2021

Science Review

20**21**

Science Review

GBIF SECRETARIAT

Foreword

JOE MILLER
GBIF Executive Secretary

Welcome to the latest issue of the GBIF Science Review!

Enclosed you'll find summaries for 53 peer-reviewed articles published in 2020 that made substantive use of data from the GBIF network. These cross-disciplinary exemplars are only a fraction of the year's nearly 1,000 such papers. Together they represent "the promising directions" highlighted by GBIF governing board chair Tanya Abrahamse in February 2021, upon publication of Mason Heberling's review in the *Proceedings of the National Academy of Sciences* analysing more than 4,000 GBIF-enabled peer-reviewed articles.

The Science Review also introduces a feature section, this time focused on marine research, which cuts across several topics while highlighting our partnership with OBIS, the Ocean Biodiversity Information System. As always, we encourage you to visit GBIF.org, where you can keep track of the latest finds from our literature tracking programme.

About the Science Review

DANIEL NOESGAARD
Science Communications Coordinator

The avid reader will no doubt have noticed that the Science Review in your hands looks quite different from previous years' editions, largely thanks to the latest addition to the Secretariat communications team, Javier Gamboa, and his outstanding visual design skills.
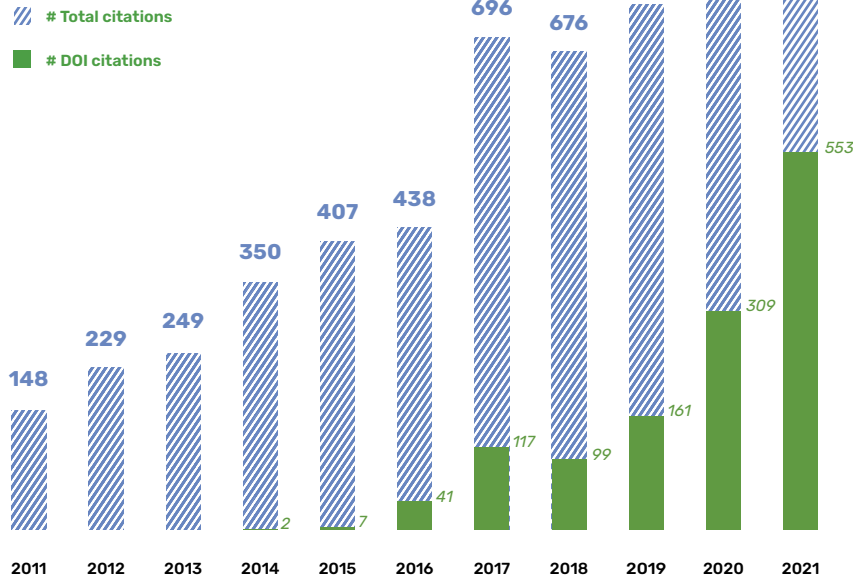
This year, we've chosen a more uniform design, giving each article an entire spread to accommodate more detailed summaries, better-structured metadata and a beautiful wide image accompanying each story. The left-hand page of each spread highlights the topic, the number of occurrences used and the geographic focus, while the right-hand has the bibliographic details, including the particulars about the authors and the journal in which the article appeared.

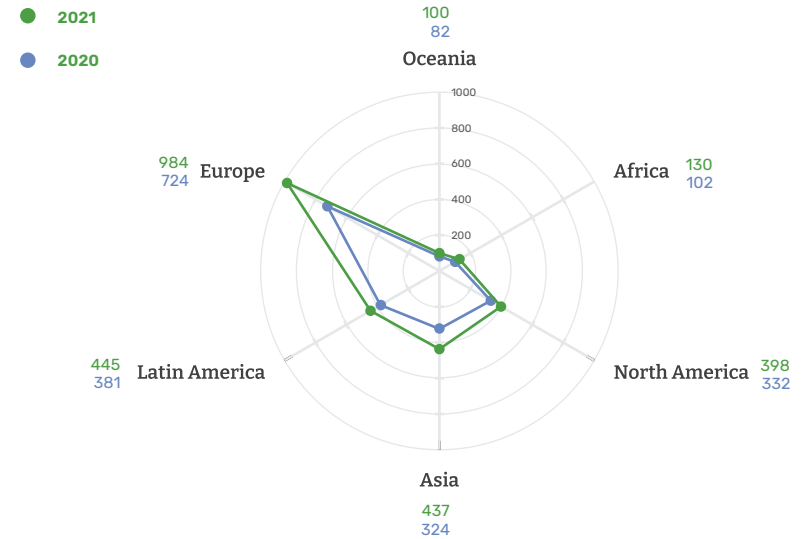We hope you enjoy reading the new Science Review—as much as we've enjoyed putting it together!

Uses and trends

These visualizations of the use of GBIF-mediated data reveal more than the growing number of peer-reviewed publications supported each year. The overlay on the graph below emphasizes authors' increasing use of DOI-based citations, a crucial practice for maintaining data provenance and scientific transparency. At right, the charts reveal the expanded geographic distribution of institutions whose researchers apply the data in their research. Each trend highlights GBIF's widening sphere of influence and impact on scientific research.
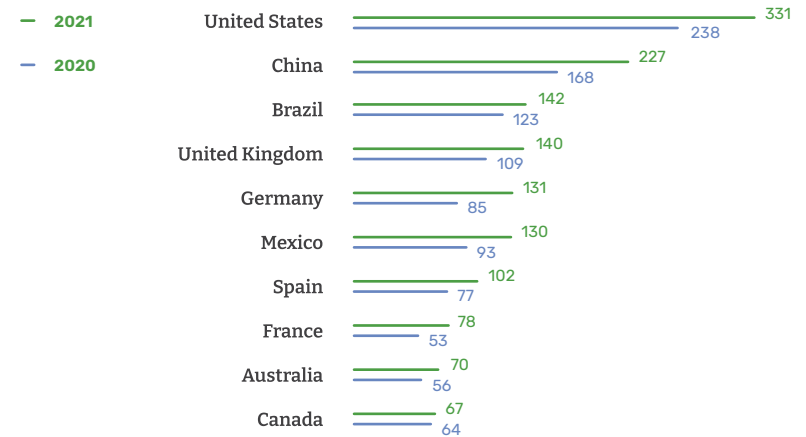
Annual number of peer-reviewed articles using GBIF-mediated data

/// # Total citations

▓ # DOI citations

Peer-reviewed articles by region

● 2021
● 2020

Peer-reviewed uses by country

— 2021
— 2020

	2021	2020
United States	331	238
China	227	168
Brazil	142	123
United Kingdom	140	109
Germany	131	85
Mexico	130	93
Spain	102	77
France	78	53
Australia	70	56
Canada	67	64

Navigation

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Topics

CITIZEN SCIENCE

TAXONOMY

BIOGEOGRAPHY

SPECIES DISTRIBUTION

BIODIVERSITY SCIENCE

DATA MANAGEMENT

INVASIVES

ECOSYSTEM SERVICES

CONSERVATION

AGRICULTURE

ECOLOGY

EVOLUTION

CLIMATE CHANGE

PHYLOGENETICS

HUMAN HEALTH

DNA

MARINE

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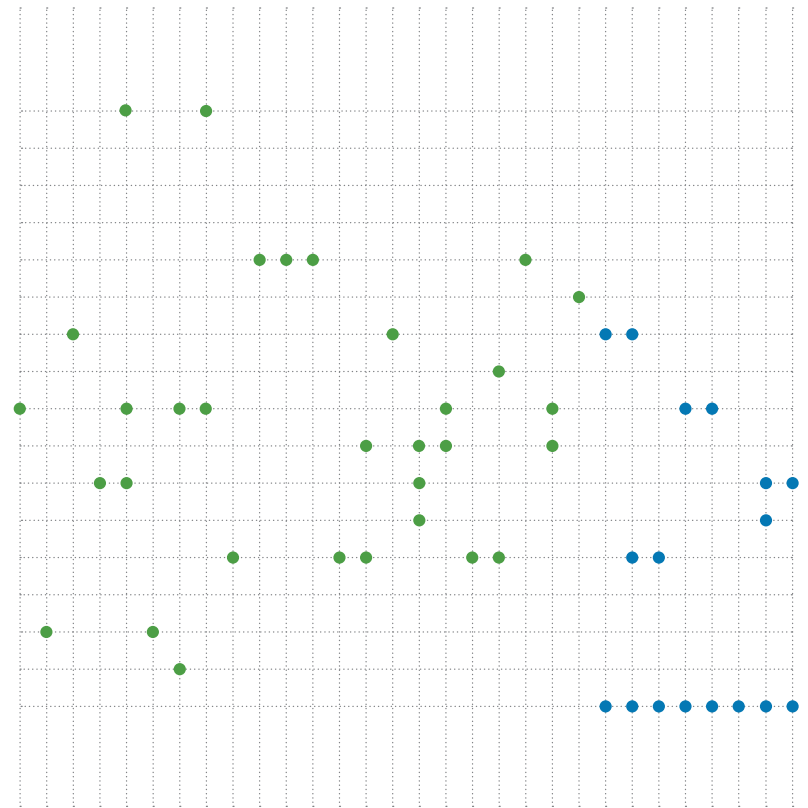
The effects of climate change in Colombia on virus-carrying mosquito

