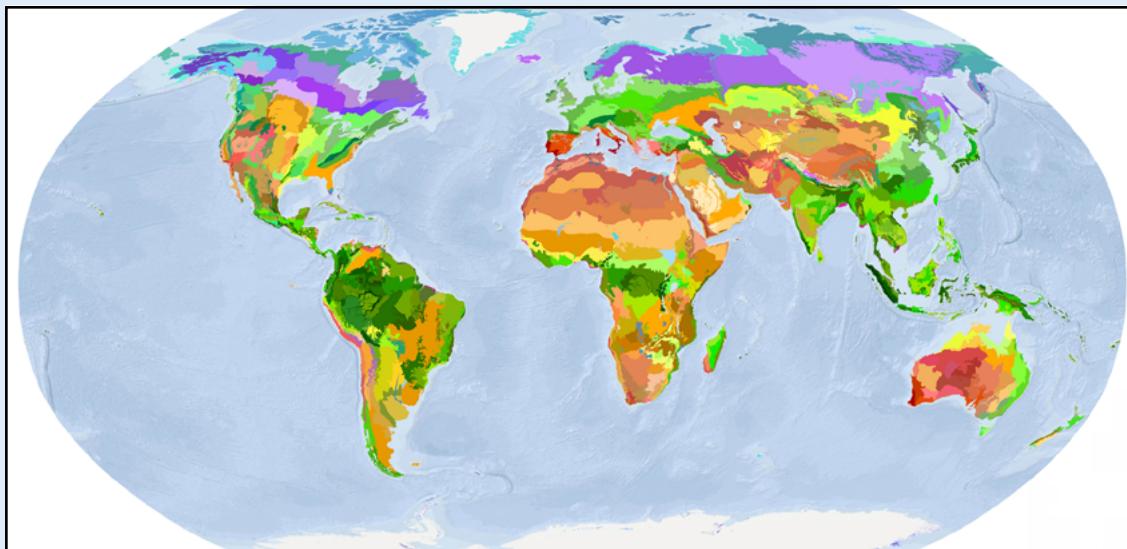
- You can provide at least one example in which you have shared biodiversity data through GBIF, used GBIF-mediated data, and/or advocated open data in your professional capacity
- You agree with the ICSU-World Data System Data Sharing Principles—in short, that data should be shared openly in a timely manner, with the fewest restrictions possible and used with proper citation
- You agree to share your contact information on GBIF.org, and possibly on websites run by GBIF nodes and partners
- You allow the GBIF Secretariat and GBIF nodes to contact you about opportunities to promote open biodiversity data at specific events
- You commit to providing details annually about at least one event, publication or process in which you have advocated for open biodiversity data

If you can check all of the above, then maybe you're the next **Biodiversity Open Data Ambassador!**

For more information about the programme and how to apply, please visit

<http://bit.ly/bodamba>

Ecology, evolution, behaviour and systematics



SERVED AS THE BASIS OF THE STATISTICAL ANALYSIS IN SMITH ET AL. 2018, THE LATEST EXPERT-LED REFINEMENT OF A GLOBAL MAP OF ECOREGIONS DEVELOPED AS PART OF THE PROPOSED GLOBAL DEAL FOR NATURE HAD ITS APPROACH VALIDATED BY THE RESEARCH. FIGURE FROM DINERSTEIN ET AL [2017] [HTTPS://DOI.ORG/10.1093/BIOSCI/BIX014](https://doi.org/10.1093/biosci/bix014) (CC BY 4.0)

DATA STORY USING SPECIES OCCURRENCE DATA AS EVIDENCE TO TEST RECEIVED BIOGEOGRAPHIC WISDOM

DATA USED: 200 MILLION SPECIES OCCURRENCES

The idea that well-defined physiographical regions both shape and define distinct groupings of species has formed a central tenet of biological sciences since Alexander von Humboldt and Alfred Russel Wallace first offered their own closely observed insights on the distribution patterns of plants and animals.

Given our current ecological and evolutionary processes, these ‘natural’ boundaries seem like an intuitively accurate way of describing patterns of biological communities. But even as biogeographic research has evolved into an increasingly computational discipline, Humboldt and Wallace’s scientific heirs haven’t challenged such concepts, tending instead to accept the validity of ecoregions on faith—or, at most, organizing new efforts by experts to refine and adjust proposed boundaries and classifications.

Stanford PhD candidate Jeffrey Smith represents the next generation of biogeographers. Armed with emerging statistical tools and libraries, massive computing power and big data in the form of 200 million occurrence records from the GBIF network,

he and his co-authors sought to use species-level evidence to weigh the validity of the ecoregion concept by asking the question:

Do ecoregion borders represent meaningful delineations between distinct biotic communities?

Despite Smith’s self-effacing description of the paper’s origins as “the result of serendipity, sarcastic comments, snacks, beer, and friends” (<https://go.nature.com/2OrSTNW>), this data-driven test was no idle pastime. Species protection, conservation planning, habitat restoration and other applied natural-resource disciplines all depend to a large extent on the validity of ecoregions as a framework for organizing and prioritizing large-scale on-the-ground actions.

To take just one high-profile example: the paper describing the proposed Global Deal for Nature (GDN: <https://doi.org/10.1093/biosci/bix014>) as a companion to the Paris Climate Agreement in 2017

is explicitly titled: “An Ecoregion-Based Approach to Protecting Half the Terrestrial Realm.” Smith and his co-authors use this latest expert-led refinement of a spatially explicit global map of ecoregions, even as they hint at the stakes involved putting the map to its first statistical test: “Despite the recognized value of categorically defined ecoregions in the development of modern biodiversity science, it is possible that they are obsolete and may even misinform research and conservation efforts.”

The experiment is elegant and, unlike many studies based on linear regression analyses and species accumulation curves, translates easily into a simple story. Like a naturalist haphazardly recording the location and identity of species they encounter on an unplanned hike, the computer model used in the study produced random but rule-based transects, painstakingly plotting occurrence data for plants, arthropods, birds, mammals, reptiles, amphibians and fungi from the GBIF network through the GDN ecoregional map, 10-km² pixel by pixel.

The analysis serves to compare two competing hypotheses regarding how many new species the model (and the naturalist) would observe as they meander indiscriminately through the landscape. The sharp-transition hypothesis predicts that the rate of observing novel species would rapidly increase upon entering a new ecoregion, while the gradual-transition hypothesis assumes little or no change in the rate of species discovery when moving within or between ecoregions. A result favouring the latter would point to relatively permeable ecoregion boundaries, calling into question their validity and use.

However, tabulating results for where and how often the model found new species, the authors found that ecoregion boundaries are better predictors of the biogeographic patterns of species accumulation than random species accumulation by distance. While the strength of the connection varies by taxa—particularly (though perhaps not unexpectedly) in the case of fungi—the results show ecoregion borders as areas of rapid species turnover, a conclusion that aligns with the sharp-transition hypothesis and generally confirms the notion that ecoregions reflect and reveal underlying evolutionary and ecological processes.

The conclusions drawn in Smith et al. 2018 offer validation that the GDN authors welcomed in their detailed follow-up on guiding principles, milestones and targets (<https://doi.org/10.1126/sciadv.aaw2869>) and provide fertile ground for additional research, like investigating the relationship between global ecoregions and phylogeny (cf. <https://doi.org/10.1111/cla.12381>).

Smith JR, Letten AD, Ke P-J, Anderson CB, Hendershot JN, Dhami MK, Diott GA, Grainger TN, Howard ME, Morrison BML, Routh D, San Juan PA, Mooney HA, Mordecai EA, Crowther TW and Daily GC (2018) A global test of ecoregions. *Nature Ecology & Evolution*. Springer Nature 2(12): 1889–1896. Available at: <https://doi.org/10.1038/s41559-018-0709-x>

Author country/area: Canada, New Zealand, Switzerland, United States

Research funding: None listed

AMENDMENTS

<https://doi.org/10.1038/s41559-019-0858-6>

**nature
ecology & evolution**

Author Correction: A global test of ecoregions

Jeffrey R. Smith , Andrew D. Letten , Po-Ju Ke , Christopher B. Anderson, J. Nicholas Hendershot, Manpreet K. Dhami, Glade A. Diott, Tess N. Grainger, Meghan E. Howard, Beth M. L. Morrison, Devin Routh, Priscilla A. San Juan, Harold A. Mooney, Erin A. Mordecai, Thomas W. Crowther and Gretchen C. Daily

Correction to: *Nature Ecology & Evolution* <https://doi.org/10.1038/s41559-018-0709-x>, published online 05 November 2018.

