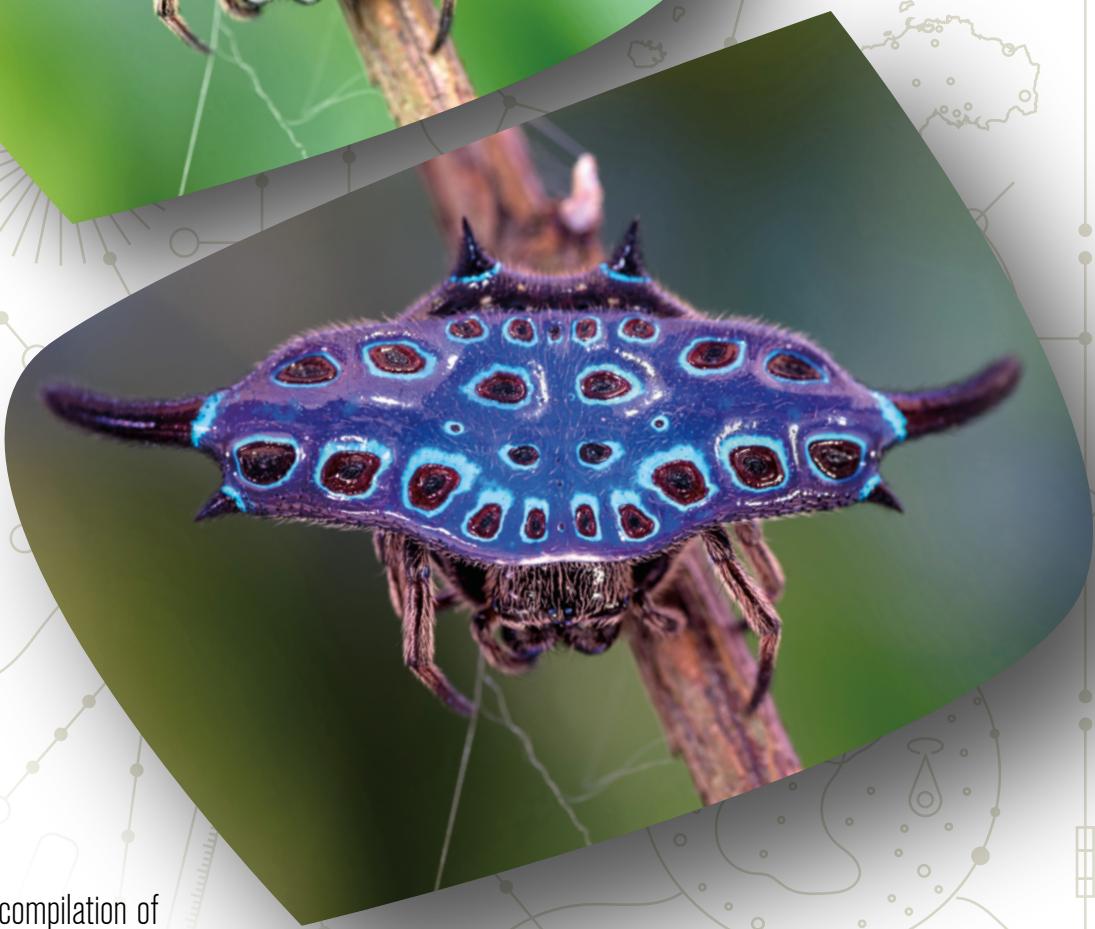


Science Review

2017



An annual compilation of
research data uses enabled by



Foreword

Use of GBIF-mediated data in scientific publications continues to grow, while data is being mobilized in new ways and from new sources.

This year's Science Review continues to document the steady growth of research that uses biodiversity data mobilized by the GBIF community. Among the typically diverse topics represented in this report, I'd like to highlight the application of biodiversity data to human health. The recognition of connections between human health and the health of animals, both domesticated and wild, is captured by the concept of "One Health". With its wealth of primary biodiversity data, GBIF is uniquely placed to contribute data relevant to studying the animal-human-ecosystem interface. However, it is worth noting that GBIF's coverage of some disease vectors could be greatly improved, even for well-known vectors such as *Aedes* mosquitoes. As always, gaps in our knowledge remain to be filled.

Identifying these gaps is a topic represented in the collection of papers on data management, as well as the focus of last year's Ebbe Nielsen Challenge. Gaps can have multiple causes. Perhaps the data simply doesn't exist, or the data does exist but hasn't yet made its way into GBIF. In this year's report the amount of GBIF-mobilized data is recorded for each paper. This figure is sometimes sobering. For example, the RAINBIO compilation of data on tropical African plants used 70,220 records made accessible by GBIF, but the study itself had a raw dataset of 977,000 records (eventually cleaned to 614,000). This raises the obvious question: why is this data not in GBIF? For this purpose, GBIF has introduced a new mechanism to help identify, prioritize and mobilize potential datasets. I encourage readers of this publication to use this tool (available at

bit.ly/gbif-suggest-dataset) when encountering data that should be available through GBIF, but isn't.

GBIF has made huge advances in mobilizing data, and as I noted in last year's report, making that data free and openly accessible. Still, a lot of data is clearly not yet freely accessible. Much of the data being generated by researchers is being stored in various external data repositories, but not in GBIF. These other repositories serve a valuable function of keeping data safe from loss and making it citable, but they do not necessarily make it easy to discover and reuse by the biodiversity community. Furthermore, its exclusion from GBIF means it hasn't benefited from the numerous data checks GBIF applies to incoming data (such as whether the taxonomic name is recognized, and whether the stated location is consistent with the latitude and longitude, to name just two).

The growing body of exciting research highlighted in this report depends on free and open access to large quantities of high-quality data. Recognizing this, the 2017 Ebbe Nielsen Challenge has the goal of encouraging the development of tools to make external data from various repositories accessible to the GBIF network, a step that will further enhance GBIF's role in supporting both fundamental and applied biodiversity research.

ROD PAGE

*Chair, GBIF Science Committee
June 2017*

*Vice Chairs : Greg Riccardi, Anders G. Finstad & Philippe Grandcolas
Members: Elizabeth Arnaud & Guy Cochrane*

Cover photos: *Gasteracantha* spp. in natural and ultraviolet light [top: flic.kr/p/V8mvDd, bottom: flic.kr/p/Ur1h7s]. © 2017 Nicky Bay (www.nickybay.com). The Singapore-based photographer runs workshops that train others in macrophotography techniques while focusing on insects, arachnids and fungi in his own work.

About the *Science Review*

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

As introduced last year, we are labelling open-access scientific articles using the symbol . We think this indicator is both valuable and practical for those interested in reading the research at a time when access often depends on institutional journal subscriptions.

Also, the comprehensive list of the year's uses remains decoupled from the printed version of the

Science Review in order to keep pace with the ever-expanding bibliographic tables (and reduce printing costs). The companion *Science Review* Sourcebook is available online at gbif.org/science-review-sourcebook-2017.

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

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

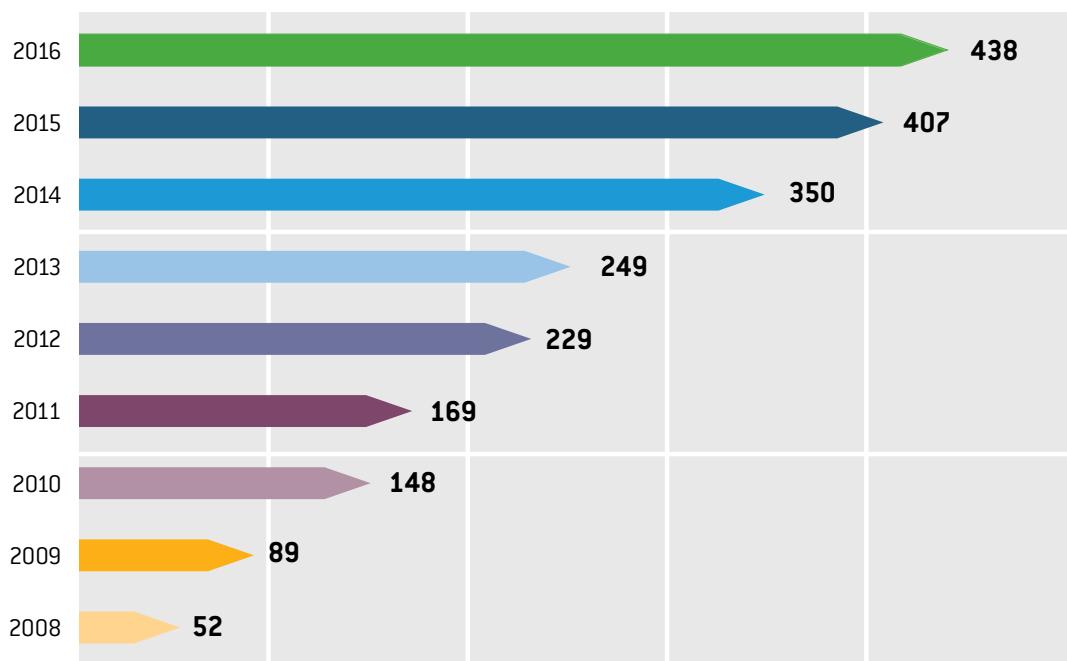
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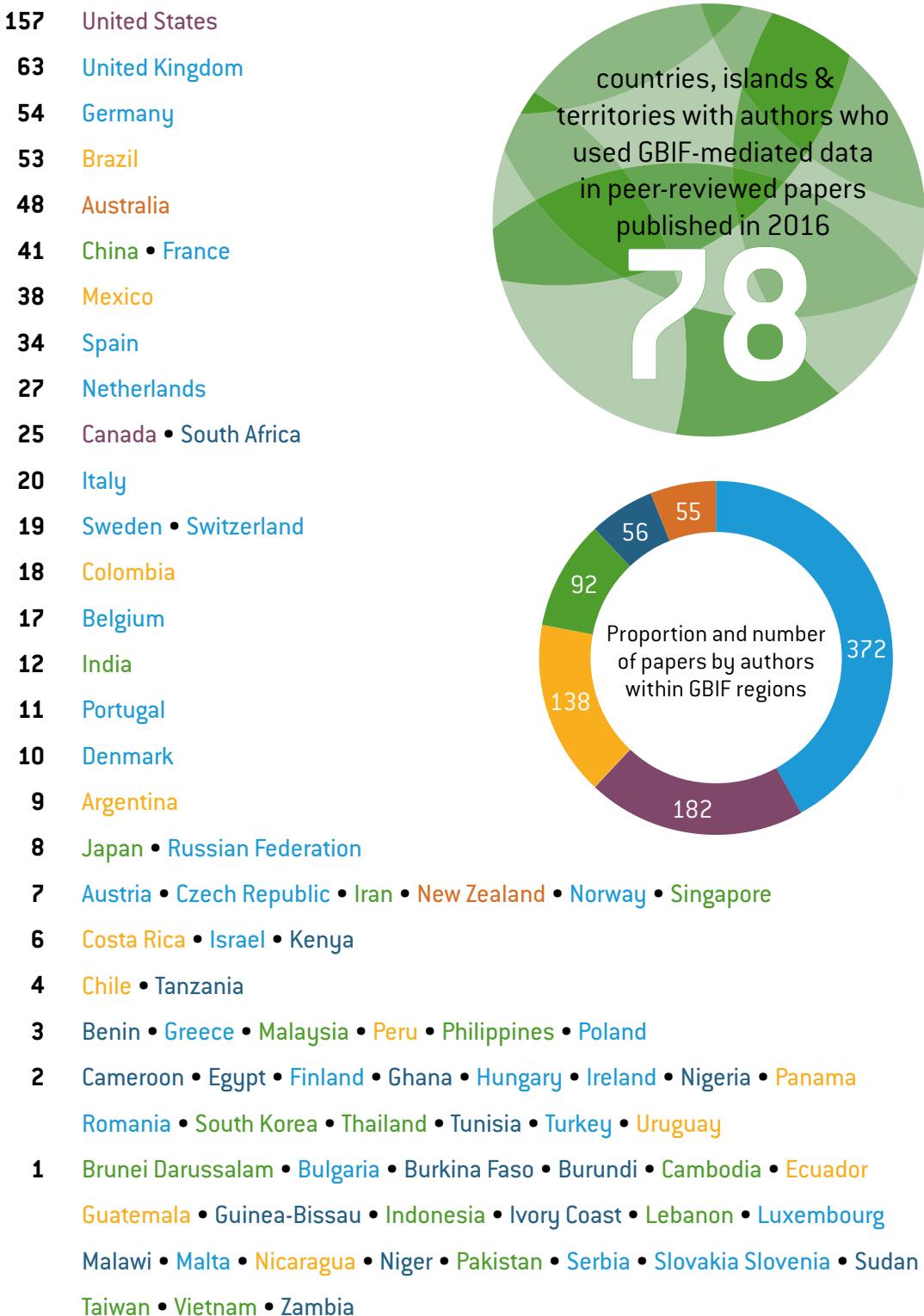
Uses and trends

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 number of countries, islands and territories whose institutions host authors who apply the data in their research articles. Each trend highlights the GBIF network's widening sphere of influence and impact on scientific research related to the biological domain.

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



NUMBER OF ARTICLES WITH AUTHORS BY COUNTRY/ISLAND/TERRITORY



Biodiversity and human health



AEDES AEGYPTI BY CYDNO [HTTP://WWW.INATURALIST.ORG/OBSERVATIONS/1573187](http://www.inaturalist.org/observations/1573187) CC BY-NC 4.0

MODELLING THE DISTRIBUTION OF THE SOUTHERN HOUSE MOSQUITO

DATA USED: 1,402 SPECIES OCCURRENCES

- ② Samy AM, Elaagip AH, Kenawy MA, Ayres CFJ, Peterson AT and Soliman DE (2016) Climate Change Influences on the Global Potential Distribution of the Mosquito *Culex quinquefasciatus*, Vector of West Nile Virus and Lymphatic Filariasis. PLOS ONE. Public Library of Science [PLoS] 11[10]: e0163863.

Author countries: Sudan, Egypt, Brazil, United States

Research funding: Fulbright

Outbreaks of vector-borne diseases may be associated with range expansion of vector populations, and predicting the potential distribution of vectors can aid disease prevention. In this study, researchers model the distribution of the southern house mosquito (*Culex quinquefasciatus*) known to carry disease-causing agents such as West Nile virus and St. Louis encephalitis virus, but also potentially Zika virus and a number of viruses that cause disease in livestock and other animals.

Under present-day conditions the potential distribution of *C. quinquefasciatus* showed high suitability in southern North America, most of South America, sub-Saharan Africa, South Asia, and most of Australia and New Zealand. Projections using

future climate scenarios revealed similar distribution patterns, however, with small, but significant increases, particularly in southern Australia.

Combining the maps of potential present-day and future distributions can identify areas, in which control and surveillance programs should be prioritized to help prevent disease outbreak.

Link to paper: <https://doi.org/10.1371/journal.pone.0163863>

ON THE ROAD TOWARDS ELIMINATION OF MALARIA IN SOUTH AMERICA

DATA USED: 2,500 SPECIES OCCURRENCES

- ② Alimi TO, Fuller DO, Herrera SV, Arevalo-Herrera M, Quinones ML, Stoler JB and Beier JC (2016) A multi-criteria decision analysis approach to assessing malaria risk in northern South America. BMC Public Health. Springer Nature.

Author countries: United States, Colombia

Research funding: The research was supported by NIH ICEMR grant: Centro Latino Americano de Investigación en Malaria (CLAIM) sponsored by NIAID/ICEMR (U19AI089702), Colciencias (719–2013)

According to the World Health Organization (WHO), the world has seen a 37 per cent decrease in malaria incidence over the last 15 years. However, the disease still imposes a significant economic and health burden

in regions where it is endemic. In 2013, South America had 427,000 confirmed cases and 82 deaths. This study uses a multi-criteria decision analysis (MCDA) to produce risk maps of malaria in the northern part of South America. The authors validate the risk maps using GBIF-mediated occurrences of three vector species (*Anopheles darlingi*, *An. Albimanus* and *An. nuneztovari*), and compared to previous studies, the maps give a continuous risk surface with high spatial detail and clearly defined gradients. The maps can be particularly useful for guiding targeted malaria interventions and potentially speeding up the process of eliminating malaria completely in South America.

Link to paper: <https://doi.org/10.1186/s12889-016-2902-7>



EIDOLON HELVUM BY AMASABAALUIZAH BY CYDNO
<HTTP://WWW.GBIF.ORG/OCCURRENCE/1211969391> CC BY-NC 4.0

TRAPPING LEISHMANIASIS IN MEXICO

DATA USED: 26,618 SPECIES OCCURRENCES

Pech-May A, Peraza-Herrera G, Moo-Llanes DA, Escobedo-Ortegón J, Berzunza-Cruz M, Becker-Fauser I, Montes De Oca-Aguilar AC and Rebollar-Téllez EA (2016) Assessing the importance of four sandfly species (Diptera: Psychodidae) as vectors of *Leishmania mexicana* in Campeche, Mexico. *Medical and Veterinary Entomology*. Wiley-Blackwell 30(3): 310–320.

Author countries: Argentina, Mexico

Research funding: CONACYT

In Latin America, the protozoan parasite *Leishmania*

mexicana is the causal agent of cutaneous leishmaniasis. Spread by sandflies, this ulcer-causing disease represents a serious public health problem in Mexico, especially in the Yucatan peninsula. In this study, researchers conducted a field study trapping sandflies in the state of Campeche and testing them for parasite presence. They captured more than 3,000 specimens belonging primarily to four species of the Psychodidae family. By DNA analysis they find 0.3 per cent of the flies to be infected with the parasite. Then, using ecological niche models based on GBIF-mediated occurrences, they demonstrate how nearly 40 per cent of the state of Campeche is suitable habitat for the flies, potentially exposing more than 100,000 people. The fly distributions overlap with those of known rodent reservoir species, increasing the evidence for the vectorial roles of the four fly species trapped in the study.

Link to paper: <https://doi.org/10.1111/mve.12169>

PREDICTING THE SPREAD OF CHIKUNGUNYA IN THE AMERICAS

DATA USED: 10,000 SPECIES OCCURRENCES

Escobar LE, Qiao H and Peterson AT (2016) Forecasting Chikungunya spread in the Americas via data-driven empirical approaches. *Parasites & Vectors*. Springer Nature.

Author countries: United States, China

Research funding: Global Emerging Infectious Disease Surveillance and Response System; Science and Technology Service Project (STS); Chinese Academy of Science; National Natural Science Foundation of China

Chikungunya (CHIKV) is a mosquito-borne viral infection that causes rashes, fever and joint symptoms. The virus is endemic to Africa and Asia and its principal vectors are *Aedes albopictus* and *A. aegypti*. In this study, researchers take a data-driven, ecological approach to predicting spread of CHIKV by focusing on the 2013 outbreak in the Americas. By compiling daunting amounts of data on airports, travel routes and aircraft passenger capacity, they anticipate CHIKV cases with high confidence in countries dominated by imported cases. Using GBIF-mediated occurrences, they model the ecological niches of the two vector species, and find that vector hotspots matched with initial reports of CHIKV cases. The approach presented in this study can be used to predict future spread of mosquito-borne diseases. CHIKV-positives travellers should be particularly aware of mosquito exposure, if travelling to identified areas of high ecological suitability.

Link to paper: <https://doi.org/10.1186/s13071-016-1403-y>

PREDICTING RISK OF MALARIA IN SOUTHEAST ASIA

DATA USED: 11,866 SPECIES OCCURRENCES

a Moyes CL, Shearer FM, Huang Z, Wiebe A, Gibson HS, Nijman V, Mohd-Azlan J, Brodie JF, Malaivijitnond S, Linkie M, Samejima H, O'Brien TG, Trainor CR, Hamada Y, Giordano AJ, Kinnaird MF, Elyazar IRF, Sinka ME, Vythilingam I, Bangs MJ, Pigott DM, Weiss DJ, Golding N and Hay SI [2016] Predicting the geographical distributions of the macaque hosts and mosquito vectors of *Plasmodium knowlesi* malaria in forested and non-forested areas. *Parasites & Vectors*. Springer Nature 9(1).

Author countries: United Kingdom, Malaysia, Canada, Thailand, Singapore, Japan, Kenya, Australia, United States, Indonesia

Research funding: none listed

In 2013, approximately 1 million cases of malaria were reported in the islands of southeast Asia, the most common cause of which is the parasite, *Plasmodium knowlesi*, with immense health, social and economic consequences in the region. In this study, researchers attempted to predict the spread of the disease by building distributions models of three reservoir species (*Macaca* spp.) as well as two mosquito vectors (*Dirus Complex* and *Leucosphyrus Complex*). Using GBIF-mediated occurrences they generated fine-scale maps of the species' distributions and explored overlaps and combined relationships with shrinking forest cover and use. The results suggest a potential increase in co-habitation of reservoir and vector species in areas with human activity, e.g. plantations and timber concessions. Overall, the study adds important knowledge to be used in future analyses of *P. knowlesi* infection risk in Southeast Asia.

Link to paper: <https://doi.org/10.1186/s13071-016-1527-0>



MASTOMYS NATALENSIS BY BATWRANGLER
<https://flic.kr/p/47HgQX> CC BY-NC-ND 2.0

PREDICTING AND PREVENTING FURTHER OUTBREAKS OF EBOLA

DATA USED: 2,254 SPECIES OCCURRENCES

a Pigott DM, Millear AI, Earl L, Morozoff C, Han BA, Shearer FM, Weiss DJ, Brady OJ, Kraemer MU, Moyes CL, Bhatt S, Gething PW, Golding N and Hay SI [2016] Updates to the zoonotic niche map of Ebola virus disease in Africa. *eLife*. eLife Sciences Organisation, Ltd. 5.

Author countries: United Kingdom, United States, Australia
Research funding: Paul G. Allen Family Foundation; National Institutes of Health; Rhodes Trust; Bill & Melinda Gates Foundation; German Academic Exchange Service (DAAD); UK Medical Research Council (MRC); UK Department for International Development (DFID); Wellcome Trust; Science & Technology Directorate

As the West African outbreak of Ebola is contained, focus shifts from control to prediction and prevention of the disease that caused more than 11,000 deaths. In their 2014 paper, Pigott and colleagues modelled the zoonotic niche of the virus through occurrences of three bat reservoir species. In this paper, the same team of researchers provide an update following an outbreak in the Democratic Republic of the Congo, and, through literature scrutiny and use of improved immunological tests, add new confirmed virus findings to the previously published database. They find evidence of Ebola virus in three animal species: Peter's mouse (*Mus setulosus*), greater forest shrew (*Sylvisorex ocellata*) and straw-coloured fruit bat (*Eidolon helvum*). By updating their model based on GBIF-mediated occurrences, they reassess the environmental suitability for the virus, increase the number of at-risk countries to 23, and highlight Cameroon, Gabon, Republic of the Congo and Equatorial Guinea as being even more suitable than previously calculated.