1

Aedes aegypti observed in Houston, TX, USA by pisum (CC BY-NC 4.0)

HEALTH

CLIMATE CHANGE

128
SPECIES OCCURRENCES

Colombia

Study shows decreases in overall bioclimatic suitability for Aedes aegypti under climate change scenarios in Colombia, but highlights other effects of warming that might increase risk of disease

Climate change has the potential to significantly alter the range of human disease vectors, such as the *Aedes aegypti* mosquito, responsible for the transmission of dengue, chikungunya and zika viruses.

In this study, researchers in Colombia—a country with abundant mosquito proliferation and limited resources for medical care and vector control—used GBIF-mediated occurrences of *A. aegypti* combined with environmental data to model the distribution of the species now and in future climates.

The prediction of areas currently suitable for the mosquito corresponds largely with the known cases of dengue, chikungunya and zika found mainly in the Caribbean and Andean regions. Significant overall reductions of up to 30 per cent, however, are predicted by 2050 and 2070. Changes will affect regions differently, as some departments such as Nariño and Cauca are likely to face expansions.

While the models may accurately predict reduced climatic suitability of the vector, warming climates may shorten time required for larval maturing and also lead to faster and more frequent feeding of the female adult mosquito, thus increasing overall transmission risk.

The study concludes that more occurrence data is needed and that future studies should take into consideration not only climate, but also socioeconomic variables and data on virus transmission dynamics.
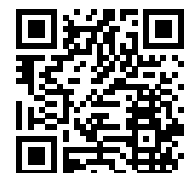
Portilla Cabrera CV and Selvaraj JJ

Colombia

Geographic shifts in the bioclimatic suitability for Aedes aegypti under climate change scenarios in Colombia

Heliyon

Habitat loss due to land conversion in US southwest deserts

2

At the Ivanpah Solar Electric Generating System in California, 300,000 mirrors track the sun in two dimensions and reflect the sunlight to boilers atop three tall power towers. Photo by National Renewable Energy Lab (CC BY-NC-ND 2.0)

ECOSYSTEM SERVICES

CONSERVATION

21,556
SPECIES OCCURRENCES

USA

McCoshum SM and Geber MA

USA

Land Conversion for Solar Facilities and Urban Sprawl in Southwest Deserts Causes Different Amounts of Habitat Loss for Ashmeadiella Bees

Using GBIF-mediated occurrences of ten *Ashmeadiella* species combined with data from the authors' own collections, they created ecological niche models predicting the potential distribution of the species. Assessing landscape layers and locations of solar power facilities, they estimated land conversion directly related to development of plants.

While the results suggested that land conversion due to development of solar facilities leads to direct habitat loss for all investigated species, the impact of urban sprawl as a whole is much greater. The study recommends incorporating pollinator conservation practices directly into the permitting processes to mitigate the effects of land conversion.

Study finds urban sprawl the bigger culprit in causing potential habitat loss for desert bees

With high potential for renewable energy production, the Southwest deserts of the United States have been promoted for solar facilities to meet increasing demands and green energy targets. Development and production, however, affects habitats and may threaten desert biodiversity.

In this study, researchers from Cornell University investigated the potential habitat loss for *Ashmeadiella* bees in Southwestern deserts due to land conversion associated with solar power plants compared with general urban sprawl.

Data on the origins of food crops

3

Pouteria sapota (Jacq.) H.E.Moore & Stearn observed in Mexico by Hannia Ayerim Tec Tuyub (CC BY-NC 4.0)

AGRICULTURE

PHYLOGENETICS

355,597
SPECIES OCCURRENCES

Paper describes a new database and phylogenetic tree to stimulate research on the macroecological and macroevolutionary patterns of crop origins

Domestication and cultivation of a few hundred wild plant species has formed the basis of our current food system. Detailed knowledge on the history of these crops, however, is limited to a few species, and research on the macroecological and macroevolutionary patterns of crop origins is scant.

This paper introduces **Crop Origins**, a comprehensive database on identities and usage of 866 food crop species with detailed information about taxonomic and geographic origins, aimed at stimulating new, comparative analyses on the origins of food crops.

Using GBIF-mediated species occurrences of the most likely wild progenitors of all crops, the author derived native ranges for which they described climate based on 19 variables from WorldClim, and assigned ecoregions based on the location of the highest number of occurrences for each progenitor.

In addition, the paper also introduces **Phylo Food**, a new phylogeny derived from a time-calibrated molecular mega-tree of nearly 75,000 plants pruned for the crop taxa. Exploring the phylogenetic patterns of the tree shows that crop species are widely distributed across major clades—with about half being rosids, 25 per cent superasterids and the remaining monocots and magnoliids.

The datasets with accompanying metadata and code are freely available online, and interested colleagues are invited to provide feedback and report inaccuracies to the author.

Milla R

Spain

The West African Plants Initiative: a model for need-driven specimen digitization

4

Crepidomanes africanum collected in Cameroon. Photo by Germinal ROUHAN / Vincent DEBLAUWE via Museum national d'Histoire naturelle, Paris (CC BY-NC-ND 4.0)

BIODIVERSITY SCIENCE

DATA MANAGEMENT

57 MILLION
SPECIES OCCURRENCES

Mauritania, Senegal, Gambia, Guinea-Bissau, Guinea, Sierra Leone, Liberia, Côte d'Ivoire, Ghana, Mali, Burkina Faso, Togo, Benin, Niger, Nigeria, Cameroon

Empowering data users—rather than specimen holding institutions—to drive digitization of herbarium sheets

The global distributions of wealth and biodiversity, respectively, are uneven and often inversely proportional. Similarly, the availability of biodiversity data tends to be highest in the wealthiest but least biodiverse regions of the world.

This study presents the West African Plants (WAP) Initiative, exploring a general model of empowering users in countries who wish to have access to data to capture and mobilize it, rather than relying on institutions in other countries holding the collections.

By connecting motivated researchers across West Africa with herbaria in Europe and North America with a desire to have their collections digitized, WAP has enabled—at an average cost of $0.50 per sheet—the mobilization of more than 190,000 primary biodiversity records in 16 countries in the region. Not all of these have been shared through GBIF yet, but as a whole represent an increase in digital accessible knowledge of West African flora by more than 50 per cent.

The study further assessed 57 million GBIF-mediated records of plant specimens globally to calculate the proportion of records by country provided by institutions in other countries as a means for exploring the model of the initiative in different regions of the world.
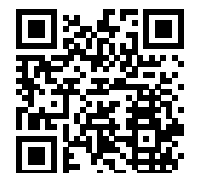
Asase A, Sainge MN, Radji RA, Ugbogu OA and Peterson AT

Ghana, Cameroon, Togo, Nigeria, USA

A new model for efficient, need-driven progress in generating primary biodiversity information resources

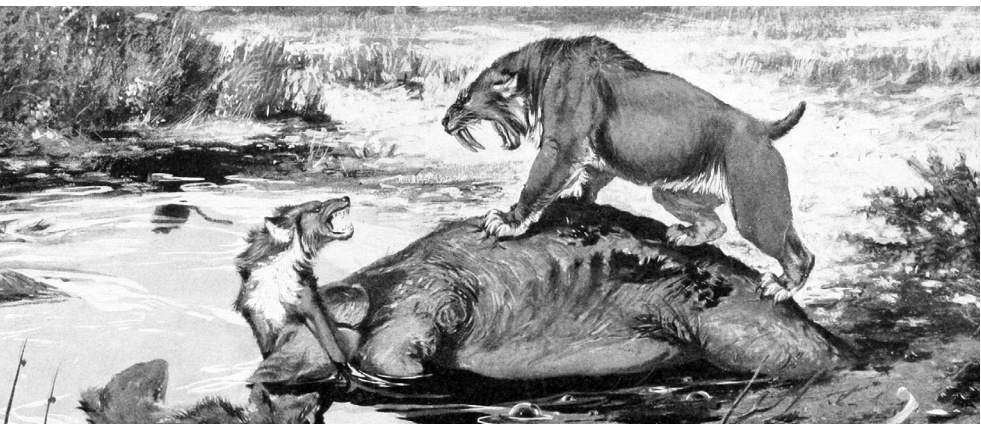# A sticky story: modelling bird distributions at La Brea tar pits