The original paper was published without unique DOIs for GBIF occurrence downloads. These have now been inserted as references 70–76, and the error has been corrected in the PDF and HTML versions of the article.

SMITH ET AL. FURTHER DEMONSTRATED THEIR COMMITMENT TO BEST PRACTICES IN OPEN SCIENCE BY PROMPTING THE JOURNAL TO PUBLISH AN AUTHOR CORRECTION ([HTTPS://DOI.ORG/10.1038/S41559-019-0858-6](https://doi.org/10.1038/s41559-019-0858-6)) THAT ADDS CITATIONS FOR DOWNLOAD DOIS OF SOURCE DATA FROM THE GBIF NETWORK.

MOLECULAR EVOLUTION IS SLIGHTLY FASTER IN THE TROPICS

DATA USED: 714,807 SPECIES OCCURRENCES

Orton MG, May JA, Ly W, Lee DJ and Adamowicz SJ [2018] Is molecular evolution faster in the tropics? *Heredity*. Springer Nature 122(5): 513–524. Available at: <https://doi.org/10.1038/s41437-018-0141-7>

Author countries/areas: Canada

Research funding: Natural Sciences and Engineering Research Council of Canada

Biodiversity increases as one moves closer to the equator—a phenomenon known as the latitudinal diversity gradient. Researchers have proposed the evolutionary speed hypothesis (ESH) as a possible underlying mechanism—explained by shorter generation times, higher mutation rates and/or faster rate of selection in the tropics. But is molecular evolution actually faster in the tropics?

In a new comprehensive study, researchers from Ontario, Canada analysed and aligned DNA barcode sequences of the mitochondrial-encoded *Cytochrome c oxidase subunit I* (COI) gene for 8,000 members of six of the largest animal phyla. They then paired closely related lineages exhibiting a difference of at least 20 degrees in median latitude as validated by GBIF-mediated occurrences and compared rates of evolution.

While the researchers only found a weak trend of higher rates in lower-latitude (51.6 per cent) vs higher-latitude (48.4 per cent) lineages, the difference was statistically significant. Some phyla, e.g. Chordata and Echinodermata, displayed stronger associations, significant even when correcting for multiple testing. So—is molecular evolution faster in the tropics? Yes, but not by much.

CLIMATIC NICHE EVOLUTION FASTER IN WARM-BLOODED VERTEBRATES

DATA USED: 294,704,442 SPECIES OCCURRENCES

Rolland J, Silvestro D, Schlüter D, Guisan A, Broennimann O and Salamin N [2018] The impact of endothermy on the climatic niche evolution and the distribution of vertebrate diversity. *Nature Ecology & Evolution*. Springer Nature 2(3): 459–464.

Available at: <https://doi.org/10.1038/s41559-017-0451-9>

Author country/area: Canada, Sweden, Switzerland

Research funding: University of British Columbia, Swedish Research Council, Knut and Alice Wallenberg Foundation

The ecological niche of a species may evolve over time, and determining the mechanisms that drive such niche evolution is a key question in evolutionary biology. With climate and temperature playing an

important role in shaping ecological niches, metabolic heat production (endodermy) may be a major factor.

To address this, authors of a large study of terrestrial vertebrates compared ecological niche evolution between birds and mammals (endoderms) and snakes, lizards and amphibians (ectoderms). By using GBIF-mediated observation occurrences combined with fossil records and paleo-temperature curves, the researchers reconstructed past climatic niches of all vertebrate groups over 270 million years.

Based on these paleoclimatic niches, they estimated the rate of niche evolution and found this to be faster in endodermic birds and mammals than in ectodermic amphibians, snakes and lizards—a result that was also significant when only considering the last 5 million years.

The slow niche evolution found in ectoderms may affect the dynamics of current ranges and patterns of biodiversity—especially when climate change will require rapid evolution of climatic tolerances.

HOST SPIDERS: DISENTANGLING THE EVOLUTION OF SPECIALIZED MORPHOLOGIES

Ceccarelli FS, Koch NM, Soto EM, Barone ML, Arnedo MA and Ramírez MJ [2018] The Grass was Greener: Repeated Evolution of Specialized Morphologies and Habitat Shifts in Ghost Spiders Following Grassland Expansion in South America. *Systematic Biology*. Oxford University Press [OUP]. Available at: <https://doi.org/10.1093/sysbio/syy028>

Author country/area: Argentina, Mexico, Spain, United States

Research funding: ANPCyT, iBOL, CONICET, Spanish Ministerio de Ciencia e Innovación, National Geographic Society

Many invertebrates have evolved to fall in with their surroundings, matching their body colour or posture with leaves or sticks as a means of hiding from prey or predators. Among the ghost spiders (subfamily Amaurobioidinae), primarily from South America, several species have slender, elongated bodies that allow them to conceal themselves completely within grass leaves.

In this study, Ceccarelli and colleagues set out to investigate the ecological processes behind morphological adaptations in ghost spiders through extensive molecular phylogenetics and trait mapping. They used GBIF-mediated occurrences from the Museo Argentino de Ciencias Naturales to ascertain the geographical range and general habitat type for each species.



ARACHOSIA PRAE SIGNIS BY JUAN JOSÉ BONANNO [HTTPS://WWW.GBIF.ORG/OCURRENCE/2006069105](https://www.gbif.org/occurrence/2006069105) (CC BY-NC 4.0)

From a dated molecular phylogeny, the authors reveal multiple switches from forests to open habitats, coinciding with the expansion of South America's grasslands during the Miocene. Although at least three grass-adapted lineages evolved independently, the study finds a common morphological characteristic, as all three present a narrowing of the prosoma (fused head and thorax), allowing the spiders to extend the front pair of legs completely and to hide within a grass leaf.

C₄ PHOTOSYNTHESIS PRESENTS NO BARRIER TO COLONIZATION OF TEMPERATE CLIMATES

DATA USED: 14,800,000 SPECIES OCCURRENCES

Watcharamongkol T, Christin P-A and Osborne CP [2018] C₄ photosynthesis evolved in warm climates but promoted migration to cooler ones. *Ecology Letters*. Wiley 21(3): 376–383. Available at: <https://doi.org/10.1111/ele.12905>

Author countries/areas: United Kingdom

Research funding: Royal Thai Government

In the hot climates of tropical and subtropical regions, plants have developed the specialized C₄ photosynthetic pathway, optimized for increased photorespiration under high temperatures. More than half of the species with this evolutionary adaptation belong to the grass family (Poaceae).

In this study, researchers used all GBIF-mediated Poaceae occurrences combined with WorldClim climate data to derive temperature ranges for more than 2,000 grass species—about half of which are C₄.

They analyse the transition of species between climates and photosynthetic types, finding that C₄ origins are more common in tropical regions, and that reversal from C₄ to C₃ almost never happens in grasses. However, transitions from tropical to temperate climates is more common for C₄ than for C₃ taxa.

While increases in the upper bounds of plant temperature niches are associated with C₄

photosynthesis, the lower bounds did not differ significantly between C₃ and C₄. Taken together, these findings suggest that C₄ presents no physiological barrier to colonization of temperate climates.

NEOTROPICAL FRUITS DISPERSED BY MEGAFAUNA, BUT ALSO LATER BY HUMANS

DATA USED: 51,084 SPECIES OCCURRENCES

van Zonneveld M, Larranaga N, Blonder B, Coradin L, Hormaza JI and Hunter D [2018] Human diets drive range expansion of megafauna-dispersed fruit species. *Proceedings of the National Academy of Sciences*. *Proceedings of the National Academy of Sciences* 115(13): 3326–3331.

Available at: <https://doi.org/10.1073/pnas.1718045115>

Author country/area: Canada, Sweden, Switzerland

Research funding: Consultative Group on International Agricultural Research (CGIAR) Forest, Trees, and Agroforestry Research Program, Ministerio de Economía y Competitividad, European Regional Development Fund, European Union, Ibero-American Program for Science and Technology

Animals help disperse and thus increase the ranges of plants and fruits that are part of their diet. Neotropical fruits once dispersed by extinct megafauna—like the giant sloth—may also have been part of human diets, but the human role in dispersal is unknown.

By comparing known fruit-producing species exclusively part of megafauna diet with species also eaten by humans, this study provides insights into the effects of human dispersal of 130 wild and cultivated neotropical fruits. Their analysis involved the use of GBIF-mediated occurrences to determine species' geographic ranges and climatic niches.

The results of the study show that the ranges of fruits in human diet are two to three times larger than those only eaten by extinct megafauna—both for cultivated and wild species.

This suggests a clear role of human food usage in expanding the ranges of species that would otherwise have contracted with the extinction of megafauna.