Link to paper: <https://doi.org/10.7554/eLife.16412>

PREDICTING ZOONOTIC SPILLOVERS UNDER FUTURE ENVIRONMENTAL STRESSORS

DATA USED: 88 SPECIES OCCURRENCES

Redding DW, Moses LM, Cunningham AA, Wood J and Jones KE [2016] Environmental-mechanistic modelling of the impact of global change on human zoonotic disease emergence: a case study of Lassa fever. *Methods in Ecology and Evolution*. Wiley-Blackwell 7(6): 646–655.

Author countries: United Kingdom, United States

Research funding: Ecosystem Services for Poverty Alleviation Programme (ESPA); Department for International Development (DFID); Economic and Social Research Council (ESRC); Natural Environment Research Council (NERC); Royal Society Wolfson Research Merit Award

A zoonotic spillover is when an infectious disease moves from its animal source or reservoir via a vector, to humans. Examples include Ebola, SARS, AIDS, and, the focus of this study, hemorrhagic fever caused by Lassa fever virus [LAS]. Integrating global environment stressors, researchers assessed the impact of climate change, population growth and land use on future emergence and spread of LAS. By use of confirmed disease cases and GBIF mediated occurrences of the Lassa virus reservoir, the natal multimammate rat (*Mastomys natalensis*), the researchers created ecological niche models examining relationships with a variety of environmental variables. The find significant associations between LAS outbreak and reservoir presence, annual precipitation, population density and rice yields. The models predict a doubling of spillover events under future scenarios. The methodology described in the study can be incorporated in epidemiological disease models to create a powerful framework for predicting spillovers of zoonotic diseases.

Link to paper: <https://doi.org/10.1111/2041-210X.12549>

MAPPING THE RISK OF TICK-BORNE DISEASE

DATA USED: 3.8 MILLION SPECIES OCCURRENCES

Estrada-Peña A and de la Fuente J (2016) Species interactions in occurrence data for a community of tick-transmitted pathogens. *Scientific Data*. Springer Nature 3: 160056.

Author countries: Spain, United States

Research funding: European Commission

Using species distributions of pathogen vectors is becoming increasingly important for predicting human and livestock infection risks. With tick-borne illnesses, such as Lyme disease and viral meningoencephalitis, the equation is expanded from vector and pathogen to include tick hosts. Based on extensive literature searches and GBIF-mediated occurrences, the authors of this data paper build a network of interactions between ticks, hosts and pathogens. They use remotely-sensed environmental data to calculate the niches of ticks and their hosts. Finally, they combine the interaction network with the niche models to create a novel framework for evaluating niche overlaps and predicting occurrences of tick-transmitted pathogens. The resulting datasets



SCIURUS AUREOGASTER BY ALFONSO GUTIÉRREZ ALDANA [HTTP://WWW.GBIF.ORG/OCCURRENCE/1262389352](http://www.gbif.org/occurrence/1262389352) CC BY-NC 4.0

were deposited with Dryad for use in future research and risk assessments. The authors note that their framework can be used to capture the impact of particular species and host-tick pairs in the circulation of pathogens.

Link to paper: <https://doi.org/10.1038/sdata.2016.56>

PREDICTING POTENTIAL ZOONOTIC HOSTS

DATA USED: 37,297 SPECIES OCCURRENCES

Stephens CR, González-Salazar C, Sánchez-Cordero V, Becker I, Rebollar-Tellez E, Rodríguez-Moreno Á, Berzunza-Cruz M, Domingo Balcells C, Gutiérrez-Granados G, Hidalgo-Mihart M, Ibarra-Cerdeña CN, Ibarra López MP, Iñiguez Dávalos LI and Ramírez Martínez MM (2016) Can You Judge a Disease Host by the Company It Keeps? Predicting Disease Hosts and Their Relative Importance: A Case Study for Leishmaniasis. PLOS Neglected Tropical Diseases. Public Library of Science (PLoS) 10(10): e0005004.

Author country: Mexico

Research funding: Universidad Nacional Autónoma de México; CONACyT

Zoonoses are diseases that can be transmitted from animals to humans, accounting for more than 60 per cent of human infectious diseases. Host animal range can be a crucial factor in predicting disease risk and potential for interventions, but some zoonoses are complex with not one, but multiple potential hosts and subsequent large ranges.

In this study, researchers from Mexico used Complex Inference Networks to predict hosts of *Leishmania* parasites, causal agent of Leishmaniasis, that transmit from sand-flies to mammalian hosts, of which only eight have been previously identified.

Using GBIF-mediated occurrences of sand-flies and mammals in Mexico they constructed a database of co-occurrences and inferred potential vector-host interactions. Ranking potential hosts by probability, they collected wildlife specimens, tested them for parasite infection, and found 22 positive species, including thirteen species of bats and one squirrel identified as hosts for the first time.

The study shows how innovative modelling of species occurrences can provide useful information about interactions and be applied to complex problems such as multi-host diseases.

Link to paper: <https://doi.org/10.1371/journal.pntd.0005004>

ORIGINS OF RENAISSANCE MEDICINE

DATA USED: 150 SPECIES

Rivera D, Verde A, Obón C, Alcaraz F, Moreno C, Egea T, Fajardo J, Palazón JA, Valdés A, Signorini MA and Bruschi P (2017) Is there nothing new under the sun? The influence of herbals and pharmacopoeias on ethnobotanical traditions in Albacete (Spain). Journal of Ethnopharmacology. Elsevier BV 195: 96–117.

Author countries: Spain, Italy

Research funding: none listed

Plants and animals have been used to make drugs for millennia. 16th century pharmacists in Western Europe preferred extremely complex herbal formulations involving dozens of ingredients, many sourced in far-away regions.

This study presents a detailed analysis of a unique set of recently discovered 16th century pharmacological manuscripts from Spain with the goal of determining ingredients, and, using GBIF-mediated data to verify species names and origin as well as influences on present medicinal knowledge.

The manuscripts describe 101 medicines of which the majority contain more than two ingredients (some as many as 35), and 85 per cent of the ingredients are of plant origin. The researchers identify more than 60 per cent of ingredients still in use today in medicine production, however, the source of these has shifted from exotic imports to cheaper, local resources.

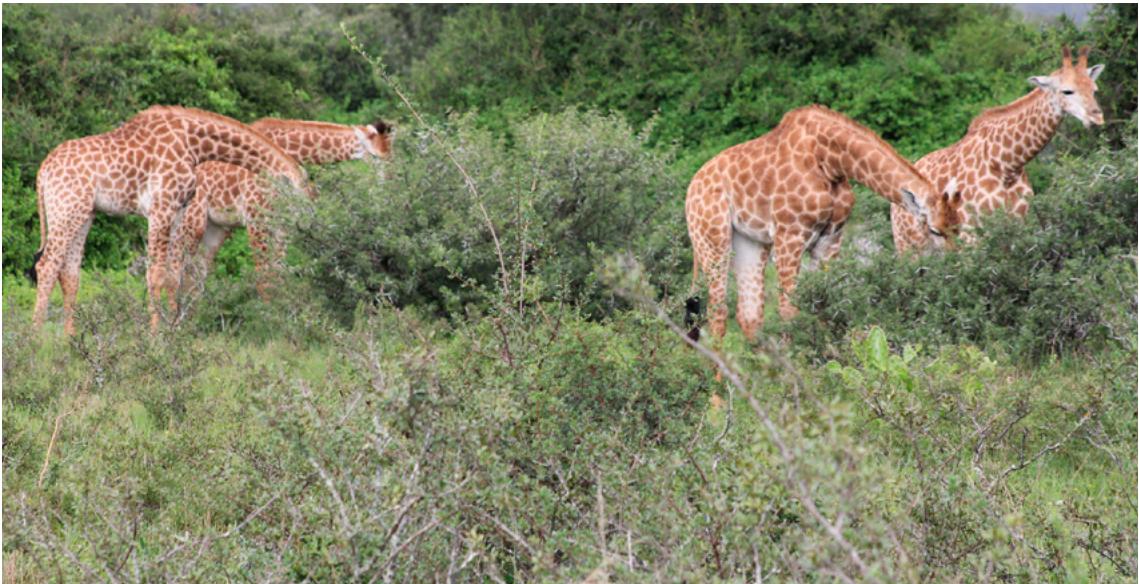
The study confirms that despite local availability of medicine ingredients, physicians had a distinct preference for exotic and expensive resources, inevitably making drugs of the Renaissance a precious affair.

Link to paper: <https://doi.org/10.1016/j.jep.2016.11.040>



IVORY FROM *ELEPHAS MAXIMUS* SUBSP. *INDICUS*, A POPULAR INGREDIENT IN RENAISSANCE MEDICINE. PHOTO BY TRISLANDER
[HTTP://WWW.GBIF.ORG/OCURRENCE/1098901646](http://www.gbif.org/occurrence/1098901646) CC BY-NC 4.0

Data management



ONE SINGLE OR SEVERAL SPECIES OF GIRAFFES (*GIRAFFA CAMELOPARDALIS*)? DEPENDS ON THE TAXONOMIC INTERPRETATION. PHOTO BY RYBER
[HTTP://WWW.GBIF.ORG/OCCURRENCE/89109526](http://WWW.GBIF.ORG/OCCURRENCE/89109526) CC BY-NC 4.0

TAXONAUT - COMPARING TAXONOMIES GRAPHICALLY

DATA USED: CHECKLIST BANK

- ② Ytow N [2016] Taxonaut: an application software for comparative display of multiple taxonomies with a use case of GBIF Species API. *Biodiversity Data Journal*. Pensoft Publishers 4: e9787.

Author country: Japan

Research funding: JSPS

The naming and classification of species is crucial for biodiversity science and relies on consistent grouping of organisms in a hierarchical structure. Taxonomies representing such hierarchies may come from a variety of sources and are not always consistent.

In this paper, winner of the inaugural Ebbe Nielsen Prize in 2002, Nozomi Ytow, presents a new Java-based application, Taxonaut, that allows for easy and user-friendly summarised comparisons of two or more taxonomies. Relying on GBIF Checklist Bank for taxonomic data, Taxonaut takes a scientific name and returns the taxonomies in which that particular taxon is included. From the results, users are able to select specific taxonomies and compare name usage in a hierarchical structure with matching taxa aligned for user-friendly comparison. Searches can also be expanded to include basionyms and synonyms, if relevant.

Taxonaut is novel methodological approach to comparative taxonomy analysis that allows non-expert users to assess and compare nomenclatural data in a fast and easy manner.

Link to paper: <https://doi.org/10.3897/BDJ.4.e9787>

ACCESSING THE OPEN TREE OF LIFE

DATA USED: 1,868 SPECIES OCCURRENCES

- ③ Michonneau F, Brown JW and Winter DJ [2016] rotl: an R package to interact with the Open Tree of Life data. *Methods in Ecology and Evolution*. Wiley-Blackwell 7(12): 1476–1481.

Author country: United States

Research funding: NIH; iDigBio; National Science Foundation

Phylogenetic trees can be tricky to assemble, but advances in genetic sequencing and informatics has made the process significantly easier. Still, published phylogenies are often only available as image files with no standard for storage and representation. The Open Tree of Life (OTL) project aims to change this, allowing researchers to assemble and maintain phylogenies in standardized environment. Using a new software package, rotl, researchers can now use the popular data processing suite, R, to directly interact programmatically with the OTL data. The present paper describes how researchers can extract relationships between taxa, but also access phylogenies from specific studies of interest. Species

data accessed via `rotl` can easily be integrated with GBIF-mediated occurrences to visualize occurrences associated with a specific study. The `rotl` package fits well into the range of R tools available to biodiversity researchers.

Link to paper: <https://doi.org/10.1111/2041-210X.12593>

IDENTIFYING DATA GAPS THROUGH VISUALIZATION

DATA USED: 10,000 SPECIES OCCURRENCES

Ⓐ Barve V and Otegui J [2016] *bdvis: visualizing biodiversity data in R*. Bioinformatics. Oxford University Press [OUP] 32[19]: 3049–3050.

Author country: United States

Research funding: Google

Informatics is an integrated part of biodiversity science, and tools are becoming essential for researchers to download, process and visualise biodiversity data. The R environment is rapidly becoming the preferred platform for all kinds of data analysis, including biodiversity. This paper introduces a new R package, `bdvis`, that enables visualization of datasets to help identify temporal, spatial and taxonomic gaps. The package accepts downloads of occurrences from GBIF (via `rgbif`), VertNet (via `rvertnet`) and iNaturalist (via `rinat`) and can help data holders to improve quality of existing datasets, and data users to understand strengths and weaknesses in datasets. Through examples, the authors demonstrate how a dataset from GBIF can be downloaded, formatted and graphically visualized in just a few simple steps. The resulting graphs provide insights into possible gaps that should be considered by data users and potentially addressed by data holders.

Link to paper: <https://doi.org/10.1093/bioinformatics/btw333>



HOODED ORIOLE (*ICTERUS CUCULLATUS*) BY BOURIQUER
HTTP://WWW.GBIF.ORG/OCCURRENCE/1253316638 CC BY-NC 4.0

BIG DATA IN BIODIVERSITY

DATA USED: 9,397 SPECIES OCCURRENCES

Franklin J, Serra-Diaz JM, Syphard AD and Regan HM [2016] Big data for forecasting the impacts of global change on plant communities. *Global Ecology and Biogeography*. Wiley-Blackwell 26[1]: 6–17.

Author country: United States

Research funding: National Science Foundation

Researchers are using big data in studies of many areas of ecology and biodiversity, and while integrating big datasets allows for addressing questions on a global scale, there are challenges faced with different types of data.

This concept paper reviews four classes of data relevant for forecasting the impacts of global change on vegetation: environmental data, species occurrences, community plots and species traits. The authors highlight how a growing number of regional and global biodiversity research initiatives use GBIF for species occurrence data, but also note that errors in spatial coordinates and taxonomic identification can lead to overestimations.

For researchers producing their own datasets, the authors point to the importance of storing these in data repositories that allows for re-use and post-publication peer review, while also ensuring proper attribution that, in turn will foster more enthusiastic data sharing and data-driven discovery. The quality of the data, however, must always be considered, as the size of a dataset alone cannot overcome problems caused by systematic errors.

Link to paper: <https://doi.org/10.1111/geb.12501>

THE CASE FOR A RUSSIAN NATIONAL BIODIVERSITY PORTAL

DATA USED: 139,909 SPECIES OCCURRENCES

Ivanova NV and Shashkov MP [2016] Biodiversity Databases in Russia: Towards a National Portal. *Arctic Science*. Canadian Science Publishing.

Author country: Russian Federation

Research funding: Russian Foundation of Basic Research

Despite being the largest country in the world and playing a key role in Arctic ecosystem conservation, Russia remains largely fragmented and digitally inaccessible when it comes to biodiversity data. More than 12,500 species of vascular plants, 1,500 vertebrates, and 100,000 invertebrates make up the Russian biodiversity, yet GBIF counts less than 0.1 occurrence per square kilometre of Russian territory.

This paper reviews existing biodiversity information

systems in Russia across species occurrences, taxonomy and digital collections. Although some systems are in place, the authors point to several problems, including a lack of willingness among researchers to share data, database platforms without functionality to allow internet access, spatial information presented as images rather than coordinates, and, systems not being updated and finally becoming unavailable as projects are completed.

Russian scientists have considerable experience in biodiversity informatics, yet lack a national platform for aggregating and sharing data. The authors conclude that formal participation in GBIF with the creation of a national node and portal is necessary to increase data mobilization and contribution to national and international biodiversity science.

Link to paper: <https://doi.org/10.1139/AS-2016-0050>

RAINBIO – A COMPILATION OF TROPICAL AFRICAN VASCULAR PLANTS

DATA USED: 70,220 SPECIES OCCURRENCES

Gilles D, Zaiss R, Blach-Overgaard A, Catarino L, Damen T, Deblauwe V, Dessein S, Dransfield J, Droissart V, Duarte MC, Engledow H, Fadeur G, Figueira R, Gereau RE, Hardy DJ, Harris DJ, de Heij J, Janssens S, Klomberg Y, Ley AC, MacKinder BA, Meerts P, van de Poel JL, Sonké B, Sosef MSM, Stévert T, Stoffelen P, Svenning J-C, Sepulchre P, van der Burgt X, Wieringa JJ and Couvreur TLP (2016) RAINBIO: a mega-database of tropical African vascular plants distributions. *PhytoKeys*. Pensoft Publishers 74: 1–18.

Author countries: France, Portugal, Denmark, Netherlands, Belgium, United Kingdom, United States, Germany

Research funding: French Foundation for Research on Biodiversity (FRB)

Tropical Africa contains high levels of species diversity, but data from the region is scarce and at best, fragmented. Biodiversity data is crucial for wise and sustainable conservation assessments, but also for understanding the shifts imposed by climate change and other human-mediated activities.

This study presents a unique compilation of 13 datasets of vascular plants in sub-Saharan tropical Africa from a variety of sources, including two GBIF-mediated datasets. Researchers carried out extensive quality checking including geo-referencing verification, taxonomic standardization, and duplication filtering, reducing the raw dataset from 977,000 to 614,000 records. As the goal was to focus on indigenous plants, the researchers used GBIF-mediated occurrences of all species to check distributions and remove 1,635 non-native species.

The final dataset comprises 25,356 species of vascular plants collected from 1782 to 2015 and includes habitat data for nearly all species. The authors have made the database available for online download under a Creative Commons BY-NC license.

Link to paper: <https://doi.org/10.3897/phytokeys.74.9723>

MAPPING DISTRIBUTION OF LICHEN TRAITS

DATA USED: 3,879,389 SPECIES OCCURRENCES

Rambold G, Zedda L, Coyle JR, Peršoh D, Köhler T and Triebel D (2016) Geographic heat maps of lichen traits derived by combining LIAS light description and GBIF occurrence data, provided on a new platform. *Biodiversity and Conservation*. Springer Nature 25(13): 2743–2751.

Author countries: Germany, United States

Research funding: None listed

Lichens are composite organisms arising from symbioses between fungi and algae or cyanobacteria, respectively, with a wide range of traits, several of which are linked to ecosystem services. To better understand the role lichens play in ecosystems, this study combines spatial occurrences of lichenized fungi mediated by GBIF with trait data, to form *LIAS gtm*, a new platform for geographical tracking of lichen traits.



POWDERED WRINKLE LICHEN (*TUCKERMANNOPSIS CHLOROPHYLLA*)
BY JK JOHNSON [HTTP://WWW.GBIF.ORG/OCCURRENCE/1052593012](http://www.gbif.org/occurrence/1052593012)
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Part of the *LIAS light* service, the resulting data matrix which is updated semi-automatically every three months, can be queried through a web interface based on traits and geographic area of interest. Visualized as heat maps, the results are easily exported and allow for further interpretation and use in research. Users can perform analyses based on both single and multiple traits, and also potentially discover novel trait-trait correlations.

The *LIAS gtm* tool offers unique insights into the geographic distribution of lichen traits.

Link to paper: <https://doi.org/10.1007/s10531-016-1199-2>

Evolution and biogeography



A FALSE TREE CORAL (*RHINOBOTHRYUM BOVALLII*) BY GREG LASLEY [HTTP://WWW.GBIF.ORG/OCCURRENCE/1249286266](http://WWW.GBIF.ORG/OCCURRENCE/1249286266) CC BY-NC 4.0

WHEN EVOLUTION GOES BANANAS

DATA USED: 3,600 SPECIES OCCURRENCES

Janssens SB, Vandelooy F, De Langhe E, Verstraete B, Smets E, Vandenhouwe I and Swennen R (2016) Evolutionary dynamics and biogeography of Musaceae reveal a correlation between the diversification of the banana family and the geological and climatic history of Southeast Asia. *New Phytologist*. Wiley-Blackwell, 1453–1465.

Author countries: Belgium, Netherlands, Tanzania

Research funding: Research Fund-Flanders (FWO)

The evolutionary patterns of plants and animals can be shaped by climate and geology. In this study of the *Musaceae* family, of which bananas and plantains (*Musa acuminata*, *Musa balbisiana*) are members, researchers investigate the diversification and biogeography the family's three genera (*Ensete*, *Musa*, and *Musella*), and draw links to the geological history of Southeast Asia. The authors sampled 44 *Musaceae* species for DNA analysis and gene alignment. Combined with GBIF-mediated occurrences they construct a new phylogenetic tree showing the ancestral ranges of the three genera and revealing the origin of *Musaceae* in northern Indo-Burma about 50 million years ago. They estimate that the divergence of *Musa* into two distinct clades took place about 10 million years later, and these diversified into numerous species 20 and 25 million years ago, respectively. The authors conclude that the diversification patterns of the banana family found in the study, mirror geological and climatic events in Southeast Asia.

Link to paper: <https://doi.org/10.1111/nph.13856>

ON THE ORIGIN OF BELLFLOWERS

DATA USED: 100,000 SPECIES OCCURRENCES

Crowl AA, Miles NW, Visger CJ, Hansen K, Ayers T, Haberle R and Cellinese N (2016) A global perspective on Campanulaceae: Biogeographic, genomic, and floral evolution. *American Journal of Botany*. Botanical Society of America, 233–245.

Author country: United States

Research funding: National Science Foundation

The bellflowers (*Campanulaceae*) are a diverse family of flowering plants encompassing more than 2,300 species across five major lineages. In this study, researchers use genetic sequence data and GBIF-mediated occurrences to provide new insights into the phylogeny and biogeography of *Campanulaceae*.

Their analysis confirms the traditionally recognized five subfamilies of the group, and provide evidence suggesting an African origin of the entire family diverging from a common ancestor about 76 million years ago.

Based on genetic studies, the authors present a hypothesis of a diploid ancestor with nine chromosome pairs. Genome duplication events leading to an increase in copies of chromosomes at the bases of clades facilitated specialization of species including the evolution of woodiness. The study is the largest to date on the *Campanulaceae* family.

Link to paper: <https://doi.org/10.3732/ajb.1500450>

BIODIVERSITY AND BIOGEOGRAPHY OF INTERTIDAL COMMUNITIES IN THE ANTARCTIC

DATA USED: 38,100 SPECIES OCCURRENCES

Griffiths HJ and Waller CL [2016] The first comprehensive description of the biodiversity and biogeography of Antarctic and Sub-Antarctic intertidal communities. *Journal of Biogeography*. Wiley-Blackwell, 1143–1155.

Author country: United Kingdom

Research funding: none listed

Marking the area between the high and low of the tide, the intertidal zone is a distinctive environment with a unique biota, often seen as the ‘canary in the coal mine’ for changes due to climate change in cool regions. This study represents a comprehensive analysis of the biodiversity and biogeography of intertidal communities in the Antarctic and sub-Antarctic regions. Compiling data from expedition records, published manuscripts, GBIF and other digital sources, the authors create a database of 3,900 occurrences across 1,416 species, noting that a general lack of standardized data makes this a challenging area to study. They are, however, able to demonstrate that the intertidal zone of the Antarctic region is far from being devoid of life. In fact, the intertidal communities of the Antarctic Peninsula prove richer and more diverse than those of southern South America.

Link to paper: <https://doi.org/10.1111/jbi.12708>

ULTRAVIOLET FLOWER PATTERN DIVERSITY

DATA USED: 335,000 SPECIES OCCURRENCES

Koski MH and Ashman T-L [2016] Macroevolutionary patterns of ultraviolet floral pigmentation explained by geography and associated bioclimatic factors. *New Phytologist*. Wiley-Blackwell, 708–718.