5

Illustration of Smilodon californicus and Canis dirus fighting over a Mammuthus columbi carcass in the La Brea Tar Pits. By Robert Bruce Horsfall, Public domain, via Wikimedia Commons

CLIMATE CHANGE

ECOLOGY

8,603,971
SPECIES OCCURRENCES

USA

Niche modelling reveals life history shifts in birds at La Brea over the last twenty millennia

The La Brea tar pits in Los Angeles, California, provide a unique opportunity to test ecological niche models and shifting distributions. This study modelled the distribution of bird species known to occur in the area, 86 of which have already been identified from skeletal remains entombed in the sticky tar for up to 40,000 years, and 97 for which remains from the pits have yet to be found.

Built using breeding survey data and GBIF-mediated occurrences for wintering and migrant species, the resulting models predicted presence at the Last Glacial Maximum (LGM) for more than 90 per cent of the identified species, suggesting reasonably accurate model range estimates.

The models also predicted suitable conditions at the LGM for more than 90 per cent of the species *not* present in tar remains but known to occur at La Brea, possibly because these were less likely to become trapped in the tar due to behavioural patterns or migratory habits—or they simply haven't been recovered yet.

Combined, the analyses revealed a small decrease in species richness from the LGM to today, likely due to distribution shifts following warming climates.

Zink RM, Botero-Cañola S, Martinez H and Herzberg KM

USA

Rapid Least Concern: towards automating Red List assessments

6

Euphorbia blodgettii Engelm. ex Hitchc. observed in Bermuda by Mike Oldham (CC BY-NC 4.0)

CONSERVATION

Bermuda

Prize-winning tool simplifies and automates plant Red List assessments and enables direct submission to IUCN

Supporting global conservation planning and safe-guarding critical habitat, the IUCN Red List of Threatened Species™ is a crucial resource for protecting biodiversity worldwide. While coverage among vertebrates is good, plants, fungi and invertebrates represent major gaps—potentially due to complicated and time-consuming procedures involved in assessing species.

Addressing the challenge of accelerating the generation of Least Concern (LC) Red List assessments, Rapid Least Concern (RLC), a simple but prize-winning web-based

tool, takes advantage of free and open biodiversity data from GBIF to perform fast analyses of single or multiple plant species, outputting files compliant with direct submission to the IUCN database.

Based on a species, the tool derives the number of unique, native occurrences and the number of regions in which the species is present while calculating the extent of occurrence (EOO) and area of occupancy (AOO). Set thresholds for each of these values determine whether a species can be designated LC.

Using Bermuda as a case study, the authors compiled a list of 172 native plant species, of which only 38 had been previously assessed. Using RLC on the remaining 134 species, they were able to increase the number of assessed species to 85 per cent, of which 109 species could be designated LC and were thus submitted to IUCN for inclusion in the Red List.
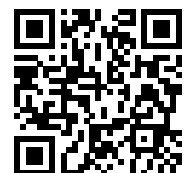
Bachman S, Walker B, Barrios S, Copeland A and Moat J

UK, Bermuda

Rapid Least Concern: towards automating Red List assessments

Biodiversity Data Journal

Global drivers of marine and terrestrial biodiversity

7

Stenopus hispidus observed in Indonesia by Erik Schlogl *(CC BY-NC 4.0)*

ECOLOGY

EVOLUTION

Study models species richness across marine and terrestrial domains to identify prevailing environmental features

Drivers of biodiversity are often studied with specific taxonomic or geographical focuses, and while many such studies have significantly advanced ecology and conservation, until now, limited data availability has hindered truly global studies.

In a massive study analysing distribution data from GBIF and other sources of more than 67,000 vertebrate and invertebrate species across terrestrial and marine domains, researchers used artificial neural networks to predict global species richness and how it relates to

environmental features in each domain. Quantifying contributions of environmental drivers, the produced models identified sunlight and temperature as the most important factors shaping biodiversity across domains. In the ocean, depth and oxygen were also important, while terrestrial biodiversity was more influenced by precipitation and primary production.

The study also confirmed known latitudinal gradients, but pointed out that latitude in itself is not a mechanism but a proxy for, e.g. sunlight and temperature. Attempts to forecast impacts of climate change should, therefore, model these mechanisms directly.

Not all patterns of biodiversity could be explained by environmental drivers. The models under-predicted richness in several coral reefs and montane forests while tending to over-predict richness in regions with steep biogeographic boundaries and on isolated islands.

Gagné TO, Reygondeau G, Jenkins CN, Sexton JO, Bograd SJ, Hazen EL and Van Houtan KS

USA, Canada, Brazil

The ghost fruits of Madagascar

8

Propithecus verreauxi observed in southern Madagascar by figschool (CC BY 4.0)

CONSERVATION

EVOLUTION

ECOLOGY

487,759
SPECIES OCCURRENCES

Madagascar

Study analyses seed dispersal in Madagascar's endemic flora to identify plants whose dispersal partners may be extinct

With extreme levels of endemism, Madagascar is home to plants and vertebrates, of which more than 80 per cent exist nowhere else on the planet. Some plants have evolved in mutualistic relationships with frugivore lemurs as seed dispersers, almost all of which are severely threatened.

In this study, authors explore seed dispersal on the island, analysing more than 3,000 flowering plants, identifying disperser animal groups, animal co-occurrences based on GBIF-mediated data, and comparing seed and gape (mouth) size to predict anachronistic species where no apparent extant disperser is available.

Their results find only 179 plant species with direct evidence of dispersal by extant frugivores in Madagascar. Based on seed size and disperser groups, two species, *Erythrina hazomboay* and *Borassus madagascariensis* appear to have completely lost their main dispersers to extinction.

With more than 100 species, lemurs are the main mammal disperser in Madagascar. Sixteen per cent of the analysed plant species, however, lacked co-occurring lemur species with an appropriate gape size, suggesting that local extinctions are leading to dysfunctional dispersal.
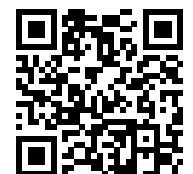
Albert-Daviaud A, Buerki S, Onjalalaina GE, Perillo S, Rabarijaona R, Razafindratsima OH, Sato H, Valenta K, Wright PC and Stuppy W

UK, USA, Madagascar, Japan

Improving legume crops by mapping stress resilience in wild relatives

9

Mung bean (Vigna radiata) observed in Maharashtra, India by swanand kesari (CC BY-NC 4.0)

Analysing intercrossing studies combined with genomic and phylogenetic data, the authors defined four delineated *Vigna* gene pools. Using GBIF-mediated occurrences they modelled the distribution of 84 taxa to score their levels of resilience against heat and drought.

While the study found high levels of pest and disease resistance in 75 per cent of taxa, abiotic stress resilience occurs in less than 30 per cent. Combined with poor germplasm conservation, the authors recommend prioritizing the collection of these rare, resilient species for breeding before they are extirpated.

van Zonneveld M, Rakha M, Tan S yee, Chou Y-Y, Chang C-H, Yen J-Y, Schafleitner R, Nair R, Naito K and Solberg SØ

Chinese Taipei, Egypt, Malaysia, India, Japan, Norway

CONSERVATION

AGRICULTURE

CLIMATE CHANGE

26,210
SPECIES OCCURRENCES

Study assesses abiotic and biotic stress resilience in legume gene pools to uncover breeding potential of wild relatives

Vigna is a tropical legume with more than 88 taxa, including important crops such as mung bean and cowpea—cheap and excellent sources of proteins in human diets, but also attractive soil improvement crops due to symbiotic nitrogen-fixing properties.

With climate change and increased stressors, this study examines the *Vigna* gene pool to identify patterns of resilience in wild relatives in order to improve varieties that will better sustain legume crop production in the future.