FOSSILIZED POLLEN OF CHARISMATIC SOUTHERN HEMISPHERE PLANT FOUND IN WESTERN GREENLAND

DATA USED: 45,440 SPECIES OCCURRENCES

Grímsson F, Grimm GW, Potts AJ, Zetter R and Renner SS [2017] A Winteraceae pollen tetrad from the early Paleocene of western Greenland, and the fossil record of Winteraceae in Laurasia and Gondwana. *Journal of Biogeography*. Wiley 45(3): 567–581.
Available at: <https://doi.org/10.1111/jbi.13154>.

Author country/area: Austria, France, Germany, South Africa
Research funding: Austrian Science Fund

Comprising ~130 species in seven genera, Winteraceae is family of flowering plants with greatest diversity in the southern hemisphere. A pollen fossil found recently in a western Greenland Paleocene sediment sample tells a new story about the biogeography of Winteraceae.

Presenting the find, researchers in this study used light and electron microscopy to compare the fossilized grain with other fossils and extant pollen, describing the new species *Pseudowinterapollis agatdalensis* (after the valley where the fossil was found).

Using GBIF-mediated Winteraceae occurrences, the researchers derive climate and vegetation profiles for extant genera of the family. The paleoflora of Western Greenland suggests a fully humid temperate climate with biomes analogous to those now occupied by extant Winteraceae genera in Australasia.

The evidence presented in the study implies that Winteraceae is not just a charismatic family of the Southern hemisphere, but likely provides important clues to understanding global biogeographic evolution of flowering plants.



PSEUDOWINTERA COLORATA BY KRZYSZTOF ZIARNEK, KENRAIZ <HTTP://BIT.LY/32RL607> (CC BY-SA 4.0)

GLOBAL SURVEY SHOWS GENETIC STRUCTURE PREDICTED BY RANGE SIZE AND LATITUDE

Pelletier TA and Carstens BC [2018] Geographical range size and latitude predict population genetic structure in a global survey. *Biology Letters*. The Royal Society 14(1): 20170566.

Available at: <https://doi.org/10.1098/rsbl.2017.0566>

Author country/area: United States

Research funding: US Division of Environmental Biology

Both geographical distance and environmental barriers may influence genetic diversity within a species population. While models such as isolation-by-distance/environment have been shown to play a strong role, broad-scale studies have yet to determine if other factors might drive population diversity.

By identifying all GBIF-mediated species occurrences with associated GenBank accessions (and thus, genetic sequences), authors of this paper carried out analysis of more than 8,000 species in an unbiased assessment of such isolation models. They built a database of genetic structure predictors, including habitat type, range area and elevation.

Their results showed that a significant amount of population genetic structure can be attributed to geographical and environmental differences—and the top predictors across all analyses were related to geographical range.

The study demonstrates the potential power of having species occurrence data linked to genetic sequences, and the authors encourage increased efforts in associating such accessions.

SOME LIKE IT WARM, OTHERS COLD—BUT MOST PREFER MODERATE

DATA USED: 18,560 SPECIES OCCURRENCES

Vetaas OR, Grytnes J-A, Bhatta KP and Hawkins BA [2018] An intercontinental comparison of niche conservatism along a temperature gradient. *Journal of Biogeography*. Wiley 45(5): 1104–1113.

Available at: <https://doi.org/10.1111/jbi.13185>

Author country/area: Norway, United States

Research funding: Meltzer Research Fund

According to phylogenetic niche conservatism (PNC), closely related taxa share similar distributions along major environmental gradients, e.g. temperature. The probability of a species evolving within the range of its ancestor is therefore high.

Using a novel approach to testing the PNC theory, authors compared disjunct genera on separate continents with a shared ancestor, but few common species. By compiling GBIF-mediated occurrence data of eight woody phanerophyte genera in two regions differing in extent and complexity—the Nepalese Himalayas and the Peruvian Andes—they analysed 997 species along a temperature gradient.

All Himalayan genera showed a unimodal response with more species in the center of the temperature range. In the Andes, three genera were most speciose towards the warm end of the gradient. By statistical ranking, the authors were able to successfully predict the order of Andean genera based on Himalayan genera—and vice versa.

The study shows that temperature tolerances within a clade are conserved over time and space, and supports the notion that the highest number of species are found around the centre of the temperature range of a genus.

CLIMATIC STABILITY ALLOWS AREAS OF ENDEMISM TO PERSIST THROUGH TIME

DATA USED: 7,219 SPECIES OCCURRENCES

Pinilla-Buitrago GE, Escalante T, Gutiérrez-Velázquez A, Reyes-Castillo P and Rojas-Soto OR [2018] Areas of endemism persist through time: A palaeoclimatic analysis in the Mexican Transition Zone. *Journal of Biogeography*. Wiley 45(4): 952–961.

Available at: <https://doi.org/10.1111/jbi.13172>

Author country/area: Mexico

Research funding: CONACYT, GBIF

Endemic species are geographically restricted to a certain place. When many such species occur in the same area, the phenomenon is called an *area of endemism*. In the Mexican Transition Zone (MTZ) where the Nearctic and Neotropical biogeographical regions meet, several such areas exist, but how stable are they over time?

This study uses ecological niche models based on GBIF-mediated occurrences of 218 endemic species of beetles and mammals to identify areas of endemism in the MTZ. By transferring the models to three past periods (the Last Glacial Maximum, the mid-Holocene and the Last Interglacial), they demonstrate how two current areas of endemism have persisted throughout the periods.

While the MTZ has been a dynamic and complex region, the study reveals some climatic stability for at least the last 130,000 years, allowing for the permanence of endemic clustering in the region.

Ecosystem services



AMAZON RAINFOREST BY ALEXANDER GERST [HTTPS://WWW.FLICKR.COM/PHOTOS/ASTRO_ALEX/30626466567](https://www.flickr.com/photos/astro_alex/30626466567) [CC BY-SA 2.0]

DATA STORY HOW MUCH IS THE AMAZON FOREST WORTH?

“People think that the forest is only valuable when chopped down and sold as timber. We can show that not just biodiversity is at risk—but that deforestation actually decreases the monetary value of the Amazon.”

—Bortaldo Soares-Filho,
Federal University of Minas Gerais

As one of the most biodiverse biomes on the planet, the Amazon Forest is home to tens if not hundreds of thousands of plant and animal species that provide natural, cultural and economic values, not only to Brazil, but to the entire world. Understanding value—essentially, putting a price tag on such services—is important to researchers trying to help stakeholders make informed decisions when it comes to protecting the Amazon.

Professor Bortaldo Soares-Filho at the Center for Remote Sensing at the Federal University of Minas Gerais in Belo Horizonte, Brazil, is an expert in environmental modelling who has been working to produce science relevant to policy. Recently his

team was approached by the World Bank, proposing a valuation of the ecosystem services of the Amazon. Soares-Filho explains:

“Actually, it doesn’t really make sense to talk about the value of the Amazon—because it is invaluable! And our ability to put a monetary value on ecosystem services is still very limited.”

Realizing the importance of responding to this request, Soares-Filho and colleagues relied on experiences from previous regional valuation studies and decided to focus on very tangible services that could be translated into specific value components.

“Our study is the most comprehensive valuation study of the Brazilian Amazon and the first to be spatially explicit at a very high resolution. It relies on solid scientific models and encompasses several valuation components”.

Their approach was to estimate the impact of forest loss on the values provided by food and raw materials—through net revenues from reduced impact logging, brazil nut and rubber; greenhouse gas mitigation—through potential payments for emission

reductions; and finally, climate regulation—through added value of rainfall on hydroelectricity, soybean and beef production. The analysis of timber relied on occurrence information from GBIF, which also enabled a biodiversity analysis complementing the study with information on the potential value of non-use services, such as pollination and bioprospecting.

“All the values (use values) where there is access (roads, people, towns)—they are also more threatened by deforestation—so there is a conflict. Imminent risk of deforestation and thereby losing ecosystem service values.”

The results of the work have had an immediate effect on policy in Brazil, as Soares-Filho was invited to appear before a federal Senate hearing on a proposal to relax the main set of laws regulating conservation in private properties. The bill proposed by the administration would effectively end the legal reserve requiring land owners to set aside areas for conservation.

“This would be a major set-back for Brazil. By removing legal reserve protection, you are allowing deforestation to become rampant again, like in the early 2000s. We showed them that the Amazon has a lot of values—for example, if you deforest part of the Amazon you can reduce the net profit of soy farmers by up to 35 per cent!”