Author country: United States

Research funding: NSF; UPitt Mellon

While the colour of flowers affects interactions with pollinators, other pigments confer invisible traits such as protection against ultraviolet (UV) radiation. In this study, researchers investigated the UV absorbance of plants in the Potentilleae tribe of the rose family, and tested whether UV floral patterns were associated certain geographic or climatic properties. Initially, the researchers constructed a phylogeny of the tribe through alignment of DNA sequences from 130 species herbaria. They then assessed the absorptive properties of 177 different species by photographing flowers under UV light and measuring proportion of petals absorbing UV. They find that UV absorption is mostly present in plants with yellow petals, and although unable to predict the presence or absence

of absorption by means of geography or climate, they do find that among plants that absorb, those growing in areas with high level of UV exposure have more uniform patterns of absorption.

Link to paper: <https://doi.org/10.1111/nph.13921>

ADAPTING TO THE EXTREMES OF LIVING IN THE DESERT

DATA USED: 17,000 SPECIES OCCURRENCES

Nylinder S, Razafimandimbison SG and Anderberg AA [2016] From the Namib around the world: biogeography of the Inuleae-Plucheinae (Asteraceae). *Journal of Biogeography*. Wiley-Blackwell 43(9): 1705–1716.

Author country: Sweden

Research funding: Swedish Research Council

Deserts are usually not biodiversity hotspots, but the species adapted to the extreme and arid conditions are usually highly specialized and endemic to the area. Representing more than 250 species, the Inuleae-Plucheinae tribe is a prominent example of arid flora found globally, and this study presents a historical biogeography of the group. Using two different approaches (one based on GBIF-mediated occurrences), the researchers inferred the ancestral



INDIAN STRAWBERRY (*POTENTILLA INDICA*) BY LAURA CLARK
[HTTP://WWW.GBIF.ORG/OCCURRENCE/1262374812](http://WWW.GBIF.ORG/OCCURRENCE/1262374812) CC BY-NC 4.0

areas of the tribe to range from the Namib desert to the western Kalahari. The temporal origin is estimated to be 15.4 million years ago, coinciding with an increase in strength of the Antarctic Circumpolar Current and aridification of the Namib area, suggesting changes in climatic conditions as a driver of evolutionary radiation. The study shows how studying large groups of organisms can help uncover patterns difficult to reveal in single-species studies.

Link to paper: <https://doi.org/10.1111/jbi.12764>

MIMICS AND MODELS OF NEW WORLD SNAKES

DATA USED: 299,376 SPECIES OCCURRENCES

② Davis Rabosky AR, Cox CL, Rabosky DL, Title PO, Holmes IA, Feldman A and McGuire JA [2016] Coral snakes predict the evolution of mimicry across New World snakes. *Nature Communications*. Springer Nature 7: 11484.

Author countries: United States, Israel

Research funding: National Science Foundation; University of Michigan

Not all snakes need venom to scare predators away. A large group of harmless snakes simply mimics the appearance of noxious species as a means of deterring their enemies through deceit. In this paper, researchers studied distributional, phenotypic and phylogenetic data across all New World snakes, and investigated how shifts to mimetic coloration relate to the evolution of venomous coral snakes. Using GBIF-mediated occurrences, the researchers constructed geographic ranges of more than 1,000 species, and found that coral snakes are a strong predictor of the abundance of mimics. However, the number of observed mimetic species is much higher than expected. Phylogenetic analysis revealed at least 19 independent origins of mimetic coloration, and not surprisingly these all appear after the arrival of coral snakes. Interestingly, the researchers also find evidence of widespread loss of mimetic coloration, rejecting previous suggestions that mimicry is evolutionarily irreversible.

Link to paper: <https://doi.org/10.1038/ncomms11484>

SOWING THE SEEDS OF ZINGIBERALES

DATA USED: 55,309 SPECIES OCCURRENCES

② Benedict JC, Smith SY, Specht CD, Collinson ME, Leong-Škorničková J, Parkinson DY and Marone F [2016] Species diversity driven by morphological and ecological disparity: a case study of comparative seed morphology and anatomy across a large monocot order. *AoB Plants*. Oxford University Press [OUP] 8: plw063.

Author countries: United States, United Kingdom, Singapore, Switzerland

Research funding: Heliconia Society International; National Science Foundation; National Parks Board, Singapore; Czech Science Foundation; Integrated Infrastructure Initiative [I3]; European Community

A myriad of factors contributes to the genotypic and phenotypic diversity found in organisms on Earth, and understanding the underlying processes is a fundamental question in biology. In this study, researchers address this question by investigating the morphologically diverse angiosperm order of Zingiberales, members of which include bananas and

gingers, mainly found in the tropical and subtropical regions of the world.

Through a combination of seed analysis using X-ray microscopy and ecological niche mapping based on GBIF-mediated occurrences, the authors explore the properties of 166 taxa from eight different families.

Morphologically, an extraordinary diversity exists among Zingiberales seeds, but numerous traits unite families. The ecological niches are similar across the order as ninety per cent are distributed in the tropics and subtropics with similar parameters in terms of altitude, precipitation and temperate. One family, Zingiberaceae, however, stands out by also inhabiting frost-prone temperate regions.

Link to paper: <https://doi.org/10.1093/aobpla/plw063>



GREEN ANOLE (*ANOLIS CAROLINENSIS*) BY NICK LINDNER
[HTTP://WWW.GBIF.ORG/OCCURRENCE/1135353968](http://WWW.GBIF.ORG/OCCURRENCE/1135353968) CC BY-NC 4.0

PREDICTING FUTURE DISCOVERIES OF LIZARDS

DATA USED: 4,400 SPECIES OCCURRENCES

Meiri S [2016] Small, rare and trendy: traits and biogeography of lizards described in the 21st century. *Journal of Zoology*. Wiley-Blackwell 299(4): 251–261.

Author country: Israel

Research funding: Israel Science Foundation

The rate at which researchers are describing new species of lizards is increasing rapidly. In 2000, taxonomists described 50 new species, and this number increased to 140 in 2014.

In this study, a researcher from Tel Aviv University compiled discovery dates and species traits for all known lizard species (order Squamata excluding snakes), and deduced range sizes using occurrence data from GBIF and others. By applying statistical analysis, the researcher related traits of the discovered species to the year of discovery. The results showed that most recent discoveries (21st century) are more frequent in the tropics. The species

discovered have smaller body and range sizes, and are more likely to be nocturnal, but less likely to be burrowing. Finally, and most unfortunately, the study indicates that recent discoveries are more likely to be threatened with extinction than those described earlier, hinting at the discouraging fact that some lizard species may be lost before they are discovered.

Link to paper: <https://doi.org/10.1111/jzo.12356>

NARROWING THE GAP BETWEEN RICH AND POOR

DATA USED: 4,400,000 SPECIES OCCURRENCES

Spalink D, Drew BT, Pace MC, Zaborsky JG, Starr JR, Cameron KM, Givnish TJ and Sytsma KJ [2016] Biogeography of the cosmopolitan sedges (Cyperaceae) and the area-richness correlation in plants. *Journal of Biogeography*. Wiley-Blackwell 43[10]: 1893–1904.

Author countries: United States, Canada

Research funding: NSF; NSERC; BSA; ASPT

Why are some taxonomic groups rich in species while others are poor? Evolutionarily speaking, richness is limited by diversification rate and age, but reality is more complex. This study focused on sedges (Cyperaceae family) and the observed correlation between occupied area and its richness. Using molecular data from four genes sequenced in 384 taxa combined with GBIF-mediated occurrences, researchers modelled ancestral ranges and measured diversification rates, and tested for correlation of richness with range size, overlap, niche clade age and rate of diversification. Their results point to South America as the origin of Cyperaceae in the late Cretaceous. Increases in diversification took place three times, two of which occurred in the temperate Northern Hemisphere. Species-rich clades occupy more space and exhibit patterns consistent with niche differentiation correlating with diversification.

Link to paper: <https://doi.org/10.1111/jbi.12802>

EXPLORING MODES OF NEOTROPICAL SPECIATION

DATA USED: 4,229 SPECIES OCCURRENCES

André T, Salzman S, Wendt T and Specht CD [2016] Speciation dynamics and biogeography of Neotropical spiral gingers (Costaceae). *Molecular Phylogenetics and Evolution*. Elsevier BV 103: 55–63.

Author countries: United States, Brazil

Research funding: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior; Conselho Nacional de Desenvolvimento Científico e Tecnológico; National Geographic Society; NSF; UC Berkeley; CNR-BSP; SPUR; URAP

Speciation, the evolutionary process by which populations become distinct species, is often related to geographic alterations as uplifting mountain

ranges and rising oceans create barriers and new climates to support increased diversity. More evident in the Neotropics than anywhere, the high levels of biological diversity draw attention from researchers looking to explain evolutionary patterns. In this study, researchers examine the diversification dynamics of the Neotropical region using a phylogenetic framework of the Spiral Gingers (Costaceae family). Through GenBank downloads and *de novo* DNA sequencing combined with GBIF-mediated occurrences, the researchers produce a dated phylogeny of Costaceae showing an Eocene origin of the family with the large *Costus* genus diverging about 30 million years ago. The most-recent common ancestor of the Neotropical *Costus* clade is estimated to have occurred only 10 million years ago, with speciation without geographic separation (sympatry) being high, as opposed to the older South American clade dominated by speciation as a result of separation (allopatry).

Link to paper: <https://doi.org/10.1016/j.ympv.2016.07.008>

DEVIL'S GARDENS FOUND IN FRENCH GUIANA

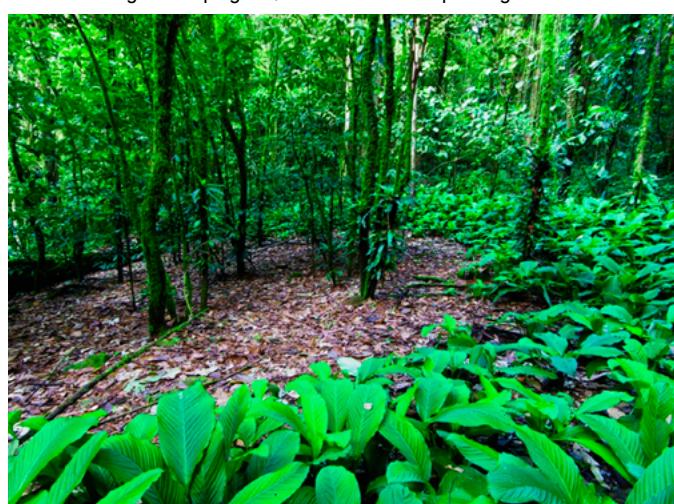
DATA USED: 3,601 SPECIES OCCURRENCES

Salas-Lopez A, Talaga S and Lalagüe H [2016] The discovery of devil's gardens: an ant–plant mutualism in the cloud forests of the Eastern Amazon. *Journal of Tropical Ecology*. Cambridge University Press [CUP] 32[03]: 264–268.

Author country: France

Research funding: French Agence Nationale de la Recherche; Centre National de la Recherche Scientifique; Fond Social Européen; Université Antilles-Guyane

Devil's gardens are a phenomenon of the Amazon, in which highly specialized ant species adapted to living within cavities of equally specialized plants, so-called myrmecophytes, attack and completely



THE LARGEST OF THE DEVIL'S GARDENS FOUND IN FRENCH GUIANA.
PHOTO USED WITH PERMISSION FROM ALEX SALAS-LOPEZ.

clear the surrounding area of non-host plants. The typical culprit, *Myrmelachista schumanni*, poisons all other plants to promote growth and reproduction of its host, typically *Duroia hirsuta*. This paper describes the discovery of Devil's gardens in French Guianan cloud forests, more than 2000 km away from previously known distributions of this rare mutualism. To investigate the factors contributing to the geographic isolation of the association, researchers used GBIF-mediated occurrences of myrmecophytes and compared these with known locations of devil's gardens, finding no evidence of host plant limitation. The authors instead suggest that the isolated phenomenon are relicts from past wider distributions, although this hypothesis needs further validation, e.g. findings in other countries with montane forests.

Link to paper: <https://doi.org/10.1017/S0266467416000195>

FERNS IN THE SKY ISLANDS OF EAST AFRICA

DATA USED: 4,313 SPECIES OCCURRENCES

Liu H-M, Zhang S-Z, Wan T, Kamau PW, Wang Z-W, Grall A, Hemp A and Schneider H (2016) Exploring the pteridophyte flora of the Eastern Afromontane biodiversity hotspot. *Journal of Systematics and Evolution*. Wiley-Blackwell 54(6): 691–705.

Author countries: China, Kenya, United Kingdom, Germany
Research funding: Scientific Research Program of Sino-Africa Joint Research Center; National Natural Science Foundation of China

Part of the East African Rift Valley, the Eastern Afromontane Biodiversity Hotspot (EABH) is a hyper-diverse region with a complex history of processes shaping species richness. The mountains of the EABH are different from other tropical mountain formations, as they do not form a continuous chain, and are often described as "sky islands".



PELLAEA CALOMELANOIS BY JOHN BARKLA
<HTTP://WWW.GBIF.ORG/OCCURRENCE/1453082858> CC BY-NC 4.0

In this study, researchers explore the origins of fern and lycophyte diversity of the sky islands of east Africa. Using a combination of traditional floras, journal articles and online resources including GBIF they identify 485 taxa in the region, a number that is only surpassed by Madagascar. The authors note that GBIF data alone reliably describes the species richness for some countries, but not all.

The study finds evidence for a distinct flora in the EABH region dominated by species preferably occurring in humid climates, while also providing framework for future studies on conservation, ecology and evolution.

Link to paper: <https://doi.org/10.1111/jse.12232>

TRACING EVOLUTION OF PHOTOSYNTHETIC PATHWAYS

DATA USED: 20,373 SPECIES OCCURRENCES

a Lundgren MR and Christin P-A (2016) Despite phylogenetic effects, C₃–C₄ lineages bridge the ecological gap to C₄ photosynthesis. *Journal of Experimental Botany*. Oxford University Press [OUP] 68(2): 241–254.

Author country: United Kingdom

Research funding: European Research Council; Royal Society University

Photosynthesis in flowering plants relies on two different biochemical pathways known as C₃ and C₄. C₄ photosynthesis evolved from C₃, particularly in warm regions where it boosts growth, and today, intermediate species with traits from both C₃ and C₄ pathways exist, though little is known about their ecology.

In this paper, researchers use GBIF-mediated occurrences combined with data on climate and soil conditions to study the distribution and phylogeny of 56 such C₃-C₄ intermediate species. They report that the group occurs across tropical and temperate regions, spanning a belt from 50°S to 65°N, and at elevations ranging from below sea level to the Andes mountains. Climates supporting C₃-C₄ intermediates feature temperatures from below zero to 30°C, and precipitation ranging from being virtually absent to extremely wet.

Precipitation and soil preferences tended to correlate with those of C₃ close relatives, however, intermediate taxa inhabit warmer climates, suggesting that the condition may facilitate evolution of the full C₄ pathway.

Link to paper: <https://doi.org/10.1093/jxb/erw451>



VERONICA PERSICA BY STEFANIAVERTUCCIO [HTTP://WWW.GBIF.ORG/OCCURRENCE/1265566440](http://WWW.GBIF.ORG/OCCURRENCE/1265566440) CC BY-NC 4.0

LIVE SHORT AND PROSPER

DATA USED: 9,374 SPECIES OCCURRENCES

ⓐ Wang J-C, Pan B-R and Albach DC [2016] Evolution of morphological and climatic adaptations in *Veronica* L. (Plantaginaceae). PeerJ. PeerJ 4: e2333.

Author countries: China, Germany

Research funding: Chinese Academy of Sciences; National Natural Science Foundation of China

Some annual flowering plants have evolved to have very short life histories, the record being less than three weeks from germination to seed set. The annual life strategy may offer advantages of being able to survive drought, heat, frost and other unfavourable periods as seeds.

The present paper presents a comparative study of perennials and annuals, and examines morphological trends and climatic factors that might favour annuality. Using a combination of genetic information, trait data and GBIF-mediated occurrences of 80 *Veronica* species, researchers found significant

differences between the two strategies, as perennials had larger leaves, petals and stamens, and annuals had larger bracts. In terms of climatic trends, annual habitats had higher temperatures, but perennial habitats were generally wetter.

All examined annual species of *Veronica* originated in the Mediterranean and southwest Asia, likely because of parallel evolution spurred by aridification.

Link to paper: <https://doi.org/10.7717/peerj.2333>.

Food and farming



A SOUNDER OF WILD BOAR (*SUS SCROFA*) BY ARIEL-SHAMIR [HTTP://WWW.GBIF.ORG/OCCURRENCE/1270051088](http://WWW.GBIF.ORG/OCCURRENCE/1270051088) CC BY-NC 4.0

IMPACT OF LAND CONSOLIDATION ON PLANT SPECIES DIVERSITY

DATA USED: 1,000 SPECIES OCCURRENCES

Osawa T, Kohyama K and Mitsuhashi H (2016) Trade-off relationship between modern agriculture and biodiversity: Heavy consolidation work has a long-term negative impact on plant species diversity. Land Use Policy. Elsevier BV, 78–84.

Author country: Japan

Research funding: Japan Society for the Promotion of Science; Ministry of the Environment, Japan

Land consolidation is used in agriculture to improve the livelihoods of farmers and to facilitate a more prosperous and efficient agricultural sector. Allowing farmers to have farms with larger areas of land, enables them to become more competitive. But what is the long-term impact of heavy land consolidation on biological diversity? In this study from Japan, researchers used plant red list data as a case study to attempt to answer this question. By compiling occurrences of 23 previously common but currently threatened plant species from GBIF and other sources, and then examining how these relate to agricultural consolidation, the authors found that threatened plants species were unlikely to inhabit consolidated areas. Unconsolidated agricultural land contained significantly higher numbers of threatened species, suggesting a negative impact on plant biodiversity of the practice.

Link to paper: <https://doi.org/10.1016/j.landusepol.2016.02.001>

WILD BOAR AND THE SPREAD OF AFRICA SWINE FEVER

DATA USED: 10,190 SPECIES OCCURRENCES

Bosch J, Iglesias I, Muñoz MJ and de la Torre A (2016) A Cartographic Tool for Managing African Swine Fever in Eurasia: Mapping Wild Boar Distribution Based on the Quality of Available Habitats. Transboundary and Emerging Diseases. Wiley-Blackwell.

Author country: Spain

Research funding: European Commission

Wild boar (*Sus scrofa*) can act as reservoirs of diseases that can infect both livestock and humans. In certain regions of Europe, populations of wild boar are responsible for maintaining and spreading African swine fever (ASF) across borders.

In this paper, authors use standardized global vegetation data combined with expert opinions to generate a map showing quality of available habitats in endemic (mainly Russia) and non-endemic (mainly EU) scenarios. They superimpose occurrences of wild boar from GBIF and other sources, as well as reported ASF cases on the generated map to assess the quality of their model.

More than half of the occurrences were in areas classified as having the highest level of suitability, indicating a good predictive ability of the model. However, ASF cases differed in the endemic and non-endemic scenario showing that wild boar play a key role ASF spread in the EU.

The presented map suggests areas that should be the focus of wildlife management and can be an important tool in epidemiological studies.

Link to paper: <https://doi.org/10.1111/tbed.12559>

EXPLORING THE CURRENT AND FUTURE NICHES OF BLUETONGUE VIRUS AND ITS VECTORS

DATA USED: 40 SPECIES OCCURRENCES

- Ⓐ Samy AM and Peterson AT [2016] Climate Change Influences on the Global Potential Distribution of Bluetongue Virus. PLOS ONE. Public Library of Science [PLoS] 11[3]: e0150489.

Author countries: United States, Egypt

Research funding: Graduate Fulbright Egyptian Mission Program [EFMP]

Bluetongue disease is a viral, but non-contagious disease of ruminants caused by the Bluetongue virus (BTV). Outbreaks in the Mediterranean region has resulted in the deaths of 800,000 sheep since 1998. In the US alone, BTV is responsible for losses amounting to US\$125 million per year. In this study, researchers built a comprehensive compilation of BTV cases and modelled the potential distribution of the virus under current and future climates. Under all future scenarios, they find that the virus is projected to expand its niche. Relating these findings to niche models for vector species (*Culicoides* spp.) based on different sources including GBIF, they find no significant differences, indicating that the virus and vectors share niches. This important observation may assist in identifying areas with no current disease reported, but at potential risk for infections in the future.

Link to paper: <https://doi.org/10.1371/journal.pone.0150489>

THE ADAPTIVE ROLE OF SEED OIL CONTENT

DATA USED: 2,567 SPECIES

- Ⓐ Sangal A and Decocq G [2016] Adaptive evolution of seed oil content in angiosperms: accounting for the global patterns of seed oils. BMC Evolutionary Biology. Springer Nature 16(1).

Author countries: France, Sweden

Research funding: French ANR

Seed oil is the primary energy source needed for germination and establishment of plants. Studying the biogeographic distribution of seed oil content is therefore fundamental to understanding mechanisms of adaptive evolution in plants.

In this study, researchers combined details of oil content of more than 2,500 species of angiosperm plants with species distributions data from GBIF

and other sources. On a broad scale, they show that tropical species have higher oil content than temperate species. This pattern is also evident at the family level.

When examining the effect of latitude, however, the correlation is only significant in three families. In two families, Sapindaceae and Sapotaceae, oil content increases with latitude, while it decreases in Papaveraceae. They also find that proportions of unsaturated fatty acids increase with latitude.

Shedding light on the role of oil seed content in plant adaptation, this study may also provide useful data for breeding of oilseed crops for human consumption.

Link to paper: <https://doi.org/10.1186/s12862-016-0752-7>

YOU SAY TOMATO, I SAY POTATO

DATA USED: 600 SPECIES

Dupin J, Matzke NJ, Särkinen T, Knapp S, Olmstead RG, Bohs L and Smith SD [2016] Bayesian estimation of the global biogeographical history of the Solanaceae. Journal of Biogeography. Wiley-Blackwell 44(4): 887–899.

Author countries: United States, Australia, United Kingdom

Research funding: National Science Foundation; University of Tennessee; Australian Research Council; Australian National University

The nightshade family [Solanaceae] is a clade of 2,800 species including important crops, such as potato, tomato and peppers, distributed across all continents except Antarctica. Despite its economic importance, the biogeographical history of the family is relatively unknown.

KANGAROO APPLE [*SOLANUM LACINIATUM*] BY JOHN BARKLA
[HTTP://WWW.GBIF.ORG/OCURRENCE/1265596713](http://www.gbif.org/occurrence/1265596713) CC BY-NC 4.0

In this study, researchers pruned a recently inferred phylogeny of the clade and used data from GBIF and other sources to determine the current distribution of around 1,000 species. Using biogeographical stochastic mapping (BSM) they identify the most probable ancestral area for extant species of

Solanaceae to be South America, and estimate that most species evolved through within-area speciation and dispersals. Movement patterns were strongly asymmetrical in all region pairs, except between Africa and Eurasia, where numbers were equal in both directions.

The study provides new insights into the biogeographical history of the nightshade family, and acts as a proof of concept for using the BSM approach for exploring frequency and directionality of biogeographical events.