Impact of deforestation on endangered mammals

Satellite photo of Borneo showing smoke from burning peat swamp forests. By Jacques Descloitres, MODIS Land Rapid Response Team, NASA/GSFC, Public domain, via Wikimedia Commons

CONSERVATION

AGRICULTURE

ECOLOGY

2,000
SPECIES OCCURRENCES

Study provides insights on the role of changing forest cover on the distribution of 35 endangered mammals

Expanding agricultural croplands and pastures lead to deforestation, a major cause of habitat loss and biodiversity decline, affecting dozens of already endangered species relying on forests for hiding, feeding and breeding.

This study by a researcher from the Polytechnic University of Tirana examines the role of changing forest cover on the distribution of 35 endangered terrestrial mammals.

Using GBIF-mediated occurrences combined with IUCN range data, the author modelled the distributions based on environmental variables and used satellite data to determine recent changes to forest cover.

With overall good performance, the models showed distributions determined particularly by elevation, distance to the nearest protected area and forested landscape, the latter a significant factor predicting occurrence in a third of carnivore species and more than half of non-carnivores.

For the large Bornean bay cat *Catopuma badia*, changes in forest cover meant changes in distribution with a tendency of occurrence mainly in areas with dense forests of more than 90 per cent coverage.

Laze K

Albania

Insights on the role of forest cover and on the changes in forest cover on thirty-five endangered mammal species distributions

Regional biosecurity is essential in stopping the spread of invasive alien species

11

Hiptage benghalensis, native to South and Southeast Asia, observed in Réunion by Jean Philippe BASUYAUX (CC BY-NC 4.0)

Faulkner KT, Robertson MP and Wilson JRU

South Africa

INVASIVES

7,242,902
SPECIES OCCURRENCES

Study predicts thousands of potential invasions and calls for stronger regional biosecurity measures to be included in global biodiversity targets

Invasive alien species are among the greatest threats to biodiversity and may easily spread from one country to another once established, as countries differ in their capacity to prevent invasions, biosecurity protocols and implementation of international standards.

This study explores the biosecurity implications in six scenarios of invasions in contiguous countries with varying levels of impact and spread. Based on the list of the world's worst invaders in the Global Invasive Species Database, the study analysed 86 species assessing introduction and invasion threats, modelling potential distributions based on GBIF-mediated occurrences to inform invasion scenarios.

Predicting more than 2,500 future invasions, the study finds that most invaders–around 60 per cent—are likely to establish in one country but not spread to neighbouring countries. Many of these invasions, however, are unlikely to be prevented due to the low response capacity of the countries in which they are predicted to occur.

More than a third of the predicted invasions are likely to spread beyond the country of introduction, with the majority of invasions causing impact in more than one country. With low preventive/responsive capacity in many countries, these scenarios call for regional cooperation around biosecurity to prevent harmful effects of future biological invasions.

Rapid sampling to inform conservation in remote Alaskan wildlife refuges

12

Dichelotarsus laevicollis collected in the Kenai National Wildlife Refuge by Matt Bowser.

CONSERVATION

SPECIES DISTRIBUTION

40,342
SPECIES OCCURRENCES

USA

Study presents a biotic inventory of an Alaskan Refuge by observations, specimens, DNA barcoding and high-throughput sequencing methods

Conserving biodiversity requires the ability to routinely document species distributions and assemblages. With a wide conservation mandate, the Kenai National Wildlife Refuge (KNWR) in Southcentral Alaska has been inventoried but lacks spatially and temporally repeated sampling.

This study tests novel biomonitoring methods in KNWR, complementing past efforts while addressing previous shortcomings. In a study area of around 900 hectares split into 42 plots, researchers used a rapid scheme to carry out sampling of plants, lichens, birds, earthworms

and terrestrial arthropods, designed to take less than one hour per visit.

Documenting 4,700 species occurrences within 200 m from plot centres, the project sampled more than 700 formally described species and an additional 274 assigned Barcode Index Numbers (BINs) based on DNA analysis. The researchers found 102 arthropod species newly reported from Alaska and five species new for North America. All occurrences were published to GBIF via VertNet.

Among three non-native species detected, *Dendrobaena octaedra* was the most widespread. Based on existing GBIF-mediated occurrences, non-native species appear to originate in the area near roads and the KNWR Visitor Center.
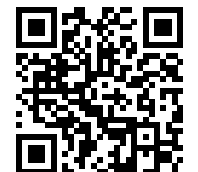
Bowser M, Brassfield R,
Dziergowski A, Eskelin T, Hester
J, Magness D, McInnis M, Melvin
T, Morton J and Stone J

USA

Global patterns of stony coral diversity

13

Acropora valida observed in New Caledonia by damienbr *(CC BY-NC 4.0)*

CONSERVATION

BIOGEOGRAPHY

109,296
SPECIES OCCURRENCES

Study explores global stony coral distributions, sampling completeness and diversity to identify priority areas for improving knowledge gaps

Shortfalls in biodiversity knowledge can lead to false estimates of global biodiversity patterns, and filling these knowledge gaps is therefore critical.

To identify areas of priority for improving shortfalls, this study focused on tropical stony corals (Scleractinia), a foundational taxon in coral reef ecosystems. Compiling occurrences of 697 Scleractinia species from GBIF and OBIS, researchers used a rarefaction and extrapolation technique based on sampling completeness to estimate species diversity patterns.

Their results showed relatively consistent sampling completeness across degrees of spatial resolutions, but varying geographically with high levels in coastal areas of Australia and Central America and low levels around Madagascar and some Pacific Islands.

The richness estimates found both latitudinal and longitudinal gradients, particularly at finer spatial resolutions, differing from previous range-based studies. The highest number of coral species was predicted in the western Indian Ocean—with greater diversity than the Indo-Pacific Coral Triangle.

Simulations revealed sampling priority areas on the northeastern coast of Australia, central Coral Triangle and coast of Madagascar to fill knowledge gaps and to help future conservation planning.
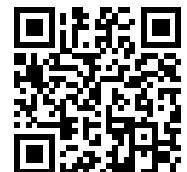
Kusumoto B, Costello MJ, Kubota Y, Shiono T, Wei C, Yasuhara M and Chao A

Japan, UK, New Zealand, Chinese Taipei, China

Large herbivores lead to taller, denser and spinier tropical plants

14

Adansonia digitata observed in Tanzania by cookswell *(CC BY-NC 4.0)*

EVOLUTION

BIOGEOGRAPHY

2,851,679
SPECIES OCCURRENCES

Study finds megafauna effect on selection of functional plant traits in the tropics

While tropical biomes sharing climate and soil characteristics exist in several parts of the world, functional plant traits and disturbance regimens vary between continents.

In this study comparing the tropical forests and savannas of Africa and South America, researchers tested the hypothesis that the extinction of megafauna in the Neotropics may explain such differences between the two regions.

Assessing functional traits of thousands of plants, the authors found significant differences when comparing biomes and continents. African species were taller and

denser than Neotropical species, particularly in the savannas. Species with spines were more frequent in Africa, while the presence of geoxyles (underground growth) was more frequent in the Neotropics.

Using GBIF-mediated occurrences, they created models to describe climatic conditions, finding that biogeographical patterns in traits could not be explained by differences in environmental variables.

Taken together, these results point to more fire-adapted species in South America and a megafauna effect on selection for more herbivory-adapted species in Africa.

Long-term and large-scale evolutionary effects of hurricanes

15

Anolis sagrei observed in Turks and Caicos Islands by David Kaposi (CC BY-NC 4.0)

EVOLUTION

CLIMATE CHANGE

6,851
SPECIES OCCURRENCES

Turks and Caicos Islands

Study in lizards suggests that severe climate events can assert selective pressure with long-lasting evolutionary impact

Extreme weather phenomena such as hurricanes and droughts can act as acute agents of natural selection, differing from the normal selective pressures affecting organisms. Being rare, such disruptions are thought to be temporary and not to have long-lasting evolutionary impacts.

Following hurricanes Irma and Maria in 2017, researchers paired a cross-generational and spatial approach to study potential evolutionary impacts on Caribbean anoles (*Anolis scriptus*). Initial investigations in the Turks and Caicos Islands found enlarged toe pads in post-hurricane lizards, thought to increase clinging performance—a useful trait during extreme winds.