BERTHOLLETTIA EXCELSA BY RENATA XAVIER
[HTTPS://WWW.GBIF.ORG/OCURRENCE/2242735480](https://www.gbif.org/occurrence/2242735480) [CC BY-NC 4.0]

The bill had already passed in the lower house of congress, but following the hearing it was rejected by the Senate. Continuing his mission to demonstrate the value of the Amazon and disseminating the results to broad audiences, Soares-Filho wants to end a paradigm:

“People think that the forest is only valuable when chopped down and sold as timber. We can show that not just biodiversity is at risk—but that deforestation actually decreases the monetary value of the Amazon.”

Strand J, Soares-Filho B, Costa MH, Oliveira U, Ribeiro SC, Pires GF, Oliveira A, Rajão R, May P, van der Hoff R, Siikamäki J, da Motta RS and Toman M (2018) Spatially explicit valuation of the Brazilian Amazon Forest’s Ecosystem Services. *Nature Sustainability*. Springer Nature 1(11): 657–664. Available at: <https://doi.org/10.1038/s41893-018-0175-0>

Author country/area: Brazil, Netherlands, United States
Research funding: None listed

ASSESSING THE GLOBAL POLLINATION CRISIS USING HISTORICAL MUSEUM COLLECTIONS

Bartomeus I, Stavert JR, Ward D and Aguado O (2019) Historical collections as a tool for assessing the global pollination crisis. *Philosophical Transactions of the Royal Society B: Biological Sciences*. The Royal Society 374(1763): 20170389.

Available at: <https://doi.org/10.1098/rstb.2017.0389>

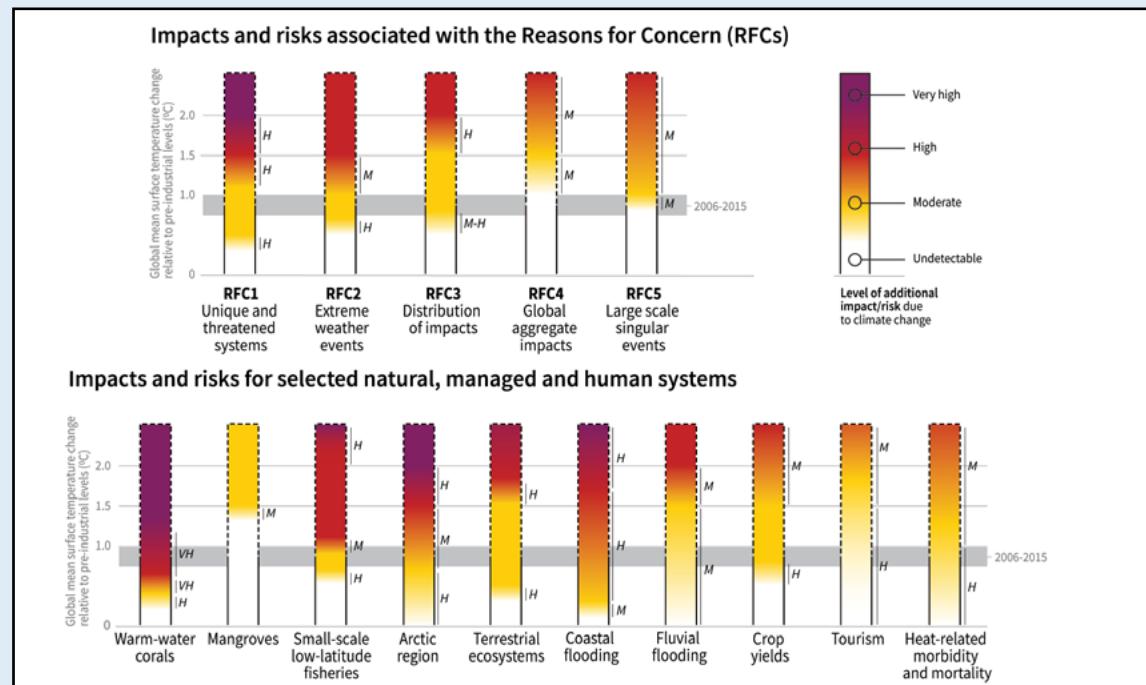
Author countries/areas: New Zealand, Spain
Research funding: BBVA Foundation

Declines among pollinators due to climate change, chemical exposure and habitat destruction are of increasing global concern. However, most of our knowledge is limited, both in terms of geography and taxonomy, as most studies tend to focus on bees in Europe and North America.

To fill some of these gaps in knowledge, this study presents a roadmap for using historical collections data—as mediated by GBIF—to assess long-term pollinator population changes. In two case studies—one of Spain and one of New Zealand—the researchers demonstrate analytical strategies and considerations for comparing historical records with modern data to derive pollinator population trends.

Their approach reveals both declines and increases across different groups, highlighting how some clades are more sensitive to disturbances than others. The study shows how strong collaborations between museum curators and researchers can help answer some of the most pressing ecological and evolutionary questions.

Climate change



IMPLICATIONS OF GLOBAL WARMING FOR PEOPLE, ECONOMIES AND ECOSYSTEMS. CROPPED FROM FIGURE IN IPCC SR15: SUMMARY FOR POLICYMAKERS*

DATA STORY DATA FROM THE GBIF NETWORK UNDERPINS BIODIVERSITY-RELATED FINDINGS IN LATEST IPCC REPORT

DATA USED: 385,681,365 SPECIES OCCURRENCES

In October 2018, the Intergovernmental Panel on Climate Change (IPCC) published its Special Report on Global Warming of 1.5 °C (SR15: <https://www.ipcc.ch/sr15>). Responding to an invitation from the countries that adopted the Paris Agreement in 2015, the report aims to “strengthen the global response to the threat of climate change, sustainable development, and efforts to eradicate poverty.”

The IPCC SR15 seeks to provide governments with comprehensive, authoritative scientific advice on how environmental risk levels will change between our world and future ones in which the global mean temperature increases by 1.5°C and 2°C above pre-industrial levels. By clearly outlining the choices and trade-offs that decision-makers face, the report also provides them with practical guidance on what’s needed to demonstrate responsible political leadership around climate change.

Links between primary biodiversity data and high-level policy documents like SR15 often border on

imperceptible, even in the best of circumstances. Comprehensive global assessments examine tens if not hundreds of thousands of scientific research articles, and climate change analyses must canvass an even more scientific, technical and socio-economic dimensions. Citations—much less data citations—refer to only a fraction of the massive bibliographies, making it nearly impossible to trace direct connections back to underlying data with any confidence.

Nearly impossible, that is. For the intrepid investigator who follows the trail of citations through the scenic distractions of supplementary materials, the link between the research that underpins SR15’s key biodiversity-related conclusions and data from the GBIF network is unmistakable. What’s more, the steady increase in the amount of GBIF-mediated data during the last decade forms a critical part of these policy-relevant findings.

In 2013, researchers Rachel Warren and Jeff Price from the University of East Anglia’s Tyndall Centre for Climate Change Research led a multi-author team that published an early, high-profile use of GBIF-mediated data in *Nature Climate Change* (Warren et al. 2013: <https://doi.org/10.1038/nclimate1887>). The paper drew on records from nearly 50,000 plant and animal species, seeking to understand how increases in global temperature will affect more common species. The findings forecasted drastic reductions in species’ geographic ranges while outlining how quick action to mitigate the impacts of climate change could reduce the scale of these losses and buy time for species to adapt.

Fast forward to 2018, when Warren and Price led publication of a fresh look at a somewhat refined question—how will limiting the increase in global temperature to 1.5°C rather than 2°C affect insects, vertebrates and plants? Writing this time in the journal *Science*, the authors analysed more than 385 million occurrence records (see the download record: <https://doi.org/10.15468/dl.kecdhx>) for 105,501 species to find that limiting warming to 1.5°C as compared to 2°C would cut geographical range losses resulting from climate change in half. The supplementary materials explicitly acknowledge how important the increased availability of data from the GBIF network was to the research.

‘Since our previous analysis in 2012, the [authors’] database has been updated and expanded to include nearly 70,000 more species of plants and animals.... Both updates to the GBIF database and increased spatial resolution enabled us to include thousands more species than were available in our earlier studies.’

In fact, this increase in data availability enabled the introduction of an entire class of animals excluded from the previous analysis—*insects*, 19,848 species of them. Their earlier omission was limiting, not only because of the role that “the little things that run the world” (as E.O. Wilson once characterized them) play preserving critical ecosystem functions and services, but also because the authors found that ‘*insects* benefit most from constraining warming to 1.5°C rather than 2°C’.