Link to paper: <https://doi.org/10.1111/jbi.12898>

MODELLING FOOD WEBS FROM PLANKTON TO TOP PREDATORS

DATA USED: 42,945 SPECIES OCCURRENCES

Halouani G, Ben Rais Lasram F, Shin Y-J, Velez L, Verley P, Hattab T, Oliveros-Ramos R, Diaz F, Ménard F, Baklouti M, Guyennan A, Romdhane MS and Le Loc'h F (2016) Modelling food web structure using an end-to-end approach in the coastal ecosystem of the Gulf of Gabes [Tunisia]. Ecological Modelling. Elsevier BV 339: 45–57.

Author countries: Tunisia, France, South Africa, Peru

Research funding: Institut de Recherche pour le Développement (IRD); JEAI IRD; ENVI-Med-MISTRALS; Fondation TOTAL; FRB

Recognized as one of the most productive areas in Mediterranean, The Gulf of Gabes is under multiple anthropogenic threats, such as overfishing and pollution.

Seeking to characterize the structure of the food web in the Gulf and model the main processes that influence species' life cycles, this study used a combination of an individual-based model

representing high trophic level organisms informed by GBIF-mediated occurrences and hydrodynamic/biochemical model representing low trophic level organisms.

The two models were linked through trophic interactions and together provide a realistic representation of the food web from smallest plankton to top predators. Comparing model simulated predator diets with stomach contents data, showed an acceptable level of similarity. The modelled size at catch also showed a close consistency when confronted with empirical data.

Overall, the model provides a foundation for future studies into the effects of anthropogenic change threatening the Gulf ecosystem.

Link to paper: <https://doi.org/10.1016/j.ecolmodel.2016.08.008>

IMPACT OF 10,000 YEARS OF HUMANS IN ALASKA

DATA USED: 27,082 SPECIES OCCURRENCES

a Dunne JA, Maschner H, Betts MW, Huntly N, Russell R, Williams RJ and Wood SA (2016) The roles and impacts of human hunter-gatherers in North Pacific marine food webs. Scientific Reports. Springer Nature 6: 21179.

Author countries: United States, Canada

Research funding: NSF; Idaho State University; Bamfield Marine Sciences Centre; Santa Fe Institute

Modern civilizations are depleting commercial fisheries leading to regulation excluding local indigenous peoples from traditional harvesting territories. This affects the Aleut peoples of the western Gulf of Alaska, who have depended on marine resources for nearly 10,000 years. This study simulates the impact of the Aleut on the ecological integrity of the region by combining anthropological data with food webs informed by GBIF-mediated occurrences. Despite being the top predator and a highly omnivorous generalist feeding on 70 different taxa, a behaviour that could potentially result in extinctions, the researchers find no evidence linking the Aleut population of *Homo sapiens* to such. In fact, the authors suggest that prey-switching behaviour promoted ecological integrity in the region.

Link to paper: <https://doi.org/10.1038/srep21179>



COMMON PANDORA (*PAGELLUS ERYTHRINUS*) BY WHODDEN
[HTTP://WWW.GBIF.ORG/OCCURRENCE/1265535366](http://WWW.GBIF.ORG/OCCURRENCE/1265535366) CC BY-NC 4.0

Impacts of climate change



PRICKLYBURR (*Datura innoxia*) BY LAURA URIBE [HTTP://WWW.GBIF.ORG/OCCURRENCE/1211983014](http://www.gbif.org/occurrence/1211983014) CC BY-NC 4.0

CLIMATE CHANGE AND MARINE FOOD-WEB STRUCTURES

DATA USED: 131,645 SPECIES OCCURRENCES

Hattab T, Leprieur F, Lasram FBR, Gravel D, Loc'h FL and Albouy C (2016) Forecasting fine-scale changes in the food-web structure of coastal marine communities under climate change. *Ecography*. Wiley-Blackwell.

Author countries: France, Tunisia, Canada

Research funding: not listed

Changing climates affect biodiversity in a number of different ways including range shifts, reorganizing local communities, and even extinctions. Marine species are not just affected by abiotic conditions such as temperature and salinity. They are connected in intricate food-web networks through competition, predation, parasitism, etc. If one species is affected, it will inevitably affect many others.

Focusing on the Gulf of Gabes in the southern Mediterranean, the authors of this study predict the impacts of climate change on species networks by combining climatic envelopes derived from GBIF-mediated occurrences with a niche food web model. Their results forecast range shifts for at least half the species under future scenarios. 14 species may be lost altogether, and with them 414 potential biotic links. The study is an important reminder that species

communities are far from just a simple collection of independent species, and that this should be considered when modelling distributions.

Link to paper: <https://doi.org/10.1111/ecog.01937>

EFFECTS OF CLIMATE AND LAND-USE CHANGE ON NORTH AMERICAN SEED PLANTS

DATA USED: 3,786,713 SPECIES OCCURRENCES

Zhang J, Nielsen SE, Chen Y, Georges D, Qin Y, Wang S-S, Svenning J-C and Thuiller W (2016) Extinction risk of North American seed plants elevated by climate and land-use change. *Journal of Applied Ecology*. Wiley-Blackwell.

Author countries: Canada, France, Denmark

Research funding: Climate Change and Emissions Management Corporation; Alberta Biodiversity Monitoring Institute; European Research Council

Climate and land-use change are expected to affect future distributions of plants and potentially lead to higher extinction rates. In this study, researchers used GBIF-mediated occurrences to examine current and future distributions of 7,465 seed plant taxa in North America. Based on the distribution models, they evaluated the vulnerability and extinction risk of each species. Their results showed that by 2080 about 2,000 species are projected to lose more than 80 per cent of their suitable habitat, however, gains of similar proportions are likely to happen for about 100

species. The ratio of loss to gain expected is 13 to one. The greatest losses are expected in southern regions, while northern latitudes can expect gains. Extinctions are likely to affect evolutionarily distinct species more, suggesting a potentially disproportionate loss of phylogenetic diversity. Overall, the study points to a rapid and severe changes in future distributions of North American plant species.

Link to paper: <https://doi.org/10.1111/1365-2664.12701>

ASSESSING THE THREAT OF AGRICULTURAL PESTS UNDER CHANGING CLIMATES

DATA USED: 18 MILLION SPECIES OCCURRENCES

ⓐ Biber-Freudenberger L, Ziemacki J, Tonnang HEZ and Borgemeister C (2016) Future Risks of Pest Species under Changing Climatic Conditions. *PLOS ONE*. Public Library of Science (PLoS) 11(4): e0153237.

Author countries: Germany, Kenya

Research funding: Volkswagen Foundation

Climate change presents many challenges to agriculture, including drought and irregular weather, especially in Africa where climate-change effects are projected to be some of the most severe in the world. Changing climatic conditions may also alter habitat suitability for pest species, which could change the threat of such pests. In this study, researchers used GBIF-mediated occurrences to model the distribution of three important pest species (*Tuta absoluta*, *Ceratitis cosyra*, and *Bactrocera invadens*) under current and future climates. Showing a good predictive performance, the models indicated that habitat suitability for the three insect pests is partially increasing across the continent, especially in those areas already overlapping with or close to most suitable sites under current climate conditions. The



BACTROCERA INVADENS BY IAEA IMAGEBANK
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three pests are likely to remain a threat to agricultural production under future climatic conditions. These results may inform management decisions and help farmers choose crops less susceptible to certain pest species.

Link to paper: <https://doi.org/10.1371/journal.pone.0153237>

PROTECTING ARTIC MIGRANTS AGAINST CLIMATE CHANGE

DATA USED: 81,503 SPECIES OCCURRENCES

Wauchope HS, Shaw JD, Varpe Ø, Lappo EG, Boertmann D, Lanctot RB and Fuller RA (2016) Rapid climate-driven loss of breeding habitat for Arctic migratory birds. *Global Change Biology*. Wiley-Blackwell.

Author countries: Australia, Norway, Russian Federation, Denmark, United States

Research funding: ARC; ARC Centre of Excellence for Environmental Decisions

Millions of birds migrate to and from the Arctic every year with some species travelling more than 20,000 km to escape the cold of the winter. Warming climates may, however, disturb breeding grounds and disrupt migratory flyways. In this study, researchers modelled climatically suitable breeding grounds of 24 Arctic specialist shorebirds and projected them to future climates as well as the last major global warming event, 6,000 years ago. The models predict a drastic decline in suitable breeding conditions by the year 2070, with as many as 20 species losing up to half their current breeding grounds. The conditions at the last warming event were far less severe. The Beringia region of Alaska and Russia with high shorebird species richness and endemism, is predicted to become unsuitable for many species. The study suggests protection of migratory stopover sites for birds having to travel further to reach suitable breeding grounds.

Link to paper: <https://doi.org/10.1111/gcb.13404>

A DOUBLE THREAT TO TROPICAL BIRDS

DATA USED: 6,286,920 SPECIES OCCURRENCES

Frishkoff LO, Karp DS, Flanders JR, Zook J, Hadly EA, Daily GC and M'Gonigle LK (2016) Climate change and habitat conversion favour the same species. *Ecology Letters*. Wiley-Blackwell 19(9): 1081–1090.

Author countries: United States, Canada, United Kingdom, Costa Rica, Sweden

Research funding: Ward Wilson Woods, Jr.; Killam; Belmont Forum

Climate change is not the only threat to species, but when amplified by anthropogenic land-use changes, a global biodiversity crisis looms. Some species are able

to thrive in human-dominated landscapes, but the diversity in such areas is very different from natural areas. In this study, researchers used census data and GBIF-mediated occurrences of more than 300 species of Neotropical birds combined with climate data to assess relationships between species' niches, origins and tolerance of human-dominated habitats. They find precipitation to be the strongest predictor, in that species originating in drier regions are more likely to occupy agriculture than forest. Interestingly, these species appear to be more resilient to changes in climate and land-use than forest-occupying species. Apparently favouring similar species, climate change and habitat conversion may homogenize global biodiversity even faster and more severely than previously anticipated.

Link to paper: <https://doi.org/10.1111/ele.12645>



WHITE ALDER (*ALNUS RHOMBIFOLIA*) BY KENNYHAN
[HTTP://WWW.GBIF.ORG/OCCURRENCE/1265541193](http://WWW.GBIF.ORG/OCCURRENCE/1265541193) CC BY-NC 4.0

ASSESSING THE EFFECT OF WARMING WATER ON MEDITERRANEAN FISHERIES

DATA USED: 25,000 SPECIES OCCURRENCES

✉ Pranovi F, Anelli Monti M, Brigolin D and Zucchetta M [2016] The Influence of the Spatial Scale on the Fishery Landings-SST Relationship. *Frontiers in Marine Science*. Frontiers Media SA 3.

Author country: Italy

Research funding: None listed

Various recent studies have shown a correlation between sea-surface temperature and fish distributions and species composition globally. This in turn affects fisheries, as other studies have shown

species shifting their ranges towards the poles. In this study, researchers investigated 40 years of fishing in the Mediterranean to determine whether changes in landings can be explained by seawater temperature. Dividing species into thermal affinity groups based on median latitude of GBIF-mediated occurrences, and aggregating the landing data in Mediterranean sub-areas, the researchers find that catches follow a general temporal trend but depend on an interaction between temperature and sub-area. They confirm that cold affinity species are negatively affected by water warming, whereas both temperate and warm affinity groups show a positive relationship with temperature. The study shows that climate change can have a major impact on global fisheries, although management strategies may prove more meaningful at a regional scale.

Link to paper: <https://doi.org/10.3389/fmars.2016.00143>

THE COMPLEXITY OF SPECIES' RESPONSE TO CLIMATE CHANGE

DATA USED: 4,733 SPECIES OCCURRENCES

✉ Harsch MA and HilleRisLambers J [2016] Climate Warming and Seasonal Precipitation Change Interact to Limit Species Distribution Shifts across Western North America. *PLOS ONE*. Public Library of Science (PLoS) 11(7): e0159184.

Author country: United States

Research funding: National Science Foundation

Many studies have predicted species distributions responding to climate warming by shifting pole-wards or towards higher elevation. In this study, researchers investigated 293 plant species in western North America to determine if distributions have shifted as expected in the past 40 years, and to gain knowledge into future responses to further climatic changes. Using species occurrences from several sources including GBIF combined with historic climate data, the researchers find that overall, plants were equally likely to shift upward as they were downward, but also that regional differences exist. Species occurring in multiple regions followed regional patterns rather than species-specific patterns. Temperature alone could not explain the direction of distribution shifts, and the researchers found that combining the effect of summer warming with seasonal precipitation change proved a better predictor, highlighting the complexity of species responding to changing climates.

Link to paper: <https://doi.org/10.1371/journal.pone.0159184>

URBAN WARMING AFFECTS LOCAL PLANT ASSEMBLAGES

DATA USED: 25,863,271 SPECIES OCCURRENCES

Duffy GA and Chown SL [2016] Urban warming favours C₄ plants in temperate European cities. *Journal of Ecology*. Wiley-Blackwell 104(6): 1618–1626.

Author country: Australia

Research funding: Australian Research Council

Urbanization represents an environmental challenge and urban land cover in 2030 is predicted to be three times the area observed in 2000. The urban heat island (UHI) phenomenon is a pronounced climatic effect that may even affect the local plant assemblages of urban areas. In this study, researchers used differences in plants' photosynthetic pathways to test the hypothesis that UHI favours so-called C₄ plants thriving in warmer climates as opposed to C₃ plants that prefer colder climates. Researchers downloaded GBIF-mediated occurrences of plants in the UK and Germany and classified species according to photosynthetic pathway- C₃ or C₄. Using remotely sensed temperature readings, the researchers showed that summer temperatures in urban regions were 2–3°C warmer in both countries. As expected, overall C₄ abundance was low in both countries, but increased significantly in urban regions with similar patterns for species richness, showing how UHI is able to restructure plant assemblages in urban areas.

Link to paper: <https://doi.org/10.1111/1365-2745.12652>

USING GENETICS TO IMPROVE ECOLOGICAL NICHE MODELS

DATA USED: 28 SPECIES OCCURRENCES

Ikeda DH, Max TL, Allan GJ, Lau MK, Shuster SM and Whitham TG [2016] Genetically informed ecological niche models improve climate change predictions. *Global Change Biology*. Wiley-Blackwell 23(1): 164–176.

Author country: United States

Research funding: NSF

To determine the effects of climate change on biodiversity, researchers often rely on modelling distributions or niches of species using a combination of occurrence records and climatic data. Such models might predict that the range of a species is likely to contract under future climates, but they may not be able to capture local adaptation.

In this study, researchers used genetic information to define ecological subregions, downloading GBIF-mediated occurrences of Fremont cottonwood (*Populus fremontii*) and modelled them separately by subregion. The models showed that genetically

distinct ecotypes differed significantly in climate niche space, showing adaptation to local environment. The models were better able to predict populations than those that did not consider the genetic component.



FREMONT COTTONWOOD (*POPULUS FREMONTII*) BY DON LOARIE
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When addressing impacts of climate change, the researchers found that ecotypes varied greatly in their response, as some were predicted to gain more than 60 per cent in suitable habitat while others stood to lose it all.

Link to paper: <https://doi.org/10.1111/gcb.13470>

THE IMPACT OF CLIMATE CHANGE ON ECOLOGICAL NETWORKS

DATA USED: 403,277 SPECIES OCCURRENCES

② Schleuning M, Fründ J, Schweiger O, Welk E, Albrecht J, Albrecht M, Beil M, Benadi G, Blüthgen N, Bruehlheide H, Böhning-Gaese K, Dehling DM, Dormann CF, Exeler N, Farwig N, Harpke A, Hickler T, Kratochwil A, Kuhlmann M, Kühn I, Michez D, Mudri-Stojnić S, Plein M, Rasmont P, Schwabe A, Settele J, Vujić A, Weiner CN, Wiemers M and Hof C (2016) Ecological networks are more sensitive to plant than to animal extinction under climate change. *Nature Communications*. Springer Nature 7: 13965.

Author countries: Germany, Canada, Poland, Switzerland, New Zealand, United Kingdom, Belgium, Serbia, Australia

Research funding: Hesse's Ministry of Higher Education, Research and the Arts; DFG; European Commission; German Academic exchange service; German Federal Environmental Foundation; German Federal Ministry of Education and Research; Climatic Impacts on Ecosystems and Climatic Adaptation Strategies; FNRS [Belgium]; BELSPO

Climate change can force species to either adapt or move, and many studies have modelled the impact of warming climates on individual species. Ecological communities, however, consists of networks of interacting species, and understanding the impact on entire ecological interaction networks is important.

Combining species distribution models based on GBIF-mediated occurrences with ecological network analyses, researchers examined the impact of climate change on more than 700 plant and animal species in pollination and seed dispersal networks in Central Europe. They also tested the hypothesis that species with narrow niches and projected losses in climatic suitability are specialist species with few biotic partners.

Their results show that the breadth of animal climatic niches is correlated with number of plant partners, however, not vice versa. Animals projected to lose climatic suitability have low diversity in plant partners, indicating that pollinators and seed dispersers with fewer plants interactions are particularly vulnerable to climate change.

Link to paper: <https://doi.org/10.1038/ncomms13965>

CLIMATE CHANGE SHIFTS GRASS PHENOLOGY

DATA USED: 5,719 SPECIES OCCURRENCES

Munson SM and Long AL (2016) Climate drives shifts in grass reproductive phenology across the western USA. *New Phytologist*. Wiley-Blackwell 213(4): 1945–1955.

Author country: United States

Research funding: US Geological Survey Ecosystems Mission Area; National Climate Change; Wildlife Science Center

In this study, researchers used herbarium records from GBIF and other sources to investigate how well grasses of the western United States cope with environmental variability.

Deriving flowering date of each grass species from the specimen collection date and relating this to climate data, the researchers found that increasing temperature variables affected flowering time differently according to photosynthetic pathway, as flowering was accelerated in C₃ plants, but delayed in C₄. For precipitation, increasing variable values generally delayed flowering. In both cases, however, the behaviour also depended on the ecoregion of the grass species, most likely attributable to species adaptation to local climates.

The results confirm that grass flowering time is largely controlled by climate change, and that grass phenology can cope with moderate changes in temperature and precipitation. This resilience, however, is most relevant if species can migrate to new locations, which is unlikely to happen at the same velocity of climate change.

Link to paper: <https://doi.org/10.1111/nph.14327>



DISTICHLIS SPICATA BY MILLIEBASDEN

[HTTP://WWW.GBIF.ORG/OCURRENCE/1453398771](http://www.gbif.org/occurrence/1453398771) CC BY-NC 4.0

Invasive alien species



GYPSY MOTH (*LYMANTRIA DISPAR*) BY MARTIN GRIMM [HTTP://WWW.GBIF.ORG/OCCURRENCE/1291061003](http://WWW.GBIF.ORG/OCCURRENCE/1291061003) CC BY-NC 4.0

CLIMATE CHANGE REDUCES RISK OF PLANT INVASION

DATA USED: 317,063 SPECIES OCCURRENCES

Allen JM and Bradley BA [2016] Out of the weeds? Reduced plant invasion risk with climate change in the continental United States. *Biological Conservation*. Elsevier BV 203: 306–312.

Author country: United States

Research funding: National Science Foundation; National Institute of Food and Agriculture, USDA; Massachusetts Agricultural Experiment Station; Department of Environmental Conservation

Invasive species represent a serious threat to ecosystems, and identifying species and areas of risk is critical for management prioritization, however, it's equally important to consider how changing climates may alter the risk picture.

In this study, researchers assembled a database of invasive plant occurrences in the continental United States from variety of sources including GBIF. Using climate data, they modelled the potential distributions of each species and find that the current observed richness of invasive plants is much lower than the predicted potential.

Under future climate scenarios, however, the potential richness is predicted to decline significantly, in some areas up to 50 per cent. Only in northern regions did the researchers find predicted increases in invasive

richness, albeit up to 175 per cent. Most predicted invasion hotspots (areas with potential richness in the top 25th percentile) remained stable through the year 2050.

Link to paper: <https://doi.org/10.1016/j.biocon.2016.09.015>

WHAT MAKES A SUCCESSFUL INVADER?

DATA USED: 381,231 SPECIES OCCURRENCES

② Bellard C, Leroy B, Thuiller W, Rysman J-F and Courchamp F [2016] Major drivers of invasion risks throughout the world. *Ecosphere*. Wiley-Blackwell 7(3): e01241.

Author countries: France, United Kingdom

Research funding: ANR; European Research Council; European Community

For invasive species to be successful, the climate in the invaded regions must be at least similar to the native region. However, other factors are also known to play an important role. To provide insight into what these factors might be and how they each contribute to successful invasions, researchers did a full investigation of abiotic and socioeconomic parameters for 95 of the world's worst invasive species. Using occurrences primarily from GBIF, they modelled the distributions of each species, and found that overall, the socioeconomic parameters such as human density and distance to airports play a role for more species than climatic parameters. However, in terms of predicting invasion success, temperature and precipitation are still most important. The authors

finally identify Western and Central Europe, Eastern North America, Central America, Eastern Australia, and some Indonesian islands as potential invasion hotspots that should be carefully monitored to prevent new invasions.

Link to paper: <https://doi.org/10.1002/ecs2.1241>

GEOGRAPHIC BIASES IN INVASIVENESS: THE CASE OF ASIAN AND AFRICAN PARAKEETS

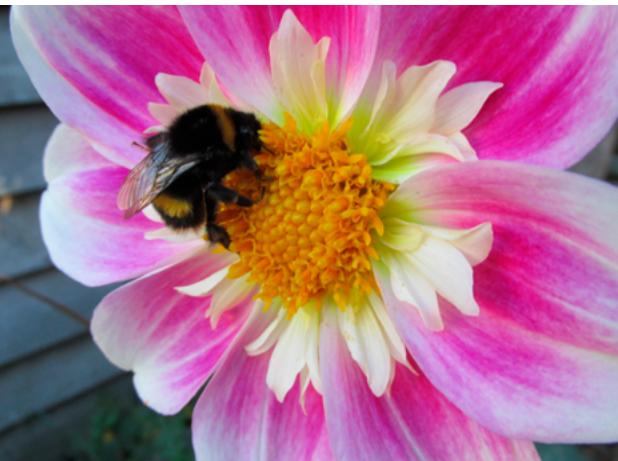
DATA USED: ~30,000 SPECIES OCCURRENCES

Cardador L, Carrete M, Gallardo B & Tellal JL [2016] Combining trade data and niche modelling improves predictions of the origin and distribution of non-native European populations of a globally invasive species. *Journal of Biogeography*.

Author country: Spain

Research funding: ESFRI LifeWatch; Severo Ochoa Program for Centres of Excellence in R+D+I

When evaluating the invasive risk of a species, researchers commonly use environmental-based predictions. This study, however, suggests that including international trade data and variability in geographical origin may lead to much more thorough risk analyses. The authors compiled occurrences of ring-necked parakeets from GBIF and other sources and built distribution models for the birds' native niches in Africa and Asia, respectively. When comparing with invasive ranges in Europe, their results show that the distribution here is mainly explained by geographical origin of the birds and time since introduction. Their models indicate that while most of Europe is suitable for the Asian population, almost no habitat is suitable for the African population. This finding is supported by recent evidence that genetic markers of established invaders mostly match those of Asian populations, although introduced in similar numbers as African birds.