When revisiting lizard populations 18 months later, they analysed hurricane survivor offspring and found that toepad size was unchanged, suggesting that trait shifts transcended generations. Broadening their focus, the authors sampled brown anoles (*Anolis sagrei*) across 12 Caribbean islands and found that hurricanes events in the past 70 years significantly predicted toepad size.

Expanding toepad analyses to the entire *Anolis* genus, the authors used GBIF-mediated occurrences and climate event data to quantify hurricane activity per species, finding a significant correlation between toepad size and hurricane activity. Together, these results show that extreme climate events can assert severe selective pressure with long-lasting evolutionary impacts.

Donihue CM, Kowaleski AM, Losos JB, Algar AC, Baeckens S, Buchkowski RW, Fabre A-C, Frank HK, Geneva AJ, Reynolds RG, Stroud JT, Velasco JA, Kolbe JJ, Mahler DL and Herrel A

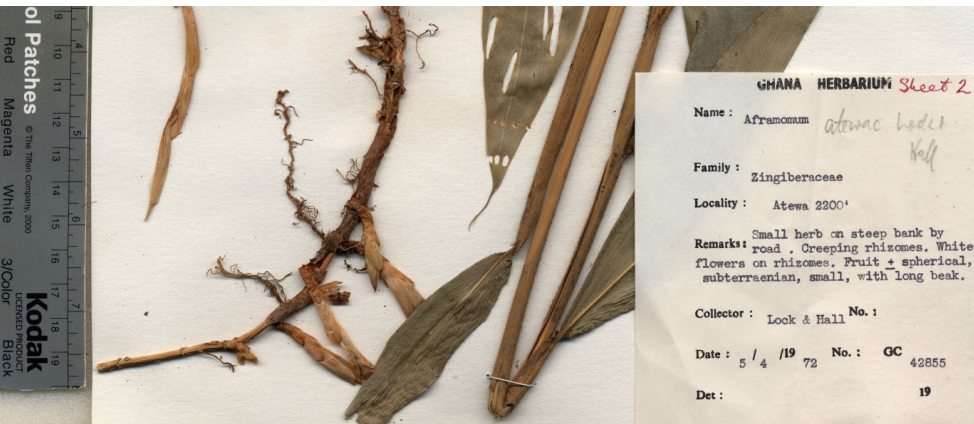UK, USA, Belgium, Australia, Mexico, Canada, France

How long does it take to discover a species?

Aframomum atewae Lock & J.B.Hall, specimen collected in Ghana in 1972.
Photo: Royal Botanic Gardens, Kew (CC BY-NC 4.0)

TAXONOMY

22,601,556
SPECIES OCCURRENCES

Study measures time lags between the discovery of a new species, the publication of its name, and subsequent collection of specimens required for a reasonable level of understanding and knowledge

The health and welfare of humans and the planet as a whole is tied to food security and biodiversity conservation, which in turn rely on knowledge and understanding of species, their characteristics and distribution. The discovery and description of new plants, however, is a lengthy process, often taking decades from the first specimen to publication.
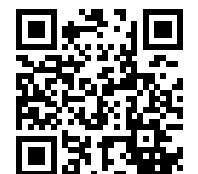
Goodwin ZA, Muñoz-Rodríguez P, Harris DJ, Wells T, Wood JRI, Filer D and Scotland RW

UK

How long does it take to discover a species?

Systematics and Biodiversity

This study attempts to flesh out the steps associated with species discovery and measure time lags between each stage. The authors recognized three key stages in the process: 1) collection of first specimen, 2) publication of name, and 3) when 15 accurately named specimens—considered the minimum for a reasonable level of understanding—are available.

Analysing 40 years of *Kew Bulletin* publications, the authors found 3,305 new seed plants described between 1970 and 2010, citing a mean of 4.9 specimens each. Only 6.2 per cent of these protologues cited more than 15 specimens.

For the time lags, the authors first explored the *Aframomum* genus, finding an average lag between first specimen and publication of name of 40.8 years, while gathering 15 specimens took on average 65 years from the first specimen.

Expanding their scope, the authors further used GBIF-mediated specimen records of more than 82,000 taxa belonging to the 20 largest angiosperm families, logging time lags for the collection of 15 specimens ranging from 58 to 74 years. Gathering the first three specimens usually took more than 30 years.

Climate change alters the global risk of invasive weeds

17

Sphagneticola trilobata (L.) Pruski observed in Macao by Jeremy J Busfield (CC BY-NC 4.0)

Shabani F, Ahmadi M, Kumar L, Solhjouy-fard S, Shafapour Tehrany M, Shabani F, Kalantar B and Esmaeili A

Australia, Iran, Switzerland, Japan

INVASIVES

CLIMATE CHANGE

32
SPECIES

Study finds overall decrease in global climatic suitability for 32 invasive species, but at the expense of some regions facing higher risk of invasion by the year 2050

Invasive weeds are a global threat with the potential to cause ecological and economic losses. Impacts of anthropogenic climate change are likely to include shifts in ranges of not only native but also invasive species.

This study focused on 32 invasive weed species and future changes to distributions and overlaps on a global scale. Using GBIF-mediated occurrences coupled with Worldclim climatic projections at varying severities, the authors created species distributions models based on the MaxEnt algorithm to visualize the current state of the invasive species compared to a prediction in the year 2050.

Current climatic conditions predicted the largest spatial overlaps of species in coastal Australia, South Africa, Madagascar, western Iberian peninsula, Morocco, Mexico, and southern Brazil, with the largest potential co-occurrence of 28 species.

By 2050, the models predicted overall suitability decreases at the global scale, but that large regions of both Africa and South America will be highly suitable and at great risk for invasions. Most of Europe will also be suitable for several invasive species and the only continent with a net gain in suitable area.

On the other hand, certain regions, like central Australia and parts of Angola, Botswana, Iran and Argentina, are predicted to be free of any risk from the 32 investigated species.

Finding new sources of antibiotics using phylogenetic, spatial, and phytochemical data

18

Anaphalis javanica observed in East Java by Cheryl Gilbert (CC BY-NC-SA 4.0)

HUMAN HEALTH

720,861
SPECIES OCCURRENCES

Indonesia

Studies of Javanese seed plants combines phylogenetics and species distribution modelling to identify "hotspots" of potential drug sources

Just 90 years after the discovery of penicillin, the world may soon be facing a post-antibiotic era, as emerging multidrug-resistant bacteria are threatening global public health. Plants have been used medicinally for thousands of years, but only a fraction have been evaluated for biological activity.

To facilitate the discovery of novel plant compounds with potential as antibiotic agents, this study classified more than 16,000 metabolites according to bioactive properties from more than 7,500 seed plant species in Java, Indonesia, one of the world's megadiverse countries. They then searched for phylogenetic signals of anti-infective properties, identifying "hot" clades of overrepresentation and "cold" clades of underrepresentation.

Using GBIF-mediated occurrences of Javanese seed plants, the authors then constructed distribution models to assess the spatial patterns of plants with anti-infective properties in relation to total plant diversity on the island.

Their phylogenetic analysis identified 26 "hot" clades, including 25 whole families, e.g. daisies/sunflowers (Asteraceae), and 24 "cold" clades, including 16 entire families, e.g. grasses (Poaceae) and orchids (Orchidaceae). The spatial analysis showed that regions with the highest diversity correlated with the highest probability of finding novel antibiotic compounds.
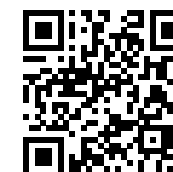
Holzmeyer L, Hartig A-K, Franke K, Brandt W, Muellner-Riehl AN, Wessjohann LA and Schnitzler J

Germany

Descriptive power of ecoregions varies across regions and taxa

19

Anaphalis javanica observed in East Java by Cheryl Gilbert (CC BY-NC-SA 4.0)

BIOGEOGRAPHY

CONSERVATION

915,738,761
SPECIES OCCURRENCES

Study finds evidence that ecoregions are more distinct for small-bodied, less vagile and tropical taxa

Ecoregions are large areas of land or water containing geographically distinct assemblages of natural communities sharing species, ecological dynamics, and environmental conditions. Used in ecological research and conservation, ecoregions need to capture and describe communities well.

Integrating maps of ecoregions with data on environmental conditions, biodiversity and species traits, this study aimed to quantify the descriptive powers of ecoregions. Using GBIF-mediated occurrences of nearly all organisms, the authors modelled abiotic and biotic predictors of ecoregion distinctness.