SR15 draws on other research supported by the GBIF network, at least secondarily, like the dozen of the 131 model predictions reviewed in Urban’s 2015 meta-analysis (<https://doi.org/10.1126/science.aaa4984>) that reported using GBIF-mediated data. But on the

“Since our previous analysis in 2012, the database has been updated and expanded to include nearly 70,000 more species of plants and animals.... Both updates to the GBIF database and increased spatial resolution enabled us to include thousands more species than were available in our earlier studies.”

—Warren et al. 2018

single page (p. 218) allocated to analysing ‘Changes in species range, abundance and extinction rates,’ SR15 refers to Warren et al. 2018 six times—for example, repeating the paper’s conclusion that limiting warming by 0.5°C could lead to a threefold reduction in the number of insect species facing extinction (defined as loss of more than half of geographic range) and halve the risk for plant and vertebrate species.

For institutions that share data through the GBIF network, the IPCC SR15 is more than a high-profile call to action. The practice of assigning DOIs to user downloads can help to reveal direct connection between policy-relevant science and the underlying data. So when asked why they share their data, GBIF publishers of any of the 5,432 datasets cited in the download can unequivocally state: to contribute to critical policy-relevant science like the first global-scale assessment of climate change impacts on insects and the IPCC’s Special Report on Global Warming of 1.5 °C.

a Warren R, Price J, Graham E, Forstenhaeusler N and VanDerWal J [2018] The projected effect on insects, vertebrates, and plants of limiting global warming to 1.5°C rather than 2°C. *Science*. American Association for the Advancement of Science (AAAS) 360(6390): 791–795. Available at: <https://doi.org/10.1126/science.aar3646>

Author country/area: Australia, United Kingdom

Research funding: Natural Environment Research Council (UK)

* IPCC, 2018: Summary for Policymakers. In: Global Warming of 1.5°C. An IPCC Special Report on the impacts of global warming of 1.5°C above pre-industrial levels and related global greenhouse gas emission pathways, in the context of strengthening the global response to the threat of climate change, sustainable development, and efforts to eradicate poverty [Masson-Delmotte, V., P. Zhai, H.-O. Pörtner, D. Roberts, J. Skea, P.R. Shukla, A. Pirani, W. Moufouma-Okia, C. Péan, R. Pidcock, S. Connors, J.B.R. Matthews, Y. Chen, X. Zhou, M.I. Gomis, E. Lonnoy, Maycock, M. Tignor, and T. Waterfield (eds.)]. World Meteorological Organization, Geneva, Switzerland, 32 pp. <http://bit.ly/sr15spm2>

TEN-DEGREE CHANGE SUFFICIENT FOR TOTAL ANNIHILATION OF LIFE ON EARTH

DATA USED: 7,219,298 SPECIES OCCURRENCES

② Strona G and Bradshaw CJA [2018] Co-extinctions annihilate planetary life during extreme environmental change. *Scientific Reports*. Springer Nature 8(1). Available at: <https://doi.org/10.1038/s41598-018-35068-1>

Author countries/areas: Australia, Italy

Research funding: None listed

Numerous studies have shown how climate change and human activities can have detrimental effects on biodiversity, eventually leading to extinctions. When one species disappears, it affects all its ecological dependencies and further co-extinctions can occur, possibly causing extinction cascades and eventually, total collapse of an ecosystem.

In an elaborate simulation study, researchers created 2,000 “virtual Earths”, populated them with virtual terrestrial species each with their own environmental tolerances calibrated using GBIF-mediated occurrences, arranged into structured food webs. The authors then exposed the virtual planets to continuous, progressive changes in temperature (heating and cooling), and while allowing for some dispersal and adaptation, ran the simulations until temperature had changed by 50° Celcius.

Considering environmental tolerances only, the authors show that a global warming of 10° would lead to the extinction of more than 60 per cent of species. For 10° cooling, fewer than 20 per cent of species would remain. However, in both scenarios, if including effects of co-extinctions, a 10° change would be sufficient for total annihilation of all life.

MINIMIZING BIODIVERSITY LOSS IN THE BRAZILIAN CERRADO

Monteiro LM, Brum FT, Pressey RL, Morellato LPC, Soares-Filho B, Lima-Ribeiro MS and Loyola R [2018] Evaluating the impact of future actions in minimizing vegetation loss from land conversion in the Brazilian Cerrado under climate change. *Biodiversity and Conservation*. Springer Nature. Available at: <https://doi.org/10.1007/s10531-018-1627-6>

Author countries/areas: Australia, Brazil

Research funding: National Council for Scientific and Technological Development (BR), Boticário Group Foundation (BR), Funding Authority for Research and Projects (BR)

Covering more than 2 million square kilometers and nearly a quarter of Brazil, the tropical ecoregion known as the Cerrado is a designated biodiversity hotspot—yet less than 10 per cent is protected. Scenic beauty and recreational value have a history of playing an

important role in conservation planning, sometimes resulting in the protection of unproductive landscapes with steep slopes and infertile soil.

To avoid this and to improve spatial prioritization in protected areas with a limited budget, this study used GBIF-mediated occurrences to model plant distributions under climate change. Coupled with land-use models, these helped evaluate the impact of four simulated conservation scenarios: implemented now or sequentially, and either focusing on maximizing species representation or conservation impact as defined by beneficial environmental outcomes arising from protection.

Their evaluation revealed little difference between the four scenarios in average species' range protected, however, focusing on conservation impact predicted vegetation losses significantly higher than in the representation-based approaches. These findings, the authors suggest, can serve as a guideline for a collaborative social, political and institutional effort to achieve the common goal of minimizing the loss of biodiversity.

HIGH-RISK CONSERVATION PLANNING REQUIRED TO COMBAT EFFECTS OF CLIMATE CHANGE

Ribeiro BR, Sales LP and Loyola R [2018] Strategies for mammal conservation under climate change in the Amazon. *Biodiversity and Conservation*. Springer Nature 27(8): 1943–1959.

Available at: <https://doi.org/10.1007/s10531-018-1518-x>

Author countries/areas: Brazil

Research funding: National Council for Scientific and Technological Development (BR), Funding Authority for Research and Projects (BR)

When planning conservation efforts, protecting climatically stable refugia is a low-risk investment, as species are considered more likely to persist in areas less affected by climate change. Such prioritization, however, is often done at the expense of less stable high-risk areas, effectively leaving inhabiting species unprotected and committed to extinction.

Proposing a novel strategy for the conservation of mammals in the Amazon, researchers used GBIF-mediated occurrences of 256 species to generate ecological niche models that served as primary input to a spatial prioritization analysis taking into consideration climate change metrics including climate anomalies and extremes.

The resulting analysis identified a network of both high-risk areas and low-risk refugia while revealing more current and future distributions of species in



DROSERA ROTUNDIFOLIA BY ВЯЧЕСЛАВ ЮСУПОВ [HTTPS://WWW.GBIF.ORG/OCURRENCE/2265893103](https://www.gbif.org/occurrence/2265893103) (CC BY-NC 4.0)

the former. The study presents a robust approach to conservation planning, taking into account uncertainties arising from alternative climate models and showing that trade-offs related to species representation can be quantified explicitly.

ASSESSING THE VULNERABILITY OF CARNIVOROUS PLANTS TO CLIMATE CHANGE

Fitzpatrick MC and Ellison AM [2018] Estimating the exposure of carnivorous plants to rapid climatic change. In: *Carnivorous Plants: Physiology, ecology, and evolution*. Oxford University Press. Available at: <https://doi.org/10.1093/oso/9780198779841.003.0028>

Author countries/areas: United States

Research funding: None listed

Deriving nutrients from trapping and consuming animals, carnivorous plants have adapted to growing in unique microhabitats and soil conditions that can be difficult to categorize. This poses challenges when trying to predict how these plants respond to changes in climate using traditional modelling approaches.

In a new book examining the physiology, ecology and evolution of carnivorous plants, authors of a chapter dedicated to estimating the response to climate change attempt to overcome some of these challenges and assess the vulnerability of this group.

Through weighted ensemble models and calculation of bioclimatic velocities—i.e. the rate at which the climate is changing—the authors show that most locations where carnivorous plants occur are projected to decrease in suitability. In fact, for 65 per cent of examined species climate change would lead to substantial declines in habitat.

With no near-term solution to climate change, the authors propose a conservation strategy focusing

on immediate threats, such as limiting habitat conversion, poaching and competition from invasive species.

FUTURE CLIMATE LEAVES LITTLE ROOM FOR EASTERN AMAZON BATS

Costa WF, Ribeiro M, Saraiva AM, Imperatriz-Fonseca VL and Giannini TC [2018] Bat diversity in Carajás National Forest (Eastern Amazon) and potential impacts on ecosystem services under climate change. *Biological Conservation*. Elsevier BV 218: 200–210.