BOMBUS TERRESTRIS BY KATY JOHNS
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Link to paper: <https://doi.org/10.1111/jbi.12694>

FLIGHT OF THE BUMBLEBEE

DATA USED: 8,642 SPECIES OCCURRENCES

a Acosta AL, Giannini TC, Imperatriz-Fonseca VL and Saraiva AM [2016] Worldwide Alien Invasion: A Methodological Approach to Forecast the Potential Spread of a Highly Invasive Pollinator. *PLOS ONE*. Public Library of Science [PLoS], e0148295.

Author country: Brazil

Research funding: São Paulo State Research Foundation; National Counsel of Technological and Scientific Development

The worldwide number of alien species invasions is rapidly increasing, and new methods of predicting vulnerable areas are required. In this study, researchers suggest a new methodological framework for assessing habitat invasion susceptibility on a global scale by focusing on the bumblebee, *Bombus terrestris*. The native range of the bee is in Europe, but it has invaded several regions including South America, Oceania and Asia. Using occurrences primarily from GBIF, the authors modelled habitat suitability based on environmental topoclimatic data to create a global map of areas particularly susceptible to invasion by the bumblebee. Countries that were identified as vulnerable, including Australia, Brazil and Uruguay, may use the findings of this study to develop action plans for monitoring bumblebee invasion.

Link to paper: <https://doi.org/10.1371/journal.pone.0148295>

THE GLOBAL THREAT OF INVASIVE ALIEN SPECIES

DATA USED: 78,000 SPECIES OCCURRENCES

a Bellard C, Genovesi P and Jeschke JM [2016] Global patterns in threats to vertebrates by biological invasions. *Proceedings of the Royal Society B: Biological Sciences*. The Royal Society, 20152454.

Author countries: France, Italy, Germany

Research funding: European Research Council; ANR

Studies have shown that invasive alien species (IAS) are responsible for a fifth of animal extinctions for which the causes are well-known, but are invasive species a treat to global biodiversity? In this paper, researchers assessed the spatial and taxonomic relationship between IAS and threatened vertebrates worldwide. Using GBIF-mediated occurrences and IUCN Red List data, they determine that IAS play a role in more than a quarter of all threatened vertebrates. Birds and amphibians have the highest share of IAS-threatened species, and the largest IAS-threatened proportion is found among critically

endangered species. The study identifies the frog fungus *Batrachochytrium dendrobatidis* as the IAS that threatens most vertebrate species (amphibians only), whereas rats combined threaten nearly as many species across all vertebrate classes. They finally show how the effects of IAS aren't equally distributed worldwide, and point to major centres of IAS-threatened species in the Americas, India, Indonesia, Australia and New Zealand.

Link to paper: <https://doi.org/10.1098/rspb.2015.2454>

THE IMPACT OF ALASKA'S FIRST INVASIVE FRESHWATER PLANT

DATA USED: 52,820 SPECIES OCCURRENCES

Luizza MW, Evangelista PH, Jarnevich CS, West A and Stewart H (2016) Integrating subsistence practice and species distribution modeling: assessing invasive elodea's potential impact on Native Alaskan subsistence of Chinook salmon and whitefish. *Environmental Management*. Springer Nature 58(1): 144–163.

Author country: United States

Research funding: National Institute of Food and Agriculture, USDA; Colorado State University

Biodiversity in Alaska is threatened not only by changing climate, but also anthropogenic disturbances through increased resource extraction and infrastructure development. Together, these factors increase the state's vulnerability to biological invasions. In this interdisciplinary paper, researchers studied waterweeds (*Elodea* spp.), the first documented invasive freshwater plant in Alaska and assessed the potential threat posed by the invader to the subsistence of Alaskan Native communities by examining effect on harvest of important species, Chinook salmon and whitefish. Using GBIF-mediated occurrences, the researchers constructed suitable habitat models for *Elodea* in Alaska and find high suitability across most of the state. In future climates, the models show a slight increase in suitable habitat. Combining this data with known spawning and rearing sites for salmon and whitefish, the study identifies the nearly 1 million square kilometre Athabascan cultural domain of interior Alaska as having the highest concern, both under current and future scenarios.

Link to paper: <https://doi.org/10.1007/s00267-016-0692-4>

EXPANDING NICHES THROUGH GENETIC ADAPTATION?

DATA USED: 4,803 SPECIES OCCURRENCES

Gallien L, Thuiller W, Fort N, Boleda M, Alberto FJ, Rioux D, Lainé J and Lavergne S (2016) Is There Any Evidence for Rapid, Genetically-Based, Climatic Niche Expansion in the Invasive Common Ragweed? *PLOS ONE*. Public Library of Science [PLOS] 11(4): e0152867.

Author country: France

Research funding: French Agence Nationale de la Recherche; European Research Council

Common ragweed (*Ambrosia artemisiifolia*), an annual weed native to North America, is a highly successful invader colonizing locations across Eurasia, Australia and South America. Being highly allergenic, ragweed is a substantial public health concern. In this study, researchers investigated the invasive success of ragweed in the French Alps, an area the plant reached about sixty years ago, and attempt to link the niche expansion with genetic evolution. Using GBIF-mediated occurrences of ragweed at global and regional scales, the researchers modelled climatic niches and related these to genetic structure and phenotypic architecture gathered through a large experiment, in which they analysed DNA and tracked the development of 3,000 plants. Their results identify 36 genetic markers potentially under selection, as they showed correlation with climate niche parameters, and eight of these also correlated with quantitative traits markers. The combined results point to a rapid adaptation of ragweed during its colonization of the French Alps.

Link to paper: <https://doi.org/10.1371/journal.pone.0152867>



CANE TOAD [*RHINELLA MARINA*] BY LEK KHAUV
HTTP://WWW.GBIF.ORG/OCCURRENCE/1122958334 CC BY-NC 4.0

USING INVASIVE TOADS TO TEST EVOLUTIONARY HYPOTHESES

DATA USED: 3,384 SPECIES OCCURRENCES

Trumbo DR, Epstein B, Hohenlohe PA, Alford RA, Schwarzkopf L and Storfer A [2016] Mixed population genomics support for the central marginal hypothesis across the invasive range of the cane toad (*Rhinella marina*) in Australia. *Molecular Ecology*. Wiley-Blackwell 25[17]: 4161–4176.

Author countries: United States, Australia

Research funding: Australian Research Council; National Science Foundation; National Institute of Health

In evolutionary ecology, the central marginal hypothesis (CMH) predicts that a species cannot adapt to conditions outside their current range as genetic diversity decreases from core to the edge, because of smaller, more isolated populations in the latter. In this study, researchers tested the predictions of CMH on invasive ranges of the cane toad (*Rhinella marina*) in Australia, originally introduced as a biocontrol against sugar canes beetles. Using a combination of ecological niche modelling based on GBIF-mediated occurrences and high-throughput genetic sequencing, the researchers found the highest overall habitat suitability in Arnhem Land on the northern coast of the Northern Territory, but in this region, genetic differentiation patterns showed limited support for CMH. In the south-eastern part of the range, diversity and differentiation were, however, consistent with CMH. The study is an example of how species invasions, unfortunate as they might be, can be utilized in evolutionary hypothesis testing.

Link to paper: <https://doi.org/10.1111/mec.13754>

PREDICTING GLOBAL INVADERS AND REGIONS AT RISK OF INVASION

DATA USED: 1,540,000 SPECIES OCCURRENCES

ⓐ Wang Y and Xu Z [2016] Where are the Alien Species? Predictions of Global Plant Species Invasions under Current Environmental Conditions and the Human Footprint. *Polish Journal of Environmental Studies*. HARD Publishing Company 25[4]: 1729–1738.

Author country: China

Research funding: National Natural Science Foundation of China

Species invasion is a major global concern, and identifying potential invasive regions before they are invaded is crucial. In this study, researchers selected 308 species of invasive plant species, gathered occurrence data from GBIF, and created species distribution models based on climatic, topographic and human activity data using nine different modelling approaches. Their results show



WHITE LEADTREE [*LEUCAENA LEUCOCEPHALA*] BY TONY IWANE
[HTTP://WWW.GBIF.ORG/OCURRENCE/1253299481](http://www.gbif.org/occurrence/1253299481) CC BY-NC 4.0

invasion hotspots, defined as regions under threat from more than 100 different invasive species, in the Southeastern United States, Eastern South America, Southeast Asia, Southeast Australia and New Zealand. While abundance of alien species showed weak correlations with both mean annual temperature and precipitation, topographic wetness and solar radiation, the most significant correlation was found for human footprint. Turning to world's 100 worst invasive species, the study also examined the species with the largest potential invasive distributions, identifying among others the castorbean (*Ricinus communis*), the dwarf copperleaf (*Alternanthera sessilis*) and sweet acacia (*Vachellia farnesiana*).

Link to paper: <https://doi.org/10.1524/pjoes.62094>

THE ROLE OF CLIMATE DATA RESOLUTION ON SPECIES DISTRIBUTION MODELS

DATA USED: 35,138 SPECIES OCCURRENCES

Wan J-Z, Wang C-J and Yu F-H [2016] Impacts of the spatial scale of climate data on the modeled distribution probabilities of invasive tree species throughout the world. *Ecological Informatics*. Elsevier BV 36: 42–49.

Author countries: China, United Kingdom

Research funding: Fundamental Research Funds for the Central Universities; NSFC; National Key Research and Development Program of China

Species distribution models (SDMs) can provide valuable information on the potential range of species and are particularly useful for predicting suitability for invasive species and thus potential spread in present day and future climate scenarios. The scale of climate data used in such models, however, may affect the outcome.

Using invasive trees as a case study, researchers addressed the role of spatial scale of climate data

on species distribution models. By combining GBIF-mediated occurrences of nine invasive species with bioclimatic variables at three different resolutions, they built SDMs and compare the performance of the models and evaluate the impact of spatial scale.

In a general measure of model performance, the SDMs appear to perform well regardless of resolution. However, the average distribution probabilities increased significantly with resolution, and the most important climatic variable differed depending on resolution.

These findings suggest that the spatial scale of the climate data impacts the ability of SDMs to provide accurate predictions.

Link to paper: <https://doi.org/10.1016/j.ecoinf.2016.10.001>

INVADERS LURKING IN OUR GARDENS

DATA USED: 835,036 SPECIES OCCURRENCES

 Dullinger I, Wessely J, Bossdorf O, Dawson W, Essl F, Gatterer A, Klonner G, Kreft H, Kuttner M, Moser D, Pergl J, Pyšek P, Thuiller W, van Kleunen M, Weigelt P, Winter M and Dullinger S [2016] Climate change will increase the naturalization risk from garden plants in Europe. *Global Ecology and Biogeography*. Wiley-Blackwell 26(1): 43–53.

Author countries: Austria, Germany, United Kingdom, Czech Republic, France

Research funding: ERA-Net BiodivERsA; Austrian Science Fund; French National Research Agency; Deutsche Forschungsgemeinschaft; University of Göttingen; Czech Science Foundation; Centre of Excellence

Ornamental plants may escape our gardens and become naturalized invaders. This invasion risk may increase as changing climates provide more suitable habitat. This paper evaluates the current naturalization risk from garden plants in Europe and explores how a warmer climate might affect it. Using GBIF-mediated occurrences of all species naturalized anywhere in the world but Europe, the researchers model potential European distributions today and under future climate scenarios. Out of more than 700 species investigated, current models showed that about a quarter would find suitable habitat. Under the most severe climate change scenario, invasion hotspots (supporting more than ten per cent of the potential invaders) are predicted to double in area by the end of the century. The authors recommend raising awareness of plant invasions among gardening and ornamental trade communities, especially considering how the internet has removed any limitations on availability of plants for interested customers.

Link to paper: <https://doi.org/10.1111/geb.12512>

FROM ESCAPING PETS TO INVASIVE SPECIES

DATA USED: 7,809 SPECIES OCCURRENCES

Vall-llosera M, Woolnough AP, Anderson D and Cassey P [2016] Improved surveillance for early detection of a potential invasive species: the alien Rose-ringed parakeet *Psittacula krameri* in Australia. *Biological Invasions*. Springer Nature 19(4): 1273–1284.

Author countries: Australia, New Zealand

Research funding: Department of Economic Development, Jobs, Transport and Resources; Invasive Animals Cooperative Research Centre (CRC); Australian Research Council (ARC)

Being the most widely introduced parrot in the world, the rose-ringed parakeet (*Psittacula krameri*) is classified as an “extreme threat” to native wildlife and agriculture in Australia. The complete details of the species’ distribution and impact is, however, currently unknown.

In this study, researchers compiled a unique *P. krameri* dataset from multiple sources including GBIF, missing pet websites and government agencies, and used incursion risk and species distribution modelling to assess the potential distribution and economic impact on agricultural assets.

From 1999 to 2013, the researchers recorded incursions of more than 1100 individual birds, especially in areas around large cities, with Brisbane accounting for more than 40 per cent of cases. These numbers are almost ten times larger than previous estimates, however, far from all lead to actual invasions, as events typically include one or two individuals highly dependent on humans.

The study shows alternative data sources, like missing pet websites, can be a novel resource for understanding and assessing bird incursions.

Link to paper: <https://doi.org/10.1007/s10530-016-1332-x>



ROSE-RINGED PARAKEET [*PSITTACULA KRAMERI*] BY M. MCMASTERS
[HTTP://WWW.GBIF.ORG/OCCURRENCE/1134965843](http://WWW.GBIF.ORG/OCCURRENCE/1134965843) CC BY 2.0

INVASIVENESS RUNS IN THE FAMILY

DATA USED: 338,945 SPECIES OCCURRENCES

Harris RMB, Kriticos DJ, Remenyi T and Bindoff N [2016] Unusual suspects in the usual places: a phylo-climatic framework to identify potential future invasive species. *Biological Invasions*. Springer Nature 19(2): 577–596.

Author country: Australia

Research funding: Australian Government's National Environmental Research Programme

The threat of biological invasions is likely to change with climate conditions, and identifying species and regions of risk is becoming a priority. This study presents a general framework that relies on currently introduced and related species for recognizing species that may become invasive in the future.

By applying a series of questions, the researchers demonstrate the framework on the Australian Alps region, which is rapidly warming. For three already introduced species of hawkweed (*Hieracium* spp.) as well as a missing relative species (*H. murorum*) present in a neighbouring region, they combine GBIF-mediated occurrences and climate data to construct niche models to determine climatic suitability in the future. By considering climatically similar regions worldwide as sources, they identify another relative (*H. pringlei*), with potential to become invasive in the future.

The addition of phylogeny in the proposed framework allows for identification of potential invaders in the absence of species-specific knowledge.

Link to paper: <https://doi.org/10.1007/s10530-016-1334-8>

HIGH INVASION RISKS IN ANTARCTICA

DATA USED: 600,000 SPECIES OCCURRENCES

Pertierra LR, Aragón P, Shaw JD, Bergstrom DM, Terauds A and Olalla-Tárraga MÁ [2017] Global thermal niche models of two European grasses show high invasion risks in Antarctica. *Global Change Biology*. Wiley-Blackwell.

Author countries: Spain, Australia

Research funding: Spanish MINECO

Biological invasions are a global concern that affects not only regions in which humans live, but also remote areas such as Antarctica, previously considered pristine, have been invaded by foreign species.

Focusing on two already established non-native grasses in Antarctica, *Poa annua* and *Poa pratensis*, this study used GBIF-mediated occurrences combined with temperature data to model the distribution of the invaders, and subsequently, quantify climatic suitability in the Antarctic Peninsula.



COLORADO BUR (*SOLANUM ROSTRATUM*) BY OPUNTIA CADEREYTENSIS
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Further relating climatic suitability with human presence data, the researchers identify specific research stations, tourist sites and protected areas with the highest risk of being the source of an invasion.

The study concludes that the Antarctic Peninsula is more vulnerable to biological invasions than previously expected, and the authors suggest a need for strict management policies to minimize introduction of invasive species.

Link to paper: <https://doi.org/10.1111/gcb.13596>

INVASIVE SPECIES ALONG FOR THE RIDE

DATA USED: 9,605 SPECIES OCCURRENCES

Horvitz N, Wang R, Wan F-H and Nathan R [2016] Pervasive human-mediated large-scale invasion: analysis of spread patterns and their underlying mechanisms in 17 of China's worst invasive plants. *Journal of Ecology*. Wiley-Blackwell 105(1): 85–94.

Author countries: China, Israel

Research funding: Israel Science Foundation; Ring Foundation; National Nature Science Foundation of China; Special Fund for Scientific Research in Environmental Protection Public Interest; National Key Technology Research and Development Program of China; National Key Research and Development Program of China; Minerva Center for Movement Ecology; Adelina and Massimo Della Pergola Chair of Life Sciences

Biological invasions threaten global biodiversity and is also considered a major cause of recent extinctions. Human activity contributes to invasions through different mechanisms, but the rapid speed and patterns of invasion are largely unexplored.

In China, 268 invasive plant species have been described, and in this study, researchers trace the origin and spread rate of 17 of the worst invaders using a collection of data from herbaria, monitoring programmes, literature and own field surveys. They use GBIF-mediated data of non-invasive species to normalize their dataset, and find the average minimal speed across all species to be 1.5 km per year, with some species spreading more than 100 km per year.

These rates are unlikely to be explained by spread of seeds by the animals, water or wind, and in fact, the study finds a significant correlation between number of private-owned cars in China and counties with invasive species, providing further evidence for human-mediated spread.

Link to paper: <https://doi.org/10.1111/1365-2745.12692>

ASSESSING POTENTIAL CAUSES OF BAMBOO INVASIONS

DATA USED: 23,218 SPECIES OCCURRENCES

a Canavan S, Richardson DM, Visser V, Roux JJL, Vorontsova MS and Wilson JRU [2016] The global distribution of bamboos: assessing correlates of introduction and invasion. *AoB Plants*. Oxford University Press plw078.

Author countries: South Africa, United Kingdom

Research funding: South African National Department of Environment Affairs; DST-NRF Centre of Excellence for Invasion Biology; National Research Foundation of South Africa

Knowingly or not, humans are responsible for transporting species around the world and introducing them to new regions with beneficial, but also undesirable consequences. As global traffic and travel increase, so does the dissemination of potentially invasive species.

In this study, researchers examine the species inventory, distribution and dissemination of bamboos, a large subfamily of grasses, interesting beyond timber functions because of its versatility and total-plant utilisation. Relying on a variety of sources including GBIF, the researchers compiled a database of 1,662 bamboo species across 122 countries and territories, and identified 14 per cent as having been introduced outside native ranges.



MOSO BAMBOO (*PHYLLOSTACHYS EDULIS*) BY HARUM.KOH
[HTTP://WWW.GBIF.ORG/OCURRENCE/1088912416](http://www.gbif.org/occurrence/1088912416) CC BY-NC 4.0

Investigating morphology, they find a number of traits that correlated positively with being introduced, including runner rhizomes, culm diameter and height. Species with more cultivars are also more likely to have been introduced. Finally, and perhaps unsurprisingly, they find strong evidence linking number of introductions with risk of being invasive, suggesting that bamboo invasions are first and foremost a product of human activity rather than species differences.

Link to paper: <https://doi.org/10.1093/aobpla/plw078>

Species conservation and protected areas



AGAVE CHRYSANtha BY STEVE JONES [HTTP://WWW.GBIF.ORG/OCCURRENCE/1500266068](http://www.gbif.org/occurrence/1500266068) CC BY-NC 4.0

NO BATS, NO TEQUILA: PROMPTING PARTY PEOPLE TO PROTECT POLLINATORS

DATA USED: 2,655 SPECIES OCCURRENCES

Trejo-Salazar R-E, Eguiarte LE, Suro-Piñera D and Medellin RA [2016] Save Our Bats, Save Our Tequila: Industry and Science Join Forces to Help Bats and Agaves. *Natural Areas Journal*. *Natural Areas Journal* 36(4): 523–530.

Author countries: Mexico, United States

Research funding: none listed

As the third-largest genus in Mexican flora, *Agave* pervades the natural landscapes and cultural heritage of the Americas, providing human communities with food, fiber and distilled drinks for centuries. The best-known spirit, tequila, depends on the pollination of cultivated crops of *A. tequiliana* Weber var. *azul* by three imperiled species of nectar-eating bats. One likely contributor to the decline of these species is that commercial *Agave* isn't allowed to flower, sacrificing bat food for tequila's 'aguamiel' base.

In this study, the authors model a 'bat-friendly' approach that permits the inflorescence of between 5 and 10 per cent of cultivated plants to boost nectar supplies for hungry chiropterans. Potential mutual benefits that crop up include increased genetic diversity among commercial *Agave* clones now vulnerable to emerging plantation diseases,

suggesting how to sustain healthy populations of bats, *A. tequiliana*, as well as producers, distributors and—with the confines of their own limits—consumers of tequila.

Link to paper: <https://doi.org/10.3375/043.036.0417>

DIVERSITY OF REEF CORALS IN THE SOUTH CHINA SEA

DATA USED: 66 SPECIES OCCURRENCES

Huang D, Hoeksema BW, Affendi YA, Ang PO, Chen CA, Huang H, Lane DJW, Licuanan WY, Vibol O, Vo ST, Yeemin T and Chou LM [2016] Conservation of reef corals in the South China Sea based on species and evolutionary diversity. *Biodiversity and Conservation*. Springer Science + Business Media, 331–344.

Author countries: Singapore, Malaysia, China, Taiwan, Brunei Darussalam, Philippines, Cambodia, Vietnam, Thailand

Research funding: NUS

Building on an existing database on stony reef corals in the South China Sea, researchers used data from GBIF and others to analyse coral species richness, rarity and phylogenetic diversity in the South China Sea, and to clarify relationships between regional and global patterns of coral diversity. The resulting data point to considerable differences between examined reef areas in the region. One area (West Malaysia) contains a very high number of both regionally and

globally rare species, and another (northern Palawan) has only two, albeit extremely rare species, present only in one ecoregion. Generally, a high number of rare species is associated with high richness, with southern Vietnam being a notable exception. The authors couple their data with IUCN extinction risks, and conclude that conservation planning in the South China Sea shouldn't be based on species diversity alone.

Link to paper: <https://doi.org/10.1007/s10531-016-1052-7>

IDENTIFYING SPECIES SUITABLE FOR ECOSYSTEM RESTORATION NOW AND IN THE FUTURE

DATA USED: 28,668 SPECIES OCCURRENCES

Butterfield BJ, Copeland SM, Munson SM, Roybal CM and Wood TE [2016] Prestoration: using species in restoration that will persist now and into the future. *Restoration Ecology*. Wiley-Blackwell.

Author country: United States

Research funding: Colorado Plateau Native Plants Program; USGS

Restoration of ecosystems can be achieved through introducing species important for the structure and function of the habitat. Changing climates complicate this process as suitable habitats may shift in the future. In this paper, researchers propose the concept of "prestration", a method of selecting species that will persist not only now but also in the future. Working from the Colorado Plateau as a case study, the researchers use GBIF-mediated occurrences to construct ecological niche models for 24 species of local perennial grasses previously selected as candidate species for restoration. They then calculate the prestration potential of each species, and find that suitable area might decline by 40 per cent by mid-century. Turning again to GBIF data, the researchers are able identify new species more suitable for long-term climate changes. Adding these has the potential of making up for the losses projected for the local species.