In their results, they find evidence that ecoregion distinctness is best predicted by temperature and seasonality (presence of variations occurring at specific, regular intervals, i.e., seasons). With high average temperatures and rainfall combined with low seasonality, tropical ecoregions more strongly differentiate communities. Also, ecoregions are most distinct in regions with steeper slopes.

From a biotic perspective, ecoregion distinctiveness is more pronounced for reptiles and amphibians than mammals or birds and, in general, more pronounced for smaller-bodied species.

Overall, the study shows that ecoregions, while a powerful tool for conservation planning, do not necessarily describe communities uniformly across regions or taxa.
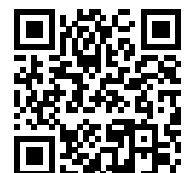
Smith JR, Hendershot JN, Nova N and Daily GC

USA

Black skin protects birds against harmful ultraviolet radiation

20

Pseudibis papillosa (Temminck, 1824) observed in Koonthakulam, Tamil Nadu, India
by Murugesh Nateshan *(CC BY-NC 4.0)*

Nicolaï MPJ, Shawkey MD, Porchetta S, Claus R and D'Alba L

Belgium

Exposure to UV radiance predicts repeated evolution of concealed black skin in birds

Nature Communications

doi.org/10.1038/ s41467-020-15894-6

EVOLUTION

2,259
SPECIES

Study of more than 2,200 bird species finds black skin a widespread trait, evolving independently more than 100 times, most likely as a protection against UV radiation

The extraordinary variety of bird colours has fascinated scientists since Darwin, but research has mainly been focused on plumage colouration. As with other vertebrates, some birds have developed black skin, but this evolutionary mechanism and its drivers have received little attention in the scientific community.

In this study, researchers examined specimens of more than 2,200 species across all bird families, categorizing species by skin colour, finding black skin on the head to be a widespread trait, present in at least 138 genera. The trait appeared to have evolved more than 100 times independently, but has been frequently lost, indicating a costly specialization only evolved when serving a particular function.

Lumping GBIF-mediated occurrences of black-skinned bird species together, the authors modelled the predicted distribution of the bird trait, which followed the so-called Gloger's rule with skin melanization increasing towards the equator. The best predictor of black skin in birds was exposure to UV radiation, while the authors found little support for hypotheses related to thermal regulation and bacterial protection.

In addition, black skin was most common in species with thin, very bright or no plumage and even more common in hatchlings. These findings together suggest that melanin-rich darkening of the skin evolved as a protection against damaging UV radiation.

Animal invaders threaten protected areas worldwide
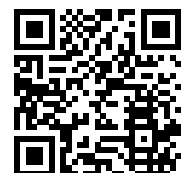
21

Lymantria dispar (Linnaeus, 1758) observed in Dunstable, MA, USA by Eli Tal. (CC BY 4.0)

INVASIVES

33,040,139
SPECIES OCCURRENCES

Study shows that terrestrial protected areas are vulnerable to invasive alien species but so far effective at preventing invasions

Protected areas (PAs) are important for conserving endemic and endangered species. Invasive alien species, however, have been identified as a serious threat to global terrestrial PAs. To mitigate, a worldwide assessment of current and potential invasion status and risk in PAs is needed.

Analysing 894 alien animal species, including amphibians, reptiles, birds, mammals and invertebrates, this study used GBIF-mediated occurrences to quantify current establishment across nearly 200,000 PAs worldwide.

Initial assessments found that more than half of the investigated species currently occur in PAs. Only 10 per cent of PAs are home to any alien species, but at least one established alien population is found within 10 km boundaries of ~90 per cent of PAs.

Modelling the climatic niches of the alien species, the authors find that more than 95 per cent of PAs are environmentally suitable for establishment by several of the investigated species.

The predicted richness of alien species in global PAs is nearly 200 times higher than what is observed, suggesting that PAs may be very sensitive to incursions but are currently effective at keeping invaders at bay.

Liu X, Blackburn TM, Song T, Wang X, Huang C and Li Y

China, UK

Animal invaders threaten protected areas worldwide

Nature Communications

doi.org/10.1038/
s41467-020-16719-2

Assessing the capacity of ecosystems to retain biological diversity under climate change

22

Senna reticulata (Willd.) H.S.Irwin & Barneby observed in Manaus, Brazil by crax (CC BY-NC 4.0)

Ferrier S, Harwood TD, Ware C
and Hoskins AJ

Australia

A globally applicable indicator
of the capacity of terrestrial
ecosystems to retain biological
diversity under climate change:
The bioclimatic ecosystem
resilience index

Ecological Indicators

doi.org/10.1016/
j.ecolind.2020.106554

CONSERVATION

CLIMATE CHANGE

79,512,379
SPECIES OCCURRENCES

Bioclimatic Ecosystem Resilience Index (BERI) a new indicator addressing key aspects of ecosystem resilience under Aichi target 15

A wide range of indicators has been developed to track progress towards achieving the 20 Aichi Biodiversity Targets adopted in 2010 by the Conference of the Parties (COP) of the Convention on Biological Diversity (CBD). Target 15 on ecosystem resilience and degradation, however, was poorly served by existing indicators. In this paper, researchers from Australia introduce the Bioclimatic Ecosystem Resilience Index (BERI), tailored specifically to assess change in the capacity of ecosystems to retain biological diversity under climate change, thus addressing a key aspect of Aichi Target 15.

Occupying the middle ground between modelling of shifts in species distributions and analyses based on spatiotemporal patterns in climate alone, BERI is calculated based on input from three sources: 1) compositional-turnover models derived from species occurrences of all all terrestrial species (including GBIF-mediated data for vascular plants, reptiles and insects) combined with climate and environmental data, 2) scenarios of plausible future climates, and 3) data on observed changes in habitat condition resulting from ecosystem degradation, conservation and restoration.

As an example, the authors apply the approach to calculate and assess changes in BERI to a single forest biome (tropical and subtropical moist broadleaf forests) using turnover models for all vascular plants and habitat conditions for four different years.

The results show that in general, larger expanses of intact forest have higher BERI values, suggesting that overall levels of habitat loss and fragmentation are key determinants of the capacity of ecosystems to retain biodiversity under climate change. Projected changes in certain climate variables, however, also play an important role as some otherwise intact areas, such as parts of the Amazon, exhibited much lower BERI values than expected, potentially due to future reduction in precipitation.

Improving the accuracy of Red List assessments using open-access species occurrence data

23

Cibotium arachnoideum (C.Chr.) Holttum collected on Mt. Kinabalu, Borneo, Malaysia. Cropped specimen photo via the National Museum of Natural History, Smithsonian Institution.

Robiansyah I and Wardani W

Indonesia

Increasing accuracy: The advantage of using open access species occurrence database in the Red List assessment

Biodiversitas

CONSERVATION

128
SPECIES OCCURRENCES

Indonesia, Malasya

Study uses GBIF-mediated occurrences to re-assess conservation status of rare fern, dropping suggested designation from Endangered to Vulnerable

Assessing the conservation status and extinction risk of species for inclusion in the IUCN Red List of Threatened Species requires high-quality species occurrence data to apply criterion B, measuring the extent and area of occurrence of assessed species. With more than 1.6 billion records readily available, assessors are increasingly using GBIF-mediated data for species red-listing.

In this paper, authors from Indonesia re-evaluated a previous assessment of the fern *Cibotium arachnoideum* that relied only on specimens from a single herbarium, categorizing the species as endangered (EN). Adding additional occurrence data from GBIF, the present study more than tripled the number of records included in the assessment.

Using just 41 occurrences, the authors calculated Extent (EOO) and Area of Occurrence (AOO) using the GeoCAT tool, reaching values far higher than the previous assessment, qualifying *C. arachnoideum* for a Near Threatened (NT) designation. They further assessed the species under other criteria, and by modelling the suitable habitat of the fern, they showed that future habitat conversion is unlikely to be a serious threat.

Based on the combined results, the authors disagree with the previous EN designation and instead suggest that *C. arachnoideum* be included in the Red List as Vulnerable (VU), a lower risk category.