Available at: <https://doi.org/10.1016/j.biocon.2017.12.034>

Author countries/areas: Brazil

Research funding: National Council for Scientific and Technological Development (BR)

As flower pollinators, seed dispersers and pest controllers, bats provide important ecosystem services in the areas they inhabit. Human-induced climate change may threaten the habitats of bats, and with them, the ecosystem services provided by affected species.

In a new study of the impact of climate change on bat diversity in Carajás National Forest (Pará, Brazil), researchers collect information about more than 80 bat species present in the region. Combining with GBIF-mediated species occurrences and future climate scenarios, they create species distribution models, showing that 57 per cent of species may not find suitable habitats in Carajás under these scenarios. For nectarivorous bats, only a single species is predicted to find suitable habitat.

As more than 500 plant species (including important crops) rely on pollination and seed dispersal by these bats, the indirect consequences of climate change on ecosystem services are potentially catastrophic.

Invasive species



BUBULCUS IBIS BY DAVID MORALES RAMIREZ [HTTPS://WWW.GBIF.ORG/OCURRENCE/2013022714](https://www.gbif.org/occurrence/2013022714) [CC BY-NC 4.0]

DATA STORY PREDICTING THE FUTURE OF BIODIVERSITY USING ESSENTIAL BIODIVERSITY VARIABLES

DATA USED: 732,113 SPECIES OCCURRENCES

What's the weather going to be like tomorrow, next week—or even in ten years? This is a question researchers have worked hard on for many years. Thanks to high demand from commercial and political interests, such research has received a great deal of interest and funding, and today we have excellent weather and climate models based on standardized variables like temperature, wind speed, etc.

But what if the question was: what is biodiversity going to be like tomorrow or in ten years? It's difficult to measure biodiversity in the same way you can measure temperature. What standardized variables can be used to derive models to accurately predict changes in biodiversity?

Proposed in 2012, Essential Biodiversity Variables (EBVs) are a concept with the idea of defining standardized measurements that can be repeated and reproduced accurately in order to inform indicators of change in biodiversity. Involved in biodiversity informatics since 2003, Alex Hardisty, Director of

Informatics Projects at the School of Computer Science & Informatics at Cardiff University in the UK, has led the work of preparing what is thought to be the first EBV data product, described in a publication from early 2019:

"I was particularly interested in the challenges involved in interoperating between research infrastructures, and in previous projects we became aware of EBVs and their use as a potential unifying use-case for driving interoperability between different infrastructures."

Working in close collaboration with two research infrastructures—GBIF and the Atlas of Living Australia (ALA)—Hardisty and his team developed a workflow in three stages aimed at producing an EBV for measuring changes in the distributions of alien invasive species.

In the first stage, they gathered, filtered and harmonized occurrence data from the infrastructures, followed by the second stage, in which they merged data from the two sources and performed a range of

quality controls. In the final stage, they generated tables of time-series, calculated areas of occupancy—or AOO—by decade and produced maps and graphs of the results.

The team tested the EBV workflow on three candidate species with established alien ranges: Sydney golden wattle (*Acacia longifolia*), European wasp (*Vespa germanica*) and cattle egret (*Bubulcus ibis*). For all three species, the metrics derived from the EBV showed an exponential increase in AOO over the last few decades.

Obtaining the data and preparing it for the EBV, however, wasn't trivial and the team faced a number of challenges along the way, as described by Hardisty:

"Much to our surprise, a lot of manual manipulation was required to get data ready, and it took much longer than anticipated. There were many differences between GBIF and ALA—in data retrieval, tools available for data handling and in terms used to describe the data. As a result, the level of automation we wanted wasn't possible and we had to do a lot of manual work."

As the point of EBVs is to create reliable variables that can be measured repeatedly, steps should be taken to harmonize data formats, quality checks and assertions across research infrastructures, and to automate—a point to which Hardisty suggests working more intensely to overcome some of the inconsistencies encountered by their team:

"Some human expertise will always be necessary, but at the same time, humans are incredibly bad at keeping an accurate record of what they do, which means it can be impossible to repeat the precise steps. For EBVs, automated workflows are critical."

"Some human expertise will always be necessary, but at the same time, humans are incredibly bad at keeping an accurate record of what they do, which means it can be impossible to repeat the precise steps. For EBVs, automated workflows are critical."

—Alex R Hardisty, Cardiff University

As to the demand for EBVs and who should be responsible for producing data products, Hardisty returns to the weather and climate analogy:

"Why do we have good weather forecasting abilities today? Because of demands from the aviation and space industry, East/West political tensions in 1950-70s, even nuclear bomb development—all driving the need for predictable models. We've yet to see a real demand for routine EBV data products, however, our study has laid the groundwork for future developments. If the world wants EBVs with which it can create indicators and measure changes and trends in biodiversity, then the world has to provide the infrastructure to do that. This is driven by the political agenda—and only when this becomes hot enough will funding become available."

a Hardisty AR, Belbin L, Hoborn D, McGeoch MA, Pirzl R, Williams KJ and Kissling WD (2019) Research infrastructure challenges in preparing essential biodiversity variables data products for alien invasive species. *Environmental Research Letters*. IOP Publishing 14(2): 25005.

Available at: <https://doi.org/10.1088/1748-9326/aaf5db>

Author country/area: Australia, Denmark, Netherlands, United Kingdom

Research funding: H2020 Research Infrastructures, Australian Research Council



VEСПULA GERMANICA BY REINER RICHTER [HTTPS://WWW.GBIF.ORG/OCURRENCE/1847507468](https://www.gbif.org/occurrence/1847507468) [CC BY-NC-SA 4.0]

PLANT ENDEMISM IN GEORGIA THREATENED BY ALIEN INVADERS

DATA USED: 432,534 SPECIES OCCURRENCES

a Slodowicz D, Descombes P, Kikodze D, Broennimann O and Müller-Schärer H [2018] Areas of high conservation value at risk by plant invaders in Georgia under climate change. *Ecology and Evolution*. Wiley 8(9): 4431–4442. Available at: <https://doi.org/10.1002/ece3.4005>

Author countries/areas: Georgia, Switzerland

Research funding: European Cooperation in Science and Technology

Invasive alien species pose a serious threat to biodiversity, especially in protected areas (PA) and other areas of high conservation value with many endemic species. As changing climates may increase susceptibility of these areas, understanding and anticipating invasions is important for better management.



CENCHRUS CILIARIS BY JAMES BAILEY
HTTPS://WWW.GBIF.ORG/OCCURRENCE/1838307397 (CC BY-NC 4.0)

In this study, researchers used GBIF-mediated occurrences to map endemic species richness in Georgia—a country situated in the Caucasus mountains, known for its high plant diversity and endemism. Indeed, they identify high endemism areas in 20 per cent of the country's area, of which only 9.4 per cent overlaps with PAs.

The authors modeled the current and future distributions of 27 known invaders and mapped the richness of these species. Their results show that climatic suitability in Georgia for many invasive plants may decrease overall, however, specifically in the areas with high endemism identified in the study, it may, in fact, double.

These findings are crucial, as these important areas, located outside designated PAs are unlikely to be included in official invasive plant management programmes.

FORECASTING INVASIVE DISTRIBUTIONS AT A LOCAL LEVEL—WITH A GLOBAL PERSPECTIVE

DATA USED: 25,905 SPECIES OCCURRENCES

a Jarnevich CS, Young NE, Talbert M and Talbert C [2018] Forecasting an invasive species' distribution with global distribution data, local data, and physiological information. *Ecosphere*. Wiley 9(5): e02279. Available at: <https://doi.org/10.1002/ecs2.2279>

Author country/area: United States

Research funding: United States Geological Survey

Factors restricting the distribution of invasive alien species includes climate, topography and biotic interactions, but the contribution of each of these vary from global to local scale. When assessing the local invasion potential of a species, it's important to consider global-scale constraints as well.

Widely introduced globally as a forage species for livestock, buffelgrass (*Cenchrus ciliaris*) has become invasive in many parts of the world. This study of the species investigates differences in distribution predictors at the global and local level—in Saguaro National Park in Arizona, USA.

Using GBIF-mediated occurrences the authors derived two sets of models and when comparing local and global models, they found that while winter temperature appears to be most important predictor in both cases, topography variables, such as aspect of slopes, appeared in the local models to proxy for other climate predictors.

When projecting the models into the future, results suggests that the region—Saguaro National Park—will become more suitable to buffelgrass in the future.