Link to paper: <https://doi.org/10.1111/rec.12381>

LEAVING NO STONE UNTURNED IN EUROPE'S FIRST MARINE RESERVE

DATA USED: 3,856 SPECIES OCCURRENCES

Trowbridge CD, Little C, Ferrenburg LS, Resk HM, Kachmarik K, Plowman CQ, Stirling P and McAllen R [2016] Shallow subtidal octocorals in an Irish marine reserve. *Mar Biodiv*. Springer Science + Business Media.

Author country: United States; United Kingdom; Ireland

Research funding: National Science Foundation

Lough Hyne is fully marine, semi-enclosed, tidal



ALCYONIUM DIGITATUM BY GUIDO SCHMITZ
[HTTP://WWW.GBIF.ORG/OCURRENCE/1227715431](http://www.gbif.org/occurrence/1227715431) CC BY-NC 4.0

'lake' in the southern-most part of Ireland. The lough, connected to the Atlantic Ocean via tidal rapids, is the first marine reserve in Europe, known for high species and habitat diversity. This study is the conclusion of a two-decade monitoring programme during which researchers surveyed intertidal and shallow subtidal octocoral species at 20 sites by carefully turning rocks, photographing them, and returning them to their original location. The most commonly recorded species was the pink soft coral *Alcyonium hibernicum*, the abundance of which, however, fluctuated greatly over the period. The red octocoral *Alcyonium glomeratum* was recorded for the first time inside the lough. A previously recorded species, *Alcyonium digitatum* was notably absent, but another species, *Sarcodictyon catenatum*, not observed since the 1930s, was recorded at eight sites, presumably overlooked for eight decades due to its cryptic coloration and small size.

Link to paper: <https://doi.org/10.1007/s12526-016-0450-0>

AMPHIBIANS OF THE PHILIPPINES

DATA USED: 1,525 SPECIES

Diesmos AC, Watters JL, Huron NA, Davis DR, Alcala AC, Crombie RL, Afuang LE, Gee-Das G, Sison RV, Sanguila MB, Penrod ML, Labonte MJ, Davey CS, Leone EA, Diesmos ML, Sy EY, Welton LJ, B. R. & S. C. [2015]. Amphibians of the Philippines, Part I: Checklist of the Species. *Proceedings of the California Academy of Sciences*, 62[20], 457–539.

Author countries: Philippines, United States, Malaysia

Research funding: National Museum of the Philippines; Oklahoma Museum of Natural History; NSF; Miami University of Texas; University of Kansas Biodiversity Institute

The amphibian fauna of the Philippines is high in diversity and endemism, yet faces threats from habitat modification, invasive species, hunting, and the spread of chytrid fungus. Developing a complete species list of amphibians is essential for conservation planning and informed management decisions. Based on GBIF-mediated occurrences and records from 33 museums, the authors of this study present a revised list of all known amphibians in the Philippines with distribution maps and representative photos of most currently recognized species. New species descriptions have been steadily rising since the early 1990s due to increased sampling and awareness of species boundaries based on phylogenetic studies. Within the last 20 years alone, 27 new species have been described (nearly one-quarter of the country's recognized diversity), all endemic to the Philippines. The cryptic and underestimated diversity highlights the importance of continued efforts to study the amphibian fauna of the archipelago.

Link to paper: <http://bit.ly/2ryr4vE>

WHERE THE WILD WHEATS GROW

DATA USED: 5,863 SPECIES OCCURRENCES

 Ostrowski M-F, Prosperi J-M and David J [2016] Potential Implications of Climate Change on *Aegilops* Species Distribution: Sympatry of These Crop Wild Relatives with the Major European Crop *Triticum aestivum* and Conservation Issues. PLOS ONE. Public Library of Science (PLoS) 11(4): e0153974.

Author country: France

Research funding: Institut National de la Recherche Agronomique (INRA); Ministère de l'Enseignement et de la Recherche; Ministère de l'Agriculture

Gene exchange is a common phenomenon between crops and wild relatives when they grow in the same area. This can lead to changes in adaptation of the wild relatives to natural ecosystems. As climate change progresses, sympatry patterns might change, and in this study, researchers examined projected changes for cultivated wheat and six wild relatives (*Aegilops* spp.). Using GBIF-mediated occurrences and bioclimatic data, the researchers created niche models for each of the species, and find that by 2050, one species (*Ae. ventricosa*) might lose more than 50 per cent of suitable habitat, potentially becoming endangered. The models also showed, that European levels of sympatry will increase by 49 per cent. In some countries, the increase will be higher (e.g. five-fold in Russia), and in others it will even decrease



GOAT'S FOOT CONVOLVULUS [*IPOMOEA PES-CAPRAE*] BY CLAUDIO C. MUÑIZ
<HTTP://WWW.GBIF.ORG/OCCURRENCE/1249293275> CC BY 4.0

(e.g. UK). Concluding, the study stresses a need for increased monitoring to protect the important genetic resources of wild *Aegilops* populations.

Link to paper: <https://doi.org/10.1371/journal.pone.0153974>

PROTECTING THE COASTAL DUNES OF MEXICO

DATA USED: 2,012 SPECIES OCCURRENCES

Mendoza-González G, Martínez ML, Rojas-Soto O, Téllez-Valdés O and Arias-Del Razo I [2016] Priority areas for conservation of beach and dune vegetation of the Mexican Atlantic coast. Journal for Nature Conservation. Elsevier BV 33: 25–34.

Author countries: Mexico, United States

Research funding: Universidad Nacional Autónoma de México; CONABIO

The combination of urban development and rising sea levels is a threat to coastal ecosystems. In Mexico, coastal dunes represent one per cent of the national territory, but is home to seven per cent of the country's seed plants. This study focuses on the Atlantic coast of Mexico and identifies areas of high diversity and potential targets for conservation efforts. Using GBIF-mediated occurrences, researchers modelled the distribution of 23 species of herbaceous plants and perennial shrubs and find the highest number of typical and endemic species in areas ranging from southern Tamaulipas to central Veracruz and the northern and eastern coast of the Yucatan peninsula. Although being close to protected areas, a great deal of areas identified have no direct coastal protection. The study suggests that increased conservation efforts are needed and should takes priority over other activities, such as tourism.

Link to paper: <https://doi.org/10.1016/j.jnc.2016.04.007>

CONSERVATION STATUS OF AFRICAN REPTILES

DATA USED: 104,000 SPECIES OCCURRENCES

Tolley KA, Alexander GJ, Branch WR, Bowles P and Maritz B [2016] Conservation status and threats for African reptiles. *Biological Conservation*. Elsevier BV 204: 63–71.

Author countries: South Africa, United States

Research funding: none listed

Africa has a larger land surface than China, India, North America and Western Europe combined, and despite being home to nine of the world's biodiversity hotspots, our knowledge of Africa's fauna is poorly documented. This study aimed to elucidate knowledge gaps and conservation status of mainland African reptiles. Using GBIF-mediated occurrences, researchers quantified sampling efforts and species richness on a country level. They find species richness to be correlated to sampling, noting a potential bias. For the best sampled countries, species richness is strongly related to country area. The researchers also developed a Threat Index based on various socioeconomic factors, and find that countries with a high threat index also have the lowest levels of sampling. Combined with IUCN Red List data showing that more than half of African mainland reptiles have not been evaluated, the study highlights a need for increased data mobilization and centralization in open access databases such as GBIF.

Link to paper: <https://doi.org/10.1016/j.bioc.2016.04.006>

EFFECTS OF PROTECTED AREAS ON GLOBAL BIODIVERSITY

DATA USED: 240 MILLION SPECIES OCCURRENCES

Gray CL, Hill SLL, Newbold T, Hudson LN, Börger L, Contu S, Hoskins AJ, Ferrier S, Purvis A and Scharlemann JPW [2016] Local biodiversity is higher inside than outside terrestrial protected areas worldwide. *Nature Communications*. Springer Nature, 12306.

Author countries: United Kingdom, Australia

Research funding: University of Sussex; Natural History Museum; UK Natural Environment Research Council

The Aichi biodiversity target 11 commits parties to the Convention on Biological Diversity (CBD) to increasing protected terrestrial areas to 17 per cent by 2020. Protected areas are, however, expensive to maintain and quantifying their effectiveness is therefore crucial. This study present a global analysis of how successful protection is in terms of sustaining biodiversity.

Comparing protected sites with matched unprotected counterparts, the researchers found richness and abundance to be higher in protected sites, however,

rarefied richness did not differ. By using GBIF-mediated occurrences to determine range sizes, they also found evidence that protection has little effect on the proportion of individuals within a community that have narrow geographic ranges. Within the protected areas, the most likely explanation of the effects appeared to be differences in land use. The study reinforces the importance of protected areas, but stresses that the effectiveness of protection must be studied to be improved further.

Link to paper: <https://doi.org/10.1038/ncomms12306>

IDENTIFYING AND PRIORITIZING SITES FOR CONSERVATION PLANNING

DATA USED: 1,124,142 SPECIES OCCURRENCES

Albuquerque F and Beier P [2016] Predicted rarity-weighted richness, a new tool to prioritize sites for species representation. *Ecology and Evolution*. Wiley-Blackwell 6[22]: 8107–8114.

Author country: United States

Research funding: none listed

A major limitation for site ranking algorithms in conservation planning is lack of biodiversity data. Measurements such as vegetation communities or occurrences of a single well-inventoried taxon often act as surrogates in those cases.

This study presents a novel ranking alternative based on predicting the rarity-weighted richness using environmental data combined with species occurrences from a subset of sites in a given planning area.

The researchers applied the method to six different areas and tested the ability of the model to prioritize sites for species representation, and with just ten per cent of sites used in the model, the method performed significantly better than a random selection of sites. In one case based on birds in Spain, having just five



CLOUDBERRY (*RUBUS CHAMAEMORUS*) BY TORSTEN ERIKSSON
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per cent of sites inventoried, yielded a result 60 per cent as efficient as having all sites inventoried.

The suggested method can be a useful surrogate for prioritizing sites when just a small fraction of the landscape is inventoried.

Link to paper: <https://doi.org/10.1002/ece3.2544>

CONSERVING CROP WILD RELATIVES TO HELP FEED THE WORLD

DATA USED: 382,605 SPECIES OCCURRENCES

Phillips J, Asdal Å, Magos Brehm J, Rasmussen M and Maxted N (2016) In situ and ex situ diversity analysis of priority crop wild relatives in Norway. *Diversity and Distributions*. Wiley-Blackwell 22(11): 1112–1126.

Author countries: United Kingdom, Norway

Research funding: Norwegian Ministry of Agriculture and Food

A growing global population means higher demands for food productivity. Increased homogeneity and decreased genetic diversity in crops, however, may lead to maladaptation to changing environments. Crop wild relatives (CWR) can be used as a genetic resource to make crops better suited for the future environments. In this study, researchers created a checklist of CWR in Norway and used GBIF-mediated occurrences to model the potential distributions of the included species and identify conservation priorities. The resulting list contained 204 priority CWR taxa, including vegetables, berries and herbs, many of which were concentrated around the capital city of Oslo. The authors recommend creating a network of *in situ* genetic reserves throughout Norway to help capture the genetic diversity of priority CWR, and the collection of 177 taxa without *ex situ* accessions to be stored the Svalbard Global Seed Vault. They finally recommend reviewing and updating the CWR priority list every five years.

Link to paper: <https://doi.org/10.1111/ddi.12470>

UNDERSTANDING HISTORY TO BETTER UNDERSTAND THE FUTURE

DATA USED: 56,602 SPECIES OCCURRENCES

a Calderón L, Campagna L, Wilke T, Lormee H, Eraud C, Dunn JC, Rocha G, Zehlindjiev P, Bakaloudis DE, Metzger B, Cecere JG, Marx M and Quillfeldt P (2016) Genomic evidence of demographic fluctuations and lack of genetic structure across flyways in a long distance migrant, the European turtle dove. *BMC Evolutionary Biology*. Springer Nature 16(1).

Author countries: Germany, United States; France, United Kingdom, Spain, Bulgaria, Greece, Malta, Italy

Research funding: Deutsche Forschungsgemeinschaft; Justus Liebig University

Current changes in climate as well as human activities are affecting the evolution and distribution of species worldwide. Understanding fluctuations throughout history can help predict similar changes in the future and focus conservation efforts.

In a recent study, researchers combined genetic sequence analyses and niche modelling to characterize the demographic history and population structure of the European turtle dove (*Streptopelia turtur*), a long-distance migrant, recently designated as vulnerable.

The results of the genetic study revealed historical population fluctuations with a drastic early-Holocene expansion, and a more recent contraction, both of which are supported by the suitable habitats as shown by niche models constructed using GBIF-mediated occurrences and paleoclimatic data. The researchers found no evidence of genetic structures being linked to migratory flyways.

The combined results suggest that all turtle dove populations across Europe are equally vulnerable and relevant for conservation.

Link to paper: <https://doi.org/10.1186/s12862-016-0817-7>

USING BIOQUALITY FOR PRIORITIZING CONSERVATION EFFORTS

DATA USED: 1,970,142 SPECIES OCCURRENCES

Marshall CAM, Wieringa JJ and Hawthorne WD (2016) Bioquality Hotspots in the Tropical African Flora. *Current Biology*. Elsevier BV 26(23): 3214–3219.

Author countries: United Kingdom, Netherlands

Research funding: Clarendon Fund; Merton College; James Martin 21st Century School; BP Biofuels

Species richness is often used to identify biodiversity hotspots and to prioritize areas for conservation. This approach, however, does not consider the individual conservation status of species in assemblages and isn't very suitable for local management.

In this study, researchers suggest a new conservation framework for tropical Africa. Using mainly GBIF-mediated occurrences of African vascular plants, they summarized the global range of each species and assigned a simple star rating based on the number of degree squares occupied by a species. Plants were given either a black (fewest squares), yellow, blue or green (most squares) star rating according to distribution patterns.

Combining conservation ratings, the researchers then identified *bioquality* hotspots in areas with the highest proportion of globally rarer species, i.e. black stars.

Previously underestimated, the highest bioquality is identified in the Horn of Africa.

The framework suggested is based on the argument that areas of high bioquality is more important than areas with high species richness alone.

Link to paper: <https://doi.org/10.1016/j.cub.2016.09.045>

PESTICIDES TURN QUEENS INTO WORKERS

DATA USED: 430 SPECIES OCCURRENCES

ⓐ Dos Santos CF, Acosta AL, Dorneles AL, dos Santos PDS and Blochtein B [2016] Queens become workers: pesticides alter caste differentiation in bees. *Scientific Reports*. Springer Nature 6[1].

Author country: Brazil

Research funding: Conselho Nacional do Desenvolvimento Científico e Tecnológico (CNPq); Fundação de Amparo à Pesquisa do Estado do Rio Grande do Sul

Pesticides are used in agriculture to combat insects that threaten crop yields and quality. The chemicals used to kill or deter pests, however, are also known to have an impact on beneficial insects providing ecosystem services, such as pollination by honeybees and bumblebees. This study focuses on another group of important pollinators, the stingless bees, for which toxicological pesticide studies are lacking. Investigating the effects of a common pesticide, CPY, on stingless bee larval development, researchers used GBIF-mediated occurrences overlapped with data on use of CPY to determine relevant geographical context. Through *in vitro* queen-rearing experiments, the researchers discovered that in addition to being lethal at higher doses, CPY at sub-lethal concentrations caused 33 per cent of the larvae to develop into workers rather than queens, and this percentage increased with dose. CPY also increased development time significantly. The authors suggest developing alternative methods of pest control to reduce toxic exposure among beneficial insects.

Link to paper: <https://doi.org/10.1038/srep31605>

IDENTIFYING OVERLOOKED OCTOCORAL HABITAT

DATA USED: 114 SPECIES OCCURRENCES

ⓐ Boavida J, Assis J, Silva I and Serrão EA [2016] Overlooked habitat of a vulnerable gorgonian revealed in the Mediterranean and Eastern Atlantic by ecological niche modelling. *Scientific Reports*. Springer Nature 6[1].

Author country: Portugal

Research funding: Inqua Conservation Fund; National Geographic Society; Fundação para a Ciência e a Tecnologia

The violescent sea-whip (*Paramuricea clavata*) is a sensitive, but important structuring octocoral species in the Mediterranean and adjacent Atlantic,

threatened by fishing, recreational diving, pollution and climate change. Little is known about the habitat requirements of the sea-whip and the factors limiting its distribution.

A study aimed at increasing knowledge of *P. clavata* compiled all currently known occurrences from GBIF and other sources, and added new underwater survey records to model the ecological niche of the species. The full distribution was best explained by ocean temperatures and, in particular, slope. When restricting the suitable habitat to hard bottom areas, where larvae are more likely to settle, the researchers estimated a total area of 36,000 km², consistent with known occurrences, but also identifying novel areas including Algeria, Alboran Sea and Atlantic coasts.

The study provides new insights into the potential distribution of an important octocoral species and suggests sites as targets for further investigation and, potentially, conservation.

Link to paper: <https://doi.org/10.1038/srep36460>

CONSERVING INDIGENOUS VEGETABLES

DATA USED: 108,787 SPECIES OCCURRENCES

Solberg SØ and Chou Y-Y [2017] Conservation of Indigenous Vegetables from a Hotspot in Tropical Asia: What Did We Learn from Vavilov? *Frontiers in Plant Science*. Frontiers Media SA 7.

Author country: Taiwan

Research funding: none listed

As global populations increase and climates change, agriculture needs to produce more food under unpredictable climatic conditions. The need for crop wild relatives and the genetic diversity provided by such is greater than ever. In tropical Asia, the Indo-Burma biodiversity hotspot is a potential source for important cultivars.

This study examines the representation of indigenous vegetables in global conservation. Using tropical Asia as a case study, researchers focus on Myanmar and identify 30 target species for further examination. They compare number of available GBIF-mediated occurrences and GENESYS conserved accessions for Myanmar with other countries and regions, and find that important species have very low number of records. The researchers conclude that the overall underrepresentation of indigenous vegetables from tropical Asia is clear. They suggest prioritizing new collection missions to safeguard and utilize the potential of plant genetic resources.

Link to paper: <https://doi.org/10.3389/fpls.2016.01982>

Advancing biodiversity science



ORANGE-CROWNED WARBLER [*OREOTHLYPIS CELATA*] BY JAMIE CHAVEZ <https://flic.kr/p/j7NMkb> CC BY-NC 2.0

GETTING ABSENCE FROM PRESENCE

DATA USED: 1.7 MILLION SPECIES OCCURRENCES

Coro G, Magliozi C, Vanden Berghe E, Bailly N, Ellenbroek A & Pagano P. (2016). Estimating absence locations of marine species from data of scientific surveys in OBIS. *Ecological Modelling*, 323, 61–76.

Author countries: Italy, Belgium, Greece, Philippines

Research funding: European Commission; Presidency of the Tuscan Regional Government

The lack of a presence doesn't necessarily mean absence. When modelling species distributions based on occurrences, absence is often derived from lack of presence (pseudo-absence), but absence could be due to poor surveying or species behaviour. This paper presents a novel methodology to predict absence information from presence-only information. Using Marine Species Survey Reports from the Ocean Biogeographic Information System (OBIS), the authors developed a method which relies on the principle of predicting the absence of one species by the presence of others, thereby avoiding some sampling bias. They evaluated the performance of the method using the Atlantic cod (*Gadus morhua*) as a case study, and finally benchmarked against 1.7 million GBIF-mediated occurrences of 280 marine species. Although the method does not produce an exhaustive set of absences, it performs well and can be scaled to work regionally as well as globally.

Link to paper: <https://doi.org/10.1016/j.ecolmodel.2015.12.008>

WHY DO BIRDS ... WINTER WHERE THEY DO?

DATA USED: 6,793 SPECIES OCCURRENCES

a Pérez-Moreno H, Martínez-Meyer E, Soberón Mainero J and Rojas-Soto O (2016) Climatic patterns in the establishment of wintering areas by North American migratory birds. *Ecology and Evolution*. Wiley-Blackwell, 2022–2033.

Author countries: Mexico, United States

Research funding: Consejo Nacional de Ciencia y Tecnología (CONACYT)

When migratory birds travel to wintering grounds, what factors determine where they decide to stay? Some birds are known to follow their niches and travel to areas with climates similar to their native breeding grounds, while others prefer climates that are very different. This study presents an analysis of the monthly climatic variation of the distribution of 13 neotropical migratory birds throughout the winter season. Using GBIF-mediated occurrences and climatic data, researchers constructed monthly ecological niche models for each of the species, and their results indicate that the selection of wintering sites is driven mainly by temperature and levels of precipitation. The models also show that distributions in the early winter months vary less than late months, suggesting that the birds who arrive first, will occupy the sites with optimal climate conditions, leaving suboptimal sites to late-comers.

Link to paper: <https://doi.org/10.1002/ece3.1973>

THE IMPACT OF HUMAN LAND USE ON THE COMPOSITION OF ECOLOGICAL COMMUNITIES

DATA USED: 240 MILLION SPECIES OCCURRENCES

Newbold T, Hudson LN, Hill SLL, Contu S, Gray CL, Scharlemann JPW, Börger L, Phillips HRP, Sheil D, Lysenko I and Purvis A (2016) Global patterns of terrestrial assemblage turnover within and among land uses. *Ecography*. Wiley-Blackwell.

Author countries: United Kingdom, Norway

Research funding: Natural Environment Research Council, UK

Human land use has a negative impact of on the composition of ecological communities, also known as alpha diversity, but less is known about how the widespread modifications of natural habitats affect species turnover. In the present study, authors



GEOFFROY'S TAMARIN (*SAGUINUS GEOFFROYI*) BY HENRY DE LA TORRE
[HTTP://WWW.GBIF.ORG/OCCURRENCE/1291073189](http://WWW.GBIF.ORG/OCCURRENCE/1291073189) CC BY-NC 4.0

used data from nearly 500 studies sampling more than 14,000 sites worldwide covering all but one of the world's terrestrial biomes. Using GBIF-mediated occurrences to estimate the total range size of each species present, the authors paired biome-matched sites and calculated an endemicity-weighted compositional similarity between sites. Their results showed little evidence for difference in turnover, but they confirmed that alterations of habitats have a significant effect on community composition, especially in tropical biomes. The study reiterates the fact that human activities have a profound impact on the global structure of terrestrial ecological communities.

Link to paper: <https://doi.org/10.1111/ecog.01932>

USING DNA SEQUENCES TO IMPROVE TAXONOMIC IDENTIFICATIONS

DATA USED: 4,672 SPECIES OCCURRENCES

Smith BE, Johnston MK and Lücking R (2016) From GenBank to GBIF: Phylogeny-Based Predictive Niche Modeling Tests Accuracy of Taxonomic Identifications in Large Occurrence Data Repositories. *PLOS ONE*. Public Library of Science [PLOS], e0151232.