Mapping the geographic extent of tungiasis in sub-Saharan Africa

24

Tunga penetrans specimen collected in Gabon—slide (left) and magnification (right). Photos (merged) belonging to The Trustees of the Natural History Museum, London (CC BY 4.0)

HUMAN HEALTH

Study uses GBIF-mediated species occurrences to model the environmental suitability of tropical disease-causing parasite

Tungiasis is a tropical disease caused by the burrowing of a tiny parasitic flea, *Tunga penetrans*, in the skin of the patient leading to painful and debilitating lesions. Despite representing a significant health burden, especially in sub-Saharan Africa, knowledge of the distribution of the parasite and disease in the region is extremely limited.

Based on various variables, including data on climate, soil, vegetation, land cover and livestock densities, this study models and maps the environmental suitability of

the parasite based on known occurrences from literature and GBIF-mediated data.

The models identify suitable conditions for the parasite in nearly all of sub-Saharan Africa—with the exception of Namibia, Botswana and southern Mauritania. About half of the 44 countries with a high probability of occurrence already have reported cases of tungiasis.

An estimated total of 668 million people live in environmentally suitable areas covering 8.1 million km². In East Africa alone, the suitable area is home to 217 million people, with many living in poor rural communities with a high risk of increased suffering from tropical diseases.

While the study does not directly measure or predict tungiasis incidence, it provides insights into the potential distribution of the disease-causing parasite—valuable for future public health interventions in the region.

Deka MA

USA

Mapping the Geographic Distribution of Tungiasis in Sub-Saharan Africa

Tropical Medicine and Infectious Disease

Global assessment of human influence on modelling of bird invasions

25

Callonetta leucophrys (Vieillot, 1816) observed in South Africa by tjeerd (CC BY-NC 4.0)

INVASIVES

395,161,334
SPECIES OCCURRENCES

Study demonstrates that incorporating variables measuring human impact in distribution models significantly increases accuracy of predictions

Species distribution modelling (SDM) is a powerful tool used to estimate the invasion potential of alien species in adventive regions—areas where species have been introduced but are not yet fully established. Often based solely on macroclimatic variables, however, SDMs may overlook other conditions allowing alien species to overcome limitations imposed by broad-scale climate.

In this study, researchers explored the effect of human influence on niche conservatism and shifts by comparing native and alien distributions of 150 bird species using SDM predictions based on eight bioclimatic variables (e.g. temperature, precipitation, etc.) and/or two human impact variables: the Global Human Influence index, and, degree of urbanization.

The performance of SDMs improved significantly with the addition of human impact variables as opposed to bioclimatic variables alone. For most species, the native and alien niches were similar both in terms of climate and human impact, however, some alien expansions were registered—mostly involving colonization of colder climates and more disturbed environments.

In addition to highlighting the importance of human influence on modelling distributions of invasive species, the overall results showed that alien birds tend to invade areas with similar climatic and human impact conditions to their native range. When differences in niches are observed, these are typically related to species tolerance to human-modified habitats and time since introduction.
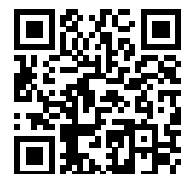
Cardador L and Blackburn TM

Spain, UK

A global assessment of human influence on niche shifts and risk predictions of bird invasions

A cross-scale assessment of productivity–diversity relationships

26

Calocedrus decurrens (Torr.) Florin observed in California, USA by Jonny Sperling (CC BY-NC 4.0)

ECOLOGY

344
SPECIES

USA

Machine learning approach shows that spatial grain mediates relationships between biodiversity and ecosystem-level productivity

This study attempts to assess the strength and directions of relationships between ecosystem-level productivity and species richness through modelling at three different spatial scales (fine, intermediate and coarse).

The models of the study were based on a large dataset of woody plant species in forests in the contiguous United States, filtered against GBIF-mediated occurrences to eliminate non-forest and alien species and to account for variation in climate, management and age.

Overall, higher values of species richness and productivity were reported in the eastern USA than in the western USA. At intermediate and coarse scales, species richness and productivity were positively correlated.

The structural equation models found a direct effect of richness on productivity and vice versa—of similar strength, increasing with spatial grain.

Richness, however, was found to be a relatively weak predictor of productivity compared to other variables such as forest age, management and biomass. With productivity and richness sharing many environmental and geographical drivers, the study is unable to distinguish between causation and correlation in the relationships.

Craven D, Sande MT, Meyer C, Gerstner K, Bennett JM, Giling DP, Hines J, Phillips HRP, May F, Bannar-Martin KH, Chase JM and Keil P

Germany, Australia, USA, Netherlands, Canada

Biases in raw opportunistic observation data may produce unreliable richness estimates

Tadorna tadorna (Linnaeus, 1758) observed in Sweden by Ulf Teghammar *(CC BY-NC 4.0)*

ECOLOGY

CONSERVATION

CITIZEN SCIENCE

1,184,984
SPECIES OCCURRENCES

Sweden

Study evaluates effects of inclusion criteria on measures of α-diversity and β-diversity when using citizen science data

Measures of biodiversity are crucial to understanding community assembly and for conservation planning. Separating transients from core species in standardized surveys is possible by applying specific inclusion criteria, but with abundant citizen science observation data available, when do we consider a species part of a local community?

Extracting occurrences published by Artportalen (Swedish Species Observation System) of 77 bird species during a 90-day breeding season at 107 frequently visited wetland sites in Sweden, this study examined the effects of varying species inclusion criteria on measures of α-diversity (species richness) and β-diversity (community dissimilarity) when relying on raw high-density opportunistic observational data vs corrected estimates using a site-use occupancy model.

Applying thresholds of 1–30 days for inclusion, they found both α and β diversity to be highly sensitive to the criteria used. Estimates of richness generated from raw data, however, were consistently lower than when based on occupancy models. The effect was even more pronounced under the criteria of consecutive days.

These results suggest that occupancy model estimates are more stable and accurate and that, despite its abundance, raw opportunistic observation data may not produce reliable local richness estimates.

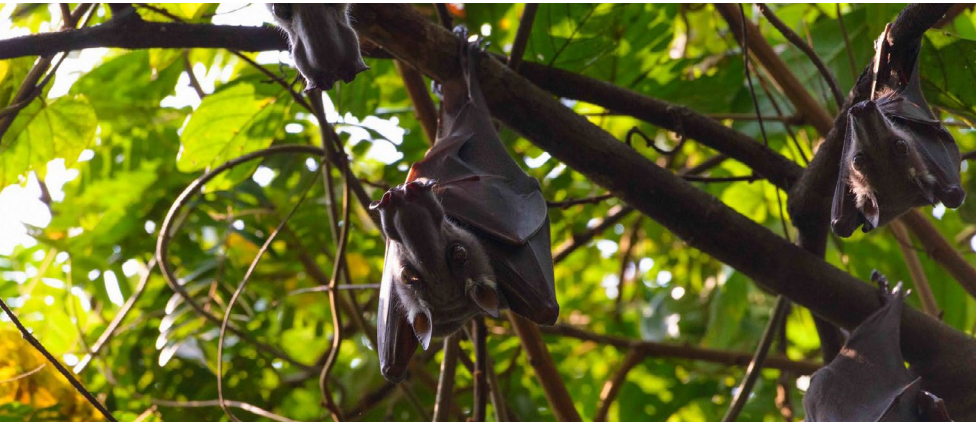Ruete A, Arlt D, Berg Å, Knape J, Żmihorski M and Pärt T

Sweden, Poland

Bats as likely Ebolavirus reservoir hosts

28

Putative Ebolavirus reservoir: Hypsignathus monstrosus observed in DR Congo by Dérozier Violette (CC BY-NC 4.0)

HUMAN HEALTH

Habitat suitability modelling of nine Ebolavirus-associated bat species fully encompasses all known disease outbreaks and provides further support to bats as prime reservoir candidates

Ebola virus disease (EVD) is caused by infections with species of the genus *Ebolavirus* with *Zaire Ebolavirus (ZEBOV)* being one of the deadliest. While the transmission cycle of ZEBOV is largely unknown, studies have pointed to bats as potential reservoirs.

This study uses GBIF-mediated occurrences to model the ecological niches of nine bat species that have tested positive for either virus RNA (three spp.) or antibodies against the virus (six spp.).

Using the maximum entropy approach, the authors derived the potential distributions of the nine bats based on climatic conditions and landcover at the sites of occurrences.

The resulting habitat suitability maps aligned well with IUCN range maps and predicted distribution in a broad transect across most of Central Africa.