ACACIA PARADOXA BY DOUGLASEUSTONBROWN HTTPS://WWW.GBIF.ORG/OCCURRENCE/1838345538 (CC BY-NC 4.0)

SOUTH AFRICA—A GLOBAL HOTSPOT FOR ACACIA INTRODUCTIONS

a Magona N, Richardson DM, Le Roux JJ and Kritzinger-Klopper S [2018] Even well-studied groups of alien species might be poorly inventoried: Australian Acacia species in South Africa as a case study. *NeoBiota*. Pensoft Publishers. Available at: <http://doi.org/10.3897/neobiota.39.23135>

Author countries/areas: South Africa

Research funding: South African National Department of Environment Affairs

Mimosa, thorn tree or wattle are some of the common names used for species belonging to *Acacia*, second most speciose genus among legumes. The majority of species are native to Australia, but South Africa is a global hotspot for foreign introductions, of which many have become naturalized and some invasive.

Taking stock of Australian *Acacia* species in South Africa, this study compiled data from herbaria,

literature, field surveys and GBIF.org on all *Acacia* occurrences in the country while assessing the current invasion status of present species.

The authors found evidence of 141 Australian *Acacia* species having been introduced to South Africa. Of these, they confirm the current presence of 33 species. Fifteen species—including *A. paradoxa* shown above—are considered invasive and five have naturalized. The remaining 13 species have yet to produce viable offspring.

Doubling previous estimates of *Acacia* species introduced to South Africa based on data collated 40 years ago, this new study represents an important update to informing management actions in the country.

Conservation and food security



COFFEA LIBERICA BY DINESH VALKE [HTTPS://WWW.FLICKR.COM/PHOTOS/DINESH_VALKE/5597839545](https://www.flickr.com/photos/dinesh_valke/5597839545) (CC BY-SA 2.0)

DATA STORY DEVELOPING AN INDICATOR FOR SUSTAINABLE DEVELOPMENT GOALS & BIODIVERSITY TARGETS USING OPEN DATA

DATA USED: 210,383,301 SPECIES OCCURRENCES

Preserving the genetic diversity of cultivated plants and domesticated animals, as well as their wild relatives, are priorities of several international agreements including the United Nations Sustainable Development Goals (SDG) Target 2.5, Aichi Biodiversity Target 13 and the Global Strategy for Plant Conservation Target 9, and Article 5 of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA). To be able to measure progress against these targets, a number of indicators have been proposed and/or deployed.

Colin Khoury of the International Center for Tropical Agriculture (CIAT) in Colombia has been involved in the development of one of these indicators.

"When I looked at the existing indicators, there were deficiencies, both in methodology and in data. Many gave a static number, but no indication of whether that was enough. It doesn't tell you that much and it doesn't tell you when you're done".

Khoury, who started on the practical end of agriculture as a farmer, returned to academia and got involved in research in agricultural diversity conservation. During his years as a PhD student he spent time at the seed bank at CIAT—home of the world collection of beans and cassava—developing a gap analysis methodology based on modelling species occurrence data that could help CIAT and other seed banks determine the completeness of their collections.

"We finished our project with reasonable results—but we thought the gap analysis had further potential. In 2017, the Biodiversity Indicators Partnership put out a call for additions to indicators for Target 13. We proposed our method and received funding for a 9 month project to develop the indicator."

Described in detail in a paper in Ecological Indicators, the proposed methodology involves simple and reproducible steps—all relying on open data. First, they create a dynamic list of relevant species for

which they download occurrence records from GBIF and from seedbank databases. Using these combined with climatic covariates, they model the potential distributions of all species. By comparing the distributions with existing germplasm collections and designated protected areas, they derive a conservation score from which the indicator can be calculated at national, regional and global scales.

Following a recent update of the World Database on Protected Areas, Khoury and colleagues have now redone the analysis and the indicator has been formally accepted.

"This is exciting news! Our indicator will be included in the Biodiversity Indicators Partnership website, which is a resource for national representatives to report progress on these targets—in our case, on Aichi Target 13."

To allow complete openness and transparency, Khoury and this team released all the data compiled and produced in the paper as part of a data paper (<https://doi.org/10.1016/j.dib.2018.11.125>) published around the same time. They also created an interactive version of the results that can be explored online (<https://ciat.cgiar.org/usefulplants-indicator>). This insistence on accessible information demonstrates how passionate Khoury and his institution are about open data—and he fully acknowledges that without GBIF, there would be no indicator.

"GBIF is one of the ways we understand living diversity—if you can't access information about it, how can you possibly preserve it?"

—Colin K. Khoury, CIAT

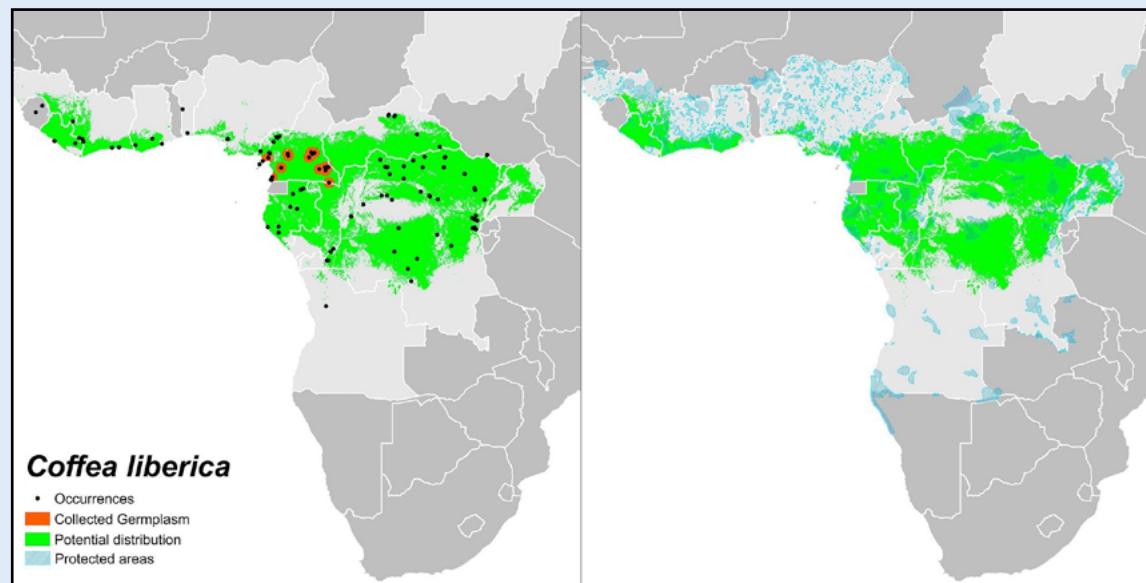
"I fell in love with seeds and diversity in agriculture at the beginning of my career. Since then I've focused on three things: how to take care of it, how to use it for good purposes, and finally how to raise awareness by making sure everyone has access to as much as possible."

He concludes, "GBIF is one of the ways we understand living diversity—if you can't access information about it, how can you possibly preserve it?"

a Khoury CK, Amariles D, Soto JS, Diaz MV, Sotelo S, Sosa CC, Ramírez-Villegas J, Achicanoy HA, Velásquez-Tibatá J, Guarino L, León B, Navarro-Racines C, Castañeda-Álvarez NP, Dempewolf H, Wiersema JH and Jarvis A (2019) Comprehensiveness of conservation of useful wild plants: An operational indicator for biodiversity and sustainable development targets. *Ecological Indicators*. Elsevier BV 98: 420–429. Available at: <https://doi.org/10.1016/j.ecolind.2018.11.016>

Author country/area: Colombia, Germany, Ireland, Peru, United States

Research funding: United Nations, European Commission, Federal Office for the Environment (DE)



POTENTIAL DISTRIBUTION MODEL FOR *COFFEA LIBERICA* BASED ON OCCURRENCE LOCATIONS. THE LIGHTER COLORED BACKGROUND DISPLAYS THE NATIVE COUNTRY BOUNDARY USED TO CLIP THE MODEL; EX SITU 'SITE WHERE GERMPLASM COLLECTED' LOCATIONS SURROUNDED BY A CA. 50 KM BUFFER (IN RED), OVER THE POTENTIAL DISTRIBUTION MODEL; POTENTIAL DISTRIBUTION OCCURRING WITHIN AND OUTSIDE OF DESIGNATED PROTECTED AREAS. FIGURE MODIFIED FROM KHOURY ET AL (2019) [HTTPS://DOI.ORG/10.1016/J.ECOLIND.2018.11.016](https://doi.org/10.1016/j.ecolind.2018.11.016) (CC BY 4.0)

A GLOBAL ASSESSMENT OF FRESHWATER FISH SURVEY EFFORT

DATA USED: 924,518 SPECIES OCCURRENCES

Pelago-Villamil P, Guisande C, Manjarrés-Hernández A, Jiménez LF, Granado-Lorencio C, García-Roselló E, González-Dacosta J, Heine J, González-Vilas L and Lobo JM (2018) Completeness of national freshwater fish species inventories around the world. *Biodiversity and Conservation*. Springer Nature 27(14): 3807–3817. Available at: <https://doi.org/10.1007/s10531-018-1630-y>

Author country/area: Colombia, Spain

Research funding: None listed

The quality of species inventories can help identify taxonomic and geographic gaps in primary biodiversity data, and the completeness of such resources can direct future surveying efforts.