Author countries: United States, Germany

Research funding: National Science Foundation

Some species are easily misidentified because they appear very similar to other species. This affects large biodiversity repositories, such as GBIF, but how can such misidentifications be corrected without having to go through millions of records? In this study, researchers present a strategy that combines DNA sequence data and specimen occurrence data to potentially find incorrectly identified specimens in large repositories such as GBIF. The researchers create ecological niche models for the lichen fungus, *Usnea longissima*, by using georeferenced specimen data that at the same time have been confirmed to represent a single species by DNA sequence data. When plotting GBIF-mediated occurrences against the verified distribution of the fungus, outliers identified potentially records for taxonomic scrutiny and revision. Revision of these outliers revealed that most were, in fact, misidentified and belonged to similar species with different distributions. The study raises interesting questions about the potential of DNA sequence data to improve the quality of species information in GBIF.

Link to paper: <https://doi.org/10.1371/journal.pone.0151232>

ARE RANGE LIMITS DEFINED BY NICHE LIMITS?

DATA USED: 88,253 SPECIES OCCURRENCES

Lee-Yaw JA, Kharouba HM, Bontrager M, Mahony C, Csergő AM, Noreen AME, Li Q, Schuster R and Angert AL (2016) A synthesis of transplant experiments and ecological niche models suggests that range limits are often niche limits. *Ecology Letters*. Wiley-Blackwell 19(6): 710–722.

Author countries: Canada, Switzerland, United States, Ireland

Research funding: Swiss National Science Foundation

The range of any given species is limited by several biotic and abiotic conditions. But to what extent can geographical range limits be explained by ecological niches? This study combined results from existing transplant experiments using both plants and animals with new ecological niche models based on GBIF-mediated occurrences to provide a comparative

approach to the question. The researchers weighed performance of transplanted species against predicted suitability in the niche models, and found that across almost all species tested, the two parameters were concordant and significantly lower outside the range than inside. The results provide compelling support for the hypothesis that range limits reflect niche limits, raising questions about the importance of dispersal limitation to species' distributions. The study combines methods and provides a robust framework for studying range limits.

Link to paper: <https://doi.org/10.1111/ele.12604>

ASSESSING COMPLETENESS OF PLANT INVENTORIES FOR AFRICA

DATA USED: 3,546,206 SPECIES OCCURRENCES

 Stropp J, Ladle RJ, M. Malhado AC, Hortal J, Gaffuri J, H. Temperley W, Olav Skøien J and Mayaux P (2016) Mapping ignorance: 300 years of collecting flowering plants in Africa. *Global Ecology and Biogeography*. Wiley-Blackwell 25(9): 1085–1096.

Author countries: Italy; Brazil, United Kingdom, Spain, Luxembourg, Belgium

Research funding: Biodiversity and Protected Areas Management; Brazilian National Council for Scientific and Technological Development; Spanish Dirección General de Correos y Telégrafos

In this study, researchers assessed the quality of occurrence data of flowering plants in Africa to determine the reliability of these records, and to systematically review botanical sampling in Africa in the past 300 years. Finally, the authors aimed to determine the overall completeness of the plant inventory for Africa. Using a download of more than three million GBIF-mediated records from 2012, the researchers make the following observations: the number of specimens collected in South Africa surpasses the total number for all other African countries, and there is a pronounced bias towards old specimens. The overall peak of sampling took place in the 1970s and 1980s, and well-sampled areas are sparse [less than one per cent of investigated units of 25 km by 25 km] and generally clustered in both time and space. The authors suggest implementation of community feedback mechanisms to allow continued improvement of data quality.

Link to paper: <https://doi.org/10.1111/geb.12468>



PHILIPPINE GROUND ORCHID (*SPATHOGLOTTIS PLICATA*) BY LEON PERRIE
[HTTP://WWW.GBIF.ORG/OCURRENCE/1135528836](http://www.gbif.org/occurrence/1135528836) CC BY-NC 4.0

ASSESSING SPECIES-LEVEL GAPS AND BIASES IN OCCURRENCE DATA

DATA USED: 4,524,585 SPECIES OCCURRENCES

Meyer C, Jetz W, Guralnick RP, Fritz SA and Kreft H (2016) Range geometry and socio-economics dominate species-level biases in occurrence information. *Global Ecology and Biogeography*. Wiley-Blackwell 25(10): 1181–1193.

Author country: Germany; United Kingdom; United States

Research funding: Deutsche Bundesstiftung Umwelt; German Academic Exchange Service; Universitätsbund Göttingen; NSF; Spatial Biodiversity Science and Conservation; Hesse's Ministry of Higher Education; German Research Foundation

Gaps in data may hamper good species distribution modelling. When assessing quality of species occurrence data, an often suggested (but rarely tested) cause of species-level variation and bias is, that species attributes, e.g. body size and diurnal activity, affect detection and collection. In this study, researchers overlaid GBIF-mediated occurrences of 3,625 mammalian species with expert-drawn range

maps, and assessed occurrences of species and higher taxonomic groups according to record count, range coverage and geographical bias. Relating these to species attributes, range geometry and socio-economic factors, the researchers found that primates stand out for below average record counts, and carnivores for below average range coverage. Marsupials, however, score high in both measures. On a global scale, coverage is, not surprisingly, positively correlated with record count. However, the



VIRGINIA RAIL (*Rallus limicola*) BY PAUL FENWICK
[HTTP://WWW.GBIF.ORG/OCCURRENCE/1272089847](http://WWW.GBIF.ORG/OCCURRENCE/1272089847) CC BY-NC 4.0

role of species attributes is remarkably minor. The study concludes by recommending increased data mobilization in institutions near data gaps and added focus on understudied species.

Link to paper: <https://doi.org/10.1111/geb.12483>

RECIPE FOR ORCHID DIVERSITY: MIX HABITAT TEMPERATURES, TOPOGRAPHY AND WATER

DATA USED: 8,935 SPECIES OCCURRENCES

Keppel G, Gillespie TW, Ormerod P and Fricker GA [2016] Habitat diversity predicts orchid diversity in the tropical south-west Pacific. *Journal of Biogeography*. Wiley-Blackwell 43(12): 2332–2342.

Author countries: Australia, United States

Research funding: University of South Australia

Age, area and isolation—researchers studying island biogeography have long presumed this trio to be the three critical factors in determining species richness.

With its dust-like seeds that disperse easily in the breeze, the famously diverse orchid family makes significant contributions to the plant species richness across the Pacific Islands. Relying on GBIF-mediated data from eight southwestern Pacific archipelagoes, this study builds on recent research suggesting that measuring the variation in an island's climate and

topography can effectively predict habitat diversity and, in turn, species richness.

The authors found that indicators of topographic complexity, temperature and precipitation can match the power of land area in predicting orchid richness and endemism in the southwest Pacific. And while isolation does help explain the decreasing pattern of Orchidaceae diversity from west to east, age fails to predict the species richness across islands and archipelagos. As a result, the study suggests refinements toward improving our understanding of the tangled banks of island biodiversity.

Link to paper: <https://doi.org/10.1111/jbi.12805>

REVEALING THE SECRET PATHS OF ILLUSIVE MIGRANTS

DATA USED: 12,951 SPECIES OCCURRENCES

Fournier AMV, Sullivan AR, Bump JK, Perkins M, Shieldcastle MC and King SL [2016] Combining citizen science species distribution models and stable isotopes reveals migratory connectivity in the secretive Virginia rail. *Journal of Applied Ecology*. Wiley-Blackwell.

Author countries: United States, Sweden, Canada

Research funding: Michigan Technological University; National Science Foundation

Some birds are extremely illusive and difficult to track systematically, making their migratory pathways hard to study and conservation management difficult. Employing stable isotope methods can provide some information, but as large geographic regions share isotope populations, such indications are often very broad. In this study, researchers use GBIF-mediated occurrences relying on citizen science observations to refine hydrogen isotope estimates of migratory origins of the secretive Virginia rail (*Rallus limicola*). Combining methods, the researchers produced high-resolution estimates of the origins of migrant birds, showing that 45 per cent of individuals from Louisiana had breeding origins outside the Mississippi flyway, and less than 20 per cent of Texas individuals originated in the Central flyway, both refuting previous assumptions. The results highlight the need for species-specific migratory studies, as management strategies based on surrogate species may be inaccurate, as indicated by the study.

Link to paper: <https://doi.org/10.1111/1365-2664.12723>

THE BIODIVERSITY SCIENCE LAB OF THE FUTURE

La Salle J, Williams KJ and Moritz C [2016] Biodiversity analysis in the digital era. *Philosophical Transactions of the Royal Society B: Biological Sciences*. The Royal Society 371(1702): 20150337.

Author country: Australia

Research funding: National Research Infrastructure for Australia; Australian Research Council; Australian Biological Resources Study; CSIRO

Using the Atlas of Living Australia as a case study, this paper breaks down the needs of a future biodiversity e-infrastructure in terms of data, tools and overall framework. In addition to species occurrences as mediated by GBIF, the authors suggest that an e-infrastructure should integrate a range of equally important data, such as genetic sequences, morphological attributes, behaviour, habitat information and species interactions. To deal with complexities and ambiguity of taxonomic naming, the authors suggest a framework that allows differing views of taxa and operational nomenclature for species that are recognized but not formally named. Visualization of phylogenies will allow for better understanding of evolutionary responses to environmental changes, and incorporating a wealth of spatial biotic and abiotic factors is key to this. The infrastructure should provide tools for discovery, access, (gap) analysis and annotation while allowing users the ability to adapt such tools to their own needs.

Link to paper: <https://doi.org/10.1098/rstb.2015.0337>

12,000 SPECIES OF TREES IN THE AMAZONIAN RAINFOREST

DATA USED: 1.5 MILLION SPECIES OCCURRENCES

Ter Steege H, Vaessen RW, Cárdenas-López D, Sabatier D, Antonelli A, de Oliveira SM, Pitman NCA, Jørgensen PM and Salomão RP [2016] The discovery of the Amazonian tree flora with an updated checklist of all known tree taxa. *Scientific Reports* 6: 29549.

Author countries: Netherlands, Colombia, France, Sweden, United States, Brazil

Research funding: MEC/MCTI/CAPES/CNPq/FAPs; Swedish Research Council; European Union

Amazonia is the most biodiverse rainforest on Earth with thousands of species of animals, and tens of thousands plant species. Whereas animal numbers are well-founded, trees are understudied and their numbers contentious. In this paper, researchers compile collection data from GBIF and offline sources to provide the first exhaustive checklist of all known Amazonian trees. Their final database contains more than 500,000 tree collection records spanning almost 12,000 species belonging to 140 families and 1225 genera. The average collection density found is only 10 per 100 km², and while some areas surrounding cities, such as Manaus, has almost 25,000 records,



YELLOW-RUMPED WARBLER [*SETOPHAGA CORONATA* SUBSP. *AUDUBONI*]
BY JOSÉ BH DÍAZ

[HTTP://WWW.GBIF.ORG/OCURRENCE/1229612499](http://www.gbif.org/occurrence/1229612499) CC BY-NC 4.0.

other remote areas totalling 320,000 km² are void of collections. The researchers find only a weak effect of population size of species on the number of collections, whereas the effect of range size was more pronounced. The paper concludes by recommending increased data exchange, curation, and digitization rather than focusing on collecting more specimens.

Link to paper: <https://doi.org/10.1038/srep29549>

SURVEYING SURVEYS OF BIRDS

DATA USED: 2,426,732 SPECIES OCCURRENCES

Peterson AT, Navarro-Sigüenza AG and Martínez-Meyer E [2016] Digital Accessible Knowledge and well-inventoried sites for birds in Mexico: baseline sites for measuring faunistic change. *PeerJ*. PeerJ 4: e2362.

Author countries: United States, Mexico

Research funding: Universidad Nacional Autónoma de México; CONACyT; Fulbright; Wildlife Institute of India.

When studying the short-term dynamics of species' distributions, re-surveying areas of interest over years and after prolonged periods of time can provide fascinating information, however, choosing sites to re-survey may be difficult. This study seeks to aid in identifying sites for re-surveying and add to a poor body of knowledge on changes in avian distributions in Mexico.

Based on bird occurrences primarily mediated by GBIF, researchers carry out extensive data quality checking, remove duplicate records and calculate levels of inventory completeness. The resulting analysis provides a summary of estimated completeness in 0.05 degree pixels. They identify sampling hotspots of contiguous pixels in almost all Mexican states, however, only three sites (El Triunfo in Chiapas, Xalapa in Veracruz, and the island of Cozumel in Quintana Roo) meet the highest criterion at more

than 90 per cent estimated completeness.

The authors suggest that other researchers use the results of this study for repeating inventories to generate knowledge on avian distribution dynamics in Mexico.

Link to paper: <https://doi.org/10.7717/peerj.2362>

MAPPING COLLECTION BIAS IN BRAZIL

DATA USED: 509,983 SPECIES OCCURRENCES

Oliveira U, Paglia AP, Brescovit AD, de Carvalho CJB, Silva DP, Rezende DT, Leite FSF, Batista JAN, Barbosa JPPP, Stehmann JR, Ascher JS, de Vasconcelos MF, De Marco P, Löwenberg-Neto P, Dias PG, Ferro VG and Santos AJ (2016) The strong influence of collection bias on biodiversity knowledge shortfalls of Brazilian terrestrial biodiversity. *Diversity and Distributions*. Wiley-Blackwell 22(12): 1232–1244.

Author country: Brazil; Singapore

Research funding: CNPq; FAPESP; FAPEMIG; Região Sudeste Brasileira; RG Goelet; NSF

Temporal and spatial variation in biological sampling may generate bias leading to shortfalls of biological knowledge, including undescribed species, poorly described species distribution, and a lack of information on tolerances and responses of species to e.g. climate changes.

In this study, researchers compiled a database of arthropod, vertebrate and angiosperm records in Brazil using data mainly from the GBIF network to test for sampling bias. Comparing taxonomic groups, they find significant differences in sampling effort with angiosperms having larger areas of high density than arthropods and vertebrates. Across all groups and biomes, however, the highest density of records falls within one kilometre of access routes, and this density increases with number of routes.

The study notes the importance of considering such collection bias in biogeographic studies, and suggests focusing on poorly sampled locations in future biodiversity surveys.

Link to paper: <https://doi.org/10.1111/ddi.12489>

FINDING NEEDLES IN THE TROPICAL HAYSTACK

DATA USED: 116,524,885 SPECIES OCCURRENCES

Zizka A, Steege H ter, Pessoa M do CR and Antonelli A (2017) Finding needles in the haystack: where to look for rare species in the American tropics. *Ecography*. Wiley-Blackwell.

Author countries: Sweden, Netherlands, Brazil

Research funding: Swedish Research Council; European Research Council; Wallenberg Academy

The biodiversity of the American tropics is remarkable, and Amazonia biome is home to an estimated 16,000

species of trees, of which as many as half may have populations of less than 1,000 individuals. However, how these rare and possibly endangered species are distributed, is unclear.

Using more than 100 million GBIF-mediated occurrences of all angiosperm species, researchers (headed by the second prize winner of the 2016 Ebbe Nielsen Challenge) identified potentially rare species in the Neotropics and characterized their distributions. Within Amazonia they find 10,000 rare species, whereas the surrounding Neotropics account for 20,000 rare species. In both case, the species are widely scattered but with concentrated centres in montane regions.

Comparing the findings to a vegetation plot dataset, the researchers find a high level of concordance, suggesting the validity of the approach, although acknowledging a potential of false positives due to sampling gaps and biases.

Link to paper: <https://doi.org/10.1111/ecog.02192>



VOCYHYSIA TUCANORUM BY MAURICIO MERCADANTE
[HTTP://WWW.GBIF.ORG/OCCURRENCE/1249271987](http://WWW.GBIF.ORG/OCCURRENCE/1249271987) CC BY-NC 4.0.

CITIZEN SCIENCE AND GLOBAL BIODIVERSITY MONITORING

DATA USED:

Ⓐ Chandler M, See L, Copas K, Bonde AMZ, López BC, Danielsen F, Legind JK, Masinde S, Miller-Rushing AJ, Newman G, Rosemartin A and Turak E (2016) Contribution of citizen science towards international biodiversity monitoring. *Biological Conservation*. Elsevier BV.

Author countries: United States, Austria, Denmark, Spain, Australia

Research funding: German Centre for Integrative Biodiversity Research (iDiv)

Citizen science (CS) is a potential source of data in many disciplines, including biodiversity monitoring. Essential Biodiversity Variables (EBVs) represent the minimum set of measurements required to capture major dimensions of biodiversity change, and while some EBVs can be monitored electronically and remotely, others require human-assisted data collection, as indeed provided by some CS projects. But what are the characteristics of such projects and to what extent do they make an impact on EBVs as measured through contributions to GBIF?

This study presents an assessment of more 3600 CS projects from around the world, of which most are based in North America or Europe. Far from all of these make their data available through GBIF, whose total records, however, are derived from CS in more than half the cases. The most extensively CS-monitored groups globally are birds, moths and trees.

Overall, the study shows that CS projects play a significant role in global biodiversity monitoring, but also that the scope of CS has the potential to expand across geography, taxonomy and additional EBVs.

Link to paper: <https://doi.org/10.1016/j.biocon.2016.09.004>

PREDICTING SPECIES RICHNESS THROUGH ENVIRONMENTAL HETEROGENEITY

DATA USED: 926,837 SPECIES OCCURRENCES

Cramer MD and Verboom GA (2016) Measures of biologically relevant environmental heterogeneity improve prediction of regional plant species richness. *Journal of Biogeography*. Wiley-Blackwell 44(3): 579–591.

Author country: South Africa

Research funding: Oppenheimer Memorial Trust; University of Cape Town

Plant species richness is influenced by resource availability, environmental stability and heterogeneity, however, most attempts to model global richness focus on absolute values of environmental variables rather than measures of their variability.

In this study, researchers hypothesized that including heterogeneities of environmental variables would improve models of plant species richness. Using GBIF-mediated occurrences of vascular plants in South Africa combined with data on climate, soil, fire frequency and distance from nearest coast, they construct a boosted regression tree (BRT) model of richness able to predict 68 per cent of species richness and 95 per cent of biome richness.

The impact of ‘roughness’, i.e. spatial heterogeneity of environmental variables was overwhelmingly important with the most critical predictor being diurnal temperature range roughness.

Facilitating regional coexistence and powering speciation, environmental heterogeneity, as shown by this study, is an important predictor of species richness to be considered in modelling.

Link to paper: <https://doi.org/10.1111/jbi.12911>



BEDSTRAW HAWK-MOTH (*HYLES GALLII*) CATERPILLAR BY KJELD BREM
HTTP://WWW.GBIF.ORG/OCCURRENCE/1052582478 CC BY-NC 4.0

PUTTING INSECTS ON THE MAP

DATA USED: 33,000 SPECIES OCCURRENCES

Ballesteros-Mejia L, Kitching IJ, Jetz W and Beck J (2016) Putting insects on the map: near-global variation in sphingid moth richness along spatial and environmental gradients. *Ecography*. Wiley-Blackwell.

Author countries: Brazil, United Kingdom, United States, Switzerland

Research funding: Swiss National Science Foundation; National Science Foundation; NASA; Synthesys; Freiwillige Akademische Gesellschaft (FAG), Basel

The role of evolutionary and ecological mechanisms in driving species distributions is a core research topic in biodiversity science. New insights, however, tend to focus on vascular plants and vertebrates, even though invertebrates make up the clear majority of species on the planet. This paper concentrated on a group of herbivorous insects, the sphingid moths, and drew on GBIF and others to compute distributions model for 789 species found outside the Americas. The researchers used these to search for links between environment and species richness and found the greatest concentration of diversity in the moist tropics. This is matched by the observation that most species ranges are found in warm and wet areas with evapotranspiration being the strongest predictor of species richness. This contrasts with studies focused



ROUGH TREE FERN (*DICKSONIA SQUARROSA*) BY LEON PERRIE
[HTTP://WWW.GBIF.ORG/OCCURRENCE/1227769163](http://WWW.GBIF.ORG/OCCURRENCE/1227769163) CC BY-NC 4.0.

on terrestrial vertebrates, where temperature is the most important predictor of richness, highlighting the need to expand studies areas beyond these taxa.

Link to paper: <https://doi.org/10.1111/ecog.02438>

CLEANING UP BIG DATA

DATA USED: 1,041,941 SPECIES OCCURRENCES

Gueta T and Carmel Y [2016] Quantifying the value of user-level data cleaning for big data: A case study using mammal distribution models. *Ecological Informatics*. Elsevier BV 34: 139–145.

Author country: Israel

Research funding: Israel Institute of Technology.

Researchers frequently combine downloads from the more than 700 million occurrence records in the GBIF network with environmental data to model distributions of species or higher level taxa. An initial step in the process often involves data cleaning to ensure the quality of the models, however, what effect do such cleaning procedures have on model performance? In this paper, researchers used one million records of Australian mammals to compare model performance before and after strict data cleaning, during which they removed among others entries with coordinates with less than 3 decimal digits and entries recorded before 1990, effectively reducing the number of records to half. The massive reduction in records significantly improved the performance of the models across all spatial scales and measurements, as both gain measures and AUC increased, most prominently for small mammals. This paper demonstrates an example of quality control and data cleaning in a world of big data.

Link to paper: <https://doi.org/10.1016/j.ecoinf.2016.06.001>

TREE FERN ECOLOGY IN NEW ZEALAND

DATA USED: 28,343 SPECIES OCCURRENCES

Brock JMR, Perry GLW, Lee WG and Burns BR [2016] Tree fern ecology in New Zealand: A model for southern temperate rainforests. *Forest Ecology and Management*. Elsevier BV 375: 112–126.

Author country: New Zealand

Research funding: University of Tasmania

Tree ferns are a clade of leptosporangiate ferns with trunk-like structures in the order Cyatheales. In New Zealand, tree ferns have been a widespread and significant component of the forest ecosystems since the Paleocene epoch. Although not a major player in modern forestry, tree ferns are harvested in vast numbers to service the international ornamental market. This paper provides an overview of New Zealand tree fern ecology and its role in forest community dynamics, in part informed by GBIF-mediated occurrences. Prominent in early forest communities after disturbances, tree ferns are limited in gamete and spore production by irradiance and nutrient levels, but may persist for more than 250 years. The main predictor of tree fern abundance is total soil phosphorus, and the key drivers of species diversity is mean temperature and solar radiation. In regenerating forest communities, tree ferns can play a major role in suppressing canopy angiosperms and conifers.

Link to paper: <https://doi.org/10.1016/j.foreco.2016.05.030>

ADDING BIOTICS TO SPECIES DISTRIBUTION MODELS

DATA USED: 33,349 SPECIES OCCURRENCES

Leach K, Montgomery WI and Reid N [2016] Modelling the influence of biotic factors on species distribution patterns. *Ecological Modelling*. Elsevier BV 337: 96–106.

Author country: United Kingdom

Research funding: Queen's University Belfast

Species distribution models (SDMs) commonly use environmental variables such as climate data to predict distributions of species. Biotic factors, however, also shape spatial distributions, and most SDMs ignore factors such as predation, parasitism, and other interactions between species. In this study, researchers used GBIF-mediated occurrences to construct models of lagomorph distributions in Europe. They then tested the predictive ability of models based solely on abiotic factors against models containing both abiotic and biotic factors using IUCN range maps to quantify the influence of biotic factors on species distribution patterns. For

the majority of European lagomorph species, the models incorporating biotic factors outperformed the models with only abiotic data, as both appear to have equal importance in shaping distributions. The paper shows that biotic factors must be taken into account in order to improve the reliability of predicting species distribution patterns and for the field of species distribution modelling to advance.