Binary modelling results of the three RNA-positive species alone covered nearly all known spillover events and outbreak sites, adding evidence to the importance of these particular species—*Epomops franqueti*, *Hypsignathus monstrosus* and *Myonycteris torquata*—as ZEBOV reservoirs.
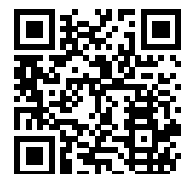
Origin of protected contraband leeches determined using metabarcoding

Hirudo verbana observed near Lytkarino, Russia by Marina Gorbunova (CC BY-NC 4.0)

CONSERVATION

DNA

Canada, Russia

How molecular analysis and metabarcoding can be used to identify protected species and their potential origin

The Convention on International Trade in Endangered Species (CITES) oversees the movement of protected and endangered species across international borders. Some species can be traded provided necessary permits are obtained, and the source of the specimen is documented.

Travelling from Russia to Canada in October 2018, a passenger was discovered at Toronto International Airport carrying more than 4,000 live European medicinal leeches (*Hirudo* spp.). As CITES provides

protection of two *Hirudo* species and as the source of the leeches was unclear, the Canadian authorities detained the animals for identification and determination of their source.

Researchers at the American Museum of Natural History identified the leeches as *H. verbana* (protected by CITES) using morphological and molecular techniques. To determine the origin of the animals, the researchers used genomic metabarcoding targeting vertebrate DNA from the blood meal in the guts of the leeches.

The analysis identified 16 distinct species—10 birds, four fish and two amphibians—none of which were domesticated animals, suggesting a wild origin. Using IUCN range maps combined with GBIF-mediated occurrences of the identified vertebrates, the researchers created a heat map of overlapping distributions, pointing to the Volga or Danube deltas as potential collection sites.

Williams KM, Barkdull M, Fahmy M, Hekkala E, Siddall ME and Kvist S

USA, Canada

Using citizen science observations to monitor urban biodiversity

30

Callaghan CT, Ozeroff I, Hitchcock C and Chandler M

USA, Australia

Japanese creeper (Parthenocissus tricuspidata) (Siebold & Zucc.) Planch.
Observed in Boston, USA by jiahuachen (CC BY-NC 4.0)

CONSERVATION

CITIZEN SCIENCE

643,000
SPECIES OCCURRENCES

USA

A multi-taxa framework scoring species by their urban tolerance and towns by their "biodiversity urbannness"

Monitoring the response of biodiversity both to threats and to restoration efforts, is essential but expensive. Broad-scale citizen science may play an important role in understanding how to best preserve and manage biodiversity in the future.

This study uses 643,000 observations in the Boston Metropolitan region, shared through iNaturalist and published in GBIF, to study the effects of urbanization on biodiversity, scoring more than 1,000 species by night-time light levels at occurring sites—derived from a remote sensing infrared imaging dataset—as a proxy for urban tolerance.

Among the most urban species were Japanese creeper (*Parthenocissus tricuspidata)* and northern seaside goldenrod *Solidago sempervirens*, while the least tolerant were Canadian bunchberry (*Cornus canadensis)* and frosted whiteface (*Leucorrhinia frigida).* The analysis highlighted a clear difference between native and non-native species, as the mean urban score was almost three times higher for non-natives.

Using the species-specific urban scores, the study then assessed 87 towns in the region by the community of species observed, ranking them by "biodiversity urbanness". This analysis revealed no bias among observers for more urban species but showed that biodiversity urbanness is negatively correlated with EVI (enhanced vegetation index) but positively correlated with the mean impervious surface of a town.

Overall, the study showcases how citizen science data can be leveraged for monitoring urban biodiversity and its responses to increased urbanization.

Poleward shifts in mangrove ranges over the past 70 years

31

Rhizophora mangle L. observed in Levy County, FL, USA by Bill stitt (CC BY-NC 4.0)

CLIMATE CHANGE

25,176
SPECIES OCCURRENCES

Study examined historical mangrove records and described significant latitudinal shifts in species worldwide, possibly driven by shifts in temperature and precipication

Adapted to live in harsh coastal conditions, mangroves tolerate saltwater immersion and wave action. Climate change brings not only increasing temperatures and shifting precipitation, but also potential changes to sea level and salinity.

To quantify global mangrove response to climate change, this study used GBIF-mediated occurrences of ten mangrove species combined with climate data and quantified the rate of latitudinal shift since the 1950s.

Their analysis revealed significant poleward shifts in nine out of ten species examined, averaging 1.3 degrees latitude per decade in North America and 1.7 degrees in Australia. The authors described higher mean shift rates in seaward zones compared to other zones, and among crypto-viviparous species (where seeds germinate while still attached to the parent tree) compared to non-viviparous.

The climate data indicated that changes in temperature and precipitation in the past 70 years were the main drivers behind the mangrove range shifts. These results can help guide conservation and management to mitigate the effects of climate change in the future.

Current status of plant and fungi collections worldwide

32

Sciodaphyllum weberbaueri collected in Peru by Sebastián Riva Regalado (CC BY-NC-ND 3.0)

BIODIVERSITY SCIENCE

81,975,817
SPECIES OCCURRENCES

Paper reviews the state of worldwide plant and fungal collections in herbaria and botanic gardens, while assessing specimen coverage in GBIF

While citizen science observations outnumber digitized specimen records from museum collections in GBIF, the opposite is true for taxonomic representation, as the most speciose citizen science datasets only contain about 20 per cent of the taxa represented in the largest museum collection datasets.

Recognizing the importance of digitizing natural history museum collections, this study provides an overview of the current state of plant and fungi collections worldwide while assessing the degree of digital accessibility and identifying main taxonomic and geographical gaps.

As of December 2019, there were 3,324 active herbaria across 178 countries containing more than 390 million specimens, though more than 45 per cent are found in European herbaria. In addition, around 107,000 plant species are represented in nearly 3,000 botanic gardens worldwide, with significant latitudinal bias as more than 90 per cent are held in northern, temperate institutions.

There are about 850,000 fungal strains available from 793 culture collections in 77 countries, but data from high-throughput sequencing suggests that millions of species are yet to be described. Only 17 per cent of described fungal species are cultured and publicly available. The study highlights initiatives such as UNITE for better understanding microbial diversity.

In terms of digitally accessible data, the study points to 85 million preserved specimens of plants and fungi available in GBIF, representing only around 21 per cent of all herbarium specimens *(NB: since the publication of the study, more than 10 million specimens have been added to GBIF).*

The study finds that data in GBIF covers 90 per cent of vascular plant species but only 55 per cent of fungi. The main geographical gaps are in Northern Africa and South and Central Asia.
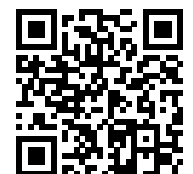
Paton A, Antonelli A, Carine M, Forzza RC, Davies N, Demissew S, Dröge G, Fulcher T, Grall A, Holstein N, Jones M, Liu U, Miller J, Moat J, Nicolson N, Ryan M, Sharrock S, Smith D, Thiers B, Victor J, Wilkinson T and Dickie J

UK, Sweden, Brazil, Ethiopia, Germany, Denmark, USA, South Africa

Cold and dark: evolution of colouration in Eurasian vipers

ascertain associations with ecogeographic variables derived from GBIF-mediated occurrences of each species.

Analyses revealed that dorsal pigmentation correlated positively with maximum precipitation and latitude, and negatively with minimum solar radiation and elevation.

Combined, these results highlight the colouration patterns of vipers as adaptive traits matching parameters of cold environments, irrespective of phylogeny, supporting the so-called thermal melanism hypothesis.

Martínez-Freiría F, Toyama KS, Freitas I and Kaliontzopoulou A

Portugal, Canada

Vipera berus (Linnaeus, 1758) observed in Sanok, Poland by olka-milosnik-robakow (CC BY-NC 4.0)

BIODIVERSITY SCIENCE

39
SPECIES

Study of dorsal pigmentation finds evidence of thermal melanism in snakes

Having fascinated biologists for centuries, animal colouration is involved in many aspects of animal ecology —including regulating temperature, attracting mates, hiding from and warning predators—and is considered an adaptive trait under strong selective pressure.

This study explores the macroevolutionary variation and drivers of dorsal pigmentation in Eurasian vipers (subfamily Viperinae), exhibiting characteristic zigzag patterns in all species. By measuring two colouration traits in 39 species, the authors quantified the dorsal pigmentation and performed phylogenetic tests to

Agricultural intensification—the main driver of wild bee decline

Andrena cineraria (Linnaeus, 1758) observed in Belgium by Stefan (