Relying on GBIF-mediated species occurrences, researchers from Colombia and Spain used KnowBR, an R package application featured in a separate section of this review (p. 11), to assess the survey completeness of freshwater fishes in all countries of the world.

The completeness results from the analysis ranged from very low, e.g. in Guinea-Bissau, to very high, e.g. in the UK. Only twenty-six nations—mainly in Europe and North America—met the requirements for having good inventories, while 35 countries mainly in Southern Africa and South America were found to have inventories of fair quality.

The freshwater fish survey completeness of the remaining 152 countries was either poor or impossible to assess due to lack of data.

USING OPEN DATA TO PREDICT PLANT CONSERVATION STATUS ON A GLOBAL SCALE

DATA USED: 165,790,878 SPECIES OCCURRENCES

Pelletier TA, Carstens BC, Tank DC, Sullivan J and Espíndola A (2018) Predicting plant conservation priorities on a global scale. *Proceedings of the National Academy of Sciences. Proceedings of the National Academy of Sciences* 115(51): 13027–13032. Available at: <https://doi.org/10.1073/pnas.1804098115>

Author country/area: United States

Research funding: National Science Foundation (US)

When assessing the extinction risk of species, plants are often neglected in favour of charismatic vertebrates, despite plants being the essential foundation in ecosystem architecture. Tools for rapid assessments for understudied species are key to improving conservation priorities worldwide.

Using a machine-learning approach, this study predicts the extinction risk of previously unassessed terrestrial plant species based on GBIF-mediated occurrence data combined with other available open data sources on environment and species traits.

In their analysis of more than 230,000 species, Pelletier and colleagues predict that up to 20 per cent belong in a Red List category above "Least Concern" (LC). They identify a core set of species consistently predicted as high risk as candidates for detailed assessment.

The framework presented in the study has low computational requirements and can be employed easily and efficiently to aid policy makers in prioritizing resources for investigating extinction risks.

ANALYSIS OF GENETIC DIVERSITY AND RICHNESS OF PLANTS IN THE CERRADO SAVANNAH BIOME

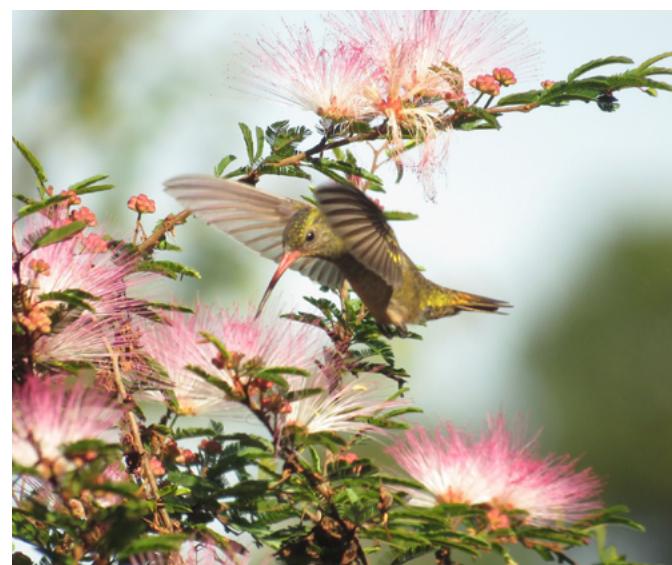
DATA USED: 4,074,709 SPECIES OCCURRENCES

Ballesteros-Mejía L, Lima JS and Collevatti RG (2018) Spatially-explicit analyses reveal the distribution of genetic diversity and plant conservation status in Cerrado biome. *Biodiversity and Conservation*. Springer Science and Business Media LLC. Available at: <https://doi.org/10.1007/s10531-018-1588-9>

Author country/area: Brazil

Research funding: National Council for Scientific and Technological Development (BR), Brazilian Federal Agency for the Support and Evaluation of Graduate Education

Mainly focusing on species diversity, conservation assessments often neglect genetic variation despite



HYLOCHARIS CHRYSURA BY DOUGLAS ALENCAR GASS
[HTTPS://WWW.GBIF.ORG/OCURRENCE/2242933986](https://www.gbif.org/occurrence/2242933986) (CC BY-NC 4.0)

being a key component representing the evolutionary potential of species and contributing to individual fitness and ecosystem function.

The Cerrado is the most diverse savannah in the world and the subject of a new, comprehensive study examining patterns of plant genetic diversity across the biome. Based on genetic data from existing literature they describe a high level of genetic richness in the northern Cerrado, however, high genetic diversity is widespread in the biome.

Using GBIF-mediated occurrences to estimate species richness combined with environmental and anthropogenic predictors, the authors modelled effects on genetic diversity and richness, finding associations with temperature and precipitation. To their surprise, however, species richness did not predict genetic richness.

The study concludes that the northern part of the Cerrado is a potential hotspot of genetic diversity that should be the focus of additional studies and protection.

CONSERVING CROP WILD RELATIVES IN SPAIN

✉ Rubio Teso ML, Parra-Quijano M, Torres E and Iriondo JM (2018) Identification and assessment of the crop wild relatives of Spain that require most urgent conservation actions. *Mediterranean Botany*. Universidad Complutense de Madrid (UCM) 39(2). Available at: <https://doi.org/10.5209/mbot.60074>

Author country/area: Colombia, Spain

Research funding: European Union

To ensure food security under increased demands and a changing climate, crop traits must adapt and yields increase. Crop wild relatives (CWR) constitute important gene pools for improving crops for future generations and they should be the focus of conservation efforts.

In a study focused on CWRs in Spain, researchers assessed the *in* and *ex situ* conservation status of important species identified according to threat level, uniqueness and crossability. Their shortlist contained 47 species for which they used GBIF-mediated occurrences to determine the *in situ* protection by designated protected areas (PA).

Their results showed that 85 per cent of target CWR species have at least one accession in a germplasm bank, and 75 per cent have populations within PAs. However, with a target of at least five populations per

species, only 37 per cent make the cut. The authors also note that 11 of the 47 species are considered endangered internationally, but not listed in national catalogues of threatened species.

INCREASING IMPACT AND FEASIBILITY OF LARGE-SCALE RESTORATION

DATA USED: 12,085 SPECIES OCCURRENCES

Strassburg BBN, Beyer HL, Crouzeilles R, Iribarrem A, Barros F, de Siqueira MF, Sánchez-Tapia A, Balmford A, Sansevero JBB, Brancalion PHS, Broadbent EN, Chazdon RL, Filho AO, Gardner TA, Gordon A, Latawiec A, Loyola R, Metzger JP, Mills M, Possingham HP, Rodrigues RR, Scaramuzza CA de M, Scarano FR, Tambosi L and Uriarte M (2018) Strategic approaches to restoring ecosystems can triple conservation gains and halve costs. *Nature Ecology & Evolution*. Springer Nature 3(1): 62–70. Available at: <https://doi.org/10.1038/s41559-018-0743-8>

Author country/area: Australia, Brazil, Poland, Sweden, United Kingdom, United States

Research funding: None listed

Fourty-seven countries have included major ecosystem restoration targets covering 350 million hectares by 2030 as part of their pledges to the Paris Climate Agreement. Through Systematic Conservation Planning (SCP) nations may maximize benefits while minimizing costs.

Using the Atlantic Forest biodiversity hotspot, a large-scale restoration target in Brazil, researchers present a novel prioritization approach based on linear programming, suggested to outperform mainstream SCP methods.

To calculate benefits, they used 1) reductions in projected species extinctions—based on distribution models created with data from GBIF and others—and 2) climate change mitigation through carbon sequestration. They used land acquisition prices and quotes from restoration companies as an estimate of total costs.

Working from a baseline model, the authors produce spatially explicit configurations maximizing cost-effective benefits. In one compromise configuration, they are able increase benefits by 257 per cent for biodiversity and 105 per cent for climate change mitigation, while reducing costs by 57 percent compared to baseline.

The results show that multicriteria spatial planning can help increase the impact and feasibility of large-scale restoration.



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