Link to paper: <https://doi.org/10.1016/j.ecolmodel.2016.06.008>

CALCULATING AND VISUALIZING PLANT PRINCIPAL STRATEGIES

DATA USED: 3,068 SPECIES

Pierce S, Negreiros D, Cerabolini BEL, Kattge J, Diaz S, Kleyer M, Shipley B, Wright SJ, Soudzilovskaya NA, Onipchenko VG, van Bodegom PM, Frenette-Dussault C, Weiher E, Pinho BX, Cornelissen JHC, Grime JP, Thompson K, Hunt R, Wilson PJ, Buffa G, Nyakunja OC, Reich PB, Caccianiga M, Mangili F, Ceriani RM, Luzzaro A, Brusa G, Siefert A, Barbosa NPU, Chapin FS III, Cornwell WK, Fang J, Fernandes GW, Garnier E, Le Stradic S, Peñuelas J, Melo FPL, Slaviero A, Tabarelli M and Tampucci D (2016) A global method for calculating plant CSR ecological strategies applied across biomes world-wide. *Functional Ecology*. Wiley-Blackwell, 444–457.

Author countries: Italy, Brazil, Germany, Argentina, Canada, Panama, Netherlands, United States, Russian Federation, United Kingdom, Tanzania, Australia, China, France, Belgium, Spain

Research funding: TRY Initiative

In plants, the competitor - stress tolerator – ruderal [CSR] theory is used to describe different principal

strategies. In this work, researchers compile functional trait records for more than 3,000 plant species supplied with GBIF-mediated taxonomic information to create a global analysis tool to derive CSR plant strategies using three simple traits: leaf area and fresh/dry weight. Calibration of the tool revealed that the high values of the traits were mutually exclusive, as dense, tough leaves were not large, while soft and acquisitive leaves were not tough. Large leaves were only seen in intermediates. The tool, called StrafeFY, is based on a simple spreadsheet that allows researchers to input trait measurements for any number of plant specimens, and retrieve a readout of CSR strategy. The tool also provides values for easy plotting of ternary graphs to visualize and compare relative proportions of CSR classes.

Link to paper: <https://doi.org/10.1111/1365-2435.12722>

MODELLING SPECIES NICHES USING EXPERT-BASED RANGE MAPS

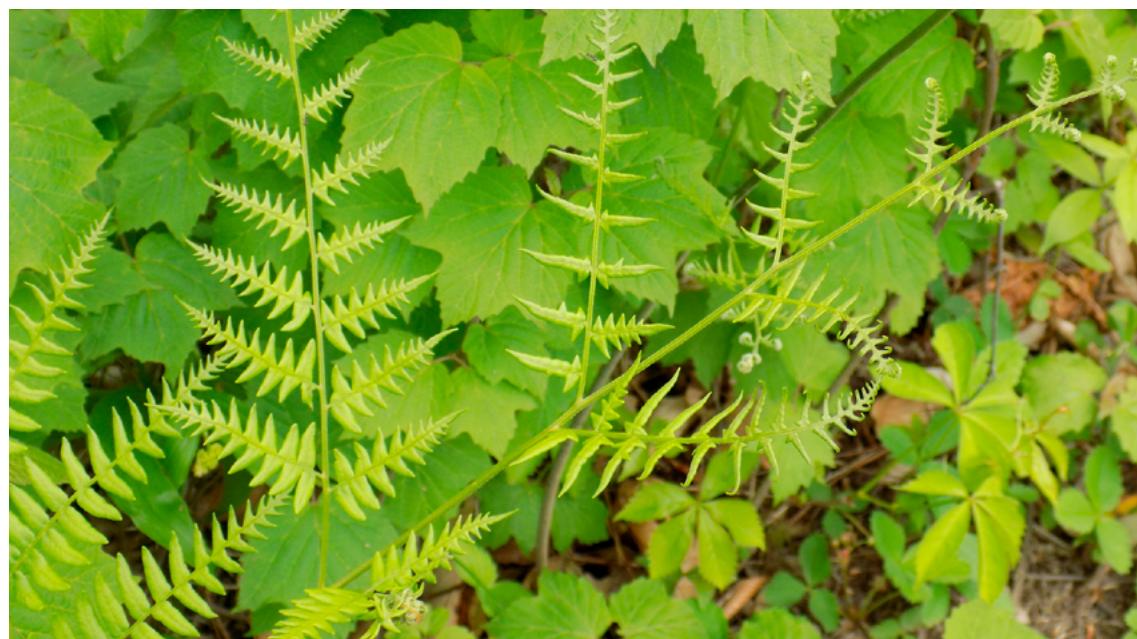
DATA USED: 4,769 SPECIES OCCURRENCES

Fourcade Y (2016) Comparing species distributions modelled from occurrence data and from expert-based range maps. Implication for predicting range shifts with climate change. *Ecological Informatics*. Elsevier BV 36: 8–14.

Author country: Sweden

Research funding: None listed

Species distribution models (SDMs) based on occurrence and environmental data are used extensively to model species' niches and predict



COMMON BRACKEN (*PTERIDIUM AQUILINUM*) BY CAILIN O'CONNOR FITZPATRICK [HTTP://WWW.GBIF.ORG/OCURRENCE/1269580807](http://www.gbif.org/occurrence/1269580807) CC BY-NC 4.0.



PULQUE AGAVE (AGAVE SALMIANA) BY CARLOS GALINDO-LEAL [HTTP://WWW.GBIF.ORG/OCURRENCE/1092903512](http://www.gbif.org/occurrence/1092903512) CC BY-NC 4.0.

e.g. the spread of invasive species or responses to changing climates. Such models can only perform as well as the data that feeds them, and are thus vulnerable to biases in the underlying data.

This study considers IUCN-derived expert-based range maps as an alternative source of species distribution information, and evaluate the modelling performance of such data compared to models using empirical occurrence data. Although using the range maps as a base for SDM involves sampling pseudo-occurrences, the researcher finds that while comparing the predicted distributions of 85 species based on either GBIF-mediated occurrences or on expert-based range maps, the two approaches produce similar results.

The author concludes by arguing that expert-based maps may be used for SDM when true occurrence data is limited or known to be biased.

Link to paper: <https://doi.org/10.1016/j.ecoinf.2016.09.002>

AGAVE LEADS THE WAY FOR LONG-NOSED BATS

DATA USED: 250 SPECIES OCCURRENCES

Gómez-Ruiz EP and Lacher TE (2016) Modelling the potential geographic distribution of an endangered pollination corridor in Mexico and the United States. *Diversity and Distributions*. Wiley-Blackwell 23(1): 67–78.

Author countries: Mexico, United States

Research funding: CONACYT; Mohamed bin Zayed Species Conservation Fund; Bat Conservation International; National Park Service; Metroparks Zoo; Cleveland Zoological Society; Society of Mammalogists; GBIF

Paniculate agave (*Agave spp.*) flower clusters are adapted to attract bats, and evidence suggests that

this attraction leads the path for Mexican long-nosed bats (*Leptonycteris nivalis*) on their annual spring migration from central Mexico to the southern United States.

In this study, researchers use agave and *L. nivalis* occurrences primarily from the GBIF network to model the distribution of relevant species, and to determine the concordance between agave species richness and bat occurrences. The modelled distributions of agave show that richness is associated with elevation, and that more species occur at higher and narrower elevation ranges. Bats co-occur in areas with more than one species of agave in 77 per cent of cases.

The combined results of the study provide convincing evidence that *L. nivalis* occurrences are correlated with distribution of Agave species, which support the proposed migratory corridor hypothesis presented in the study.

Link to paper: <https://doi.org/10.1111/ddi.12499>

CHOOSING THE RIGHT CLIMATE DATA FOR SPECIES DISTRIBUTION MODELS

DATA USED: 21,500,000 SPECIES OCCURRENCES

Bateman BL, Pidgeon AM, Radeloff VC, Flather CH, VanDerWal J, Akçakaya HR, Thogmartin WE, Albright TP, Vavrus SJ and Hegland PJ (2016) Potential breeding distributions of U.S. birds predicted with both short-term variability and long-term average climate data. *Ecological Applications*. Wiley-Blackwell 26(8): 2720–2731.

Author countries: United States, Australia

Research funding: NASA Biodiversity Program; James Cook University

When assessing the potential effects of climate change on species distributions, researchers often create models based on species occurrences and environmental variables. Such models show, for instance, that future climates may lead to species shifting their distributions to higher altitudes and/or elevations. In this study, researchers investigated the role of short-term variability versus long term averages of climate measurements for 320 bird species in the United States. Using more than 21 million GBIF-mediated occurrences, the researchers created sets of models for short- and long-term climate data, respectively. Overall, the two schemes performed well, with short-term models performing slightly better. The study shows that short-term models may produce more accurate results, but data is more difficult to process and complex to analyse, and for predicting general patterns of distribution, models based on long-term climate averages may perform adequately.

Link to paper: <https://doi.org/10.1002/eap.1416>

NEW WORLD BURYING BEETLE RESURRECTED

DATA USED: 158 SPECIES OCCURRENCES

Ⓐ Sikes DS, Trumbo ST & Peck SB [2016] Cryptic diversity in the New World burying beetle fauna: *Nicrophorus hebes* Kirby; new status as a resurrected name [Coleoptera: Silphidae: Nicrophorinae]. Arthropod Systematics & Phylogeny 74(3): 299-309. Senckenberg.

Author countries: United States, Canada

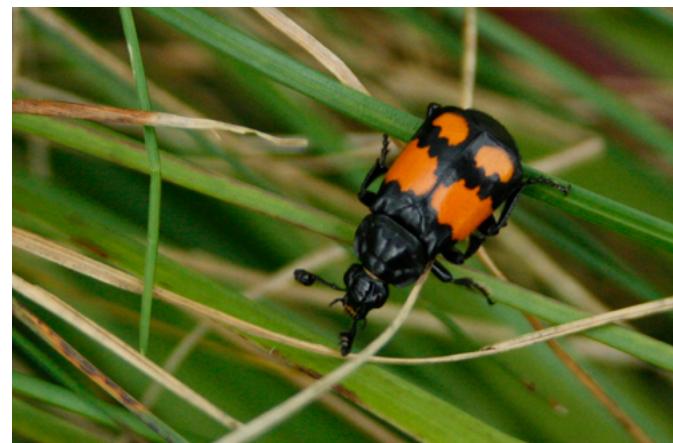
Research funding: United States Fish and Wildlife's Alaska Region NWRS Inventory and Monitoring Initiative.

Burying beetles (genus *Nicrophorus*), known for their biparental care, have been the focus of behavioural ecological studies for many years. *N. vespilloides* is distributed across most of the northern hemisphere, but recent genetic evidence from North America clusters Alaskan specimens outside the rest of the continent.

Using additional genetic data, researchers demonstrated two distinct groups, corresponding to those from Canada versus those from Alaska. In fact, the Alaskan samples clustered with Palearctic samples. Trapping individuals from both regions and setting up breeding trials, the researchers found a mating barrier preventing off-spring from reaching maturity, confirmed the genetic evidence.

The study concludes that *N. vespilloides* is in fact two species, and suggest readapting a previously used name, *N. hebes*, for the Nearctic (minus Alaska) group.

Link to paper: <http://bit.ly/2rytn1P>



NICROPHORUS VESPILLOIDES BY JAMES BAILEY

[HTTP://WWW.GBIF.ORG/OCCURRENCE/1098916406](http://WWW.GBIF.ORG/OCCURRENCE/1098916406) CC BY-NC 4.0

MAPPING CROP POLLINATION IN EUROPE

DATA USED: 120,429 SPECIES OCCURRENCES

Nogué S, Long PR, Eycott AE, de Nascimento L, Fernández-Palacios JM, Petrokofsky G, Vandvik V and Willis KJ [2016] Pollination service delivery for European crops: Challenges and opportunities. Ecological Economics. Elsevier BV 128: 1–7.

Author countries: United Kingdom, Norway, Spain

Research funding: Norwegian Academy of Science and Letters; VISTA

Crop pollination is an extremely important ecosystem service, and as much as 10 per cent of European food production depend on insect pollination. Nesting sites are threatened by land-use changes, and land managers need reliable models of pollination service delivery. Using GBIF-mediated occurrences, researchers developed distribution models for 12 bee species, and by combining distributions with crop data, they created a pollination delivery map and calculate indices for potential pollination provision and need at both species and country level. In terms of richness, the highest diversity is found in south and central Europe. Two species in particular (*Anthophora plumipes* and *Apis mellifera*) provide the highest level of pollination service. Values for delivery and efficiency on a country level do not correlate, as Denmark, for instance, shows one of the highest values of pollination delivery, but a low value in terms of efficiency.

Link to paper: <https://doi.org/10.1016/j.ecolecon.2016.03.023>

IMPROVING SPECIES DISTRIBUTION MODELS USING SATELLITE DATA

DATA USED: 50,000 SPECIES OCCURRENCES

Deblauwe V, Droissart V, Bose R, Sonké B, Blach-Overgaard A, Svenning J-C, Wieringa JJ, Ramesh BR, Stévart T and Couvreur TLP (2016) Remotely sensed temperature and precipitation data improve species distribution modelling in the tropics. *Global Ecology and Biogeography*. Wiley-Blackwell, 443–454.

Author countries: France, Belgium, Cameroon, United States, India, Denmark, Netherlands

Research funding: French Foundation for Research on Biodiversity (FRB); IRD

Species distributions models (SDMs) rely on accurate climatic data to predict the potential ranges of species, however, climatic datasets are often based on interpolations between weather stations. In regions where stations are scarce, such as the tropics, modelling can therefore be problematic. In this study, authors evaluated three alternative sources of climatic data based on remote-sensing (e.g. satellite data) by building SDMs of angiosperm plants in three different tropical regions using data from GBIF and other sources. When comparing the performance of SDMs based on WorldClim data alone versus data from remote-sensing databases, the latter performed consistently better. One explanation offered by the authors is that remote-sensing methods are able

to capture complex climatic features, such as the rain shadow effect of Mount Cameroon and flooded forest bands around the Amazon, Sangha and Congo rivers, which aren't available in interpolated climatic datasets.

Link to paper: <https://doi.org/10.1111/geb.12426>

SHEDDING LIGHT ON MESOPHOTIC CORAL ECOSYSTEMS

DATA USED: 836,971 SPECIES OCCURRENCES

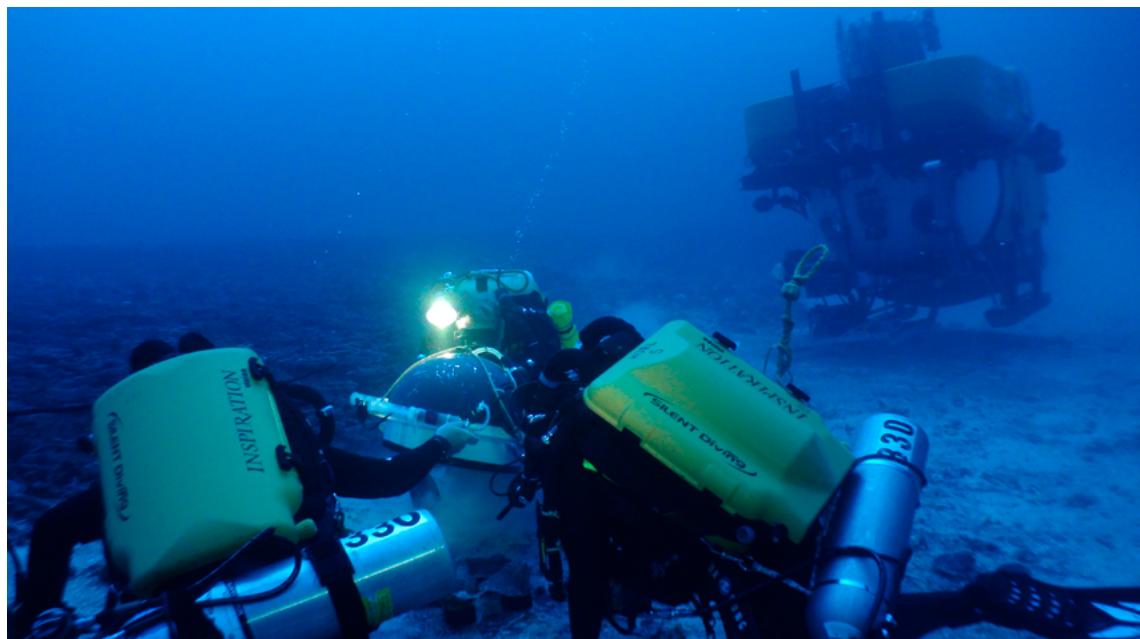
Pyle RL, Boland R, Bolick H, Bowen BW, Bradley CJ, Kane C, Kosaki RK, Langston R, Longenecker K, Montgomery A, Parrish FA, Popp BN, Rooney J, Smith CM, Wagner D and Spalding HL (2016) A comprehensive investigation of mesophotic coral ecosystems in the Hawaiian Archipelago. *PeerJ* 4: e2475.

Author country: United States

Research funding: none listed

Most coral reefs are found in shallow waters of tropical regions, but even at depths ranging from 30 to 150 meters and sometimes even deeper so-called mesophotic coral ecosystems (MCEs) exist. Here, the levels of light are low, explaining the name “meso” (meaning middle) - “photic” (meaning light).

In an interdisciplinary study spanning more than two decades, researchers characterized MCEs in the Hawaiian Archipelago using a vast and diverse set of methods to provide insights into structure,



EXPERIMENT TO DETERMINE CORAL FEEDING PATTERNS 89 METERS BELOW THE SURFACE. PHOTO BY RL PYLE
[HTTPS://DOI.ORG/10.7717/PEERJ.2475/FIG-3](https://doi.org/10.7717/PEERJ.2475/FIG-3) CC BY 4.0

composition, ecological dynamics and managements needs of MCEs in general. Their methods included field operations of photo documenting and sampling both by trained divers, remote-controlled devices and automated sensors.

Biodiversity surveys documented or collected more than 72 species of frondose macroalgae, ten species of scleractinian corals, 200 invertebrate specimens (of which three quarters remain unidentified), and also four undescribed species of fishes.

The researchers deposited voucher specimens to the Bernice P. Bishop Museum and documented occurrences in a dataset available on GBIF.org.

Link to paper: <https://doi.org/10.7717/peerj.2475>

INVESTIGATING SEED TOLERANCE TO DEHYDRATION

DATA USED: 4,200,000 SPECIES OCCURRENCES

Wyse SV and Dickie JB (2017) Predicting the global incidence of seed desiccation sensitivity. *Journal of Ecology*. Wiley-Blackwell.

Author country: United Kingdom

Research funding: UK Department for Environment, Food and Rural Affairs

Being able to tolerate dehydration is a crucial seed trait in plant regeneration, however, some species are more sensitive than others, and previous estimates based on seed banks tend to favour tolerant species and thereby underestimate proportion of desiccation-sensitive species.

In this study, researchers use a combination of models based on either shared taxonomy or habitat, to generate a non-biased estimate of the percentage of sensitive species. The taxonomic-based model used data from the Kew's Seed Information Database, while the habit-based model was based on GBIF-mediated occurrences.

Depending on statistical calculation type, the first model estimated between seven and 20 per cent desiccation-sensitive species, while the results from the model based on habitats suggested approximately eight per cent of species. Overall, the evidence suggested that the latter is the best estimate.

The study also identified the magnoliids as having the highest proportion of desiccation-sensitive species, including nutmeg, bay laurel and some magnolias.

Link to paper: <https://doi.org/10.1111/gcb.13373>

NOT ALL POLLEN ARE CREATED EQUAL

DATA USED: 3,000 SPECIES OCCURRENCES

Roger N, Moerman R, Carvalheiro LG, Aguirre-Gutiérrez J, Jacquemart A-L, Kleijn D, Lognay G, Moquet L, Quinet M, Rasmont P, Richel A, Vanderplanck M and Michez D (2016) Impact of pollen resources drift on common bumblebees in NW Europe. *Global Change Biology*. Wiley-Blackwell 23(1): 68–76.

Author countries: Belgium, Brazil, Portugal, Netherlands

Research funding: FRFC



LARGE RED-TAILED BUMBLEBEE (*BOMBUS LAPIDARIUS*) BY BRUNO DURAND.
[HTTP://WWW.GBIF.ORG/OCCURRENCE/1291146648](http://WWW.GBIF.ORG/OCCURRENCE/1291146648) CC BY-NC 4.0

Exclusively relying on pollen for survival, bees may be facing population declines due to changes in host plant availability and quality. Some generalist species, however, have remained stable for many years. In this study, researchers assessed potential changes in pollen diets for five bumblebee species in northwestern Europe, using GBIF-mediated occurrences to test if such changes were related to shifts in suitable habitats of host plants. They find evidence that four out of five species tend to forage on pollen from plants with expanding distributions. Chemical analysis of the quality of the pollen revealed no differences in nutrient composition between past and recent diets. Finally, using an experimental setup of queen-less microcolonies of *Bombus terrestris*, the researchers find no difference in pollen collection, however, productivity was higher in colonies fed diets of newly integrated resources, showing a clear impact of changing diet on colony development.

Link to paper: <https://doi.org/10.1111/gcb.13373>



WHITE MANGROVE (*LAGUNCULARIA RACEMOSA*) BY JMORALESRPC [HTTP://WWW.GBIF.ORG/OCCURRENCE/1088896079](http://WWW.GBIF.ORG/OCCURRENCE/1088896079) CC BY-NC 4.0

EXPERTS UNDERESTIMATE CLIMATIC TOLERANCE OF PLANTS

DATA USED: 608,254 SPECIES OCCURRENCES

 Curtis CA and Bradley BA [2016] Plant Distribution Data Show Broader Climatic Limits than Expert-Based Climatic Tolerance Estimates. *PLOS ONE*. Public Library of Science (PLoS) 11(11): e0166407.

Author country: United States

Research funding: NASA; National Institute of Food and Agriculture, USDA; Massachusetts Agricultural Experiment Station; Department of Environmental Conservation

The climatic niche of a species is determined by variety of parameters including tolerance to variables such as temperature and precipitation. The USDA Plants database offers climatic tolerance estimates based on expert knowledge for a wide range of plant species, and this study aimed to investigate how such estimates relate to tolerance inferred from plant distributions based on GBIF-mediated occurrences and WorldClim climate data.

By comparing tolerance values for 1800 species, the researchers find that climatic niches based on occurrence data are much broader than expert estimates. On average, plants tolerate lower minimum and higher maximum precipitation values as well as lower minimum temperatures. More than 70 per cent of the investigated species had lower minimum values for occurrence data compared to expert estimates. The observed difference increased with species range size.

The combined results suggest that expert-based estimates tend to underrepresent species' fundamental niches, and that distributions based on occurrence data produce better approximations of climatic tolerance.

Link to paper: <https://doi.org/10.1371/journal.pone.0166407>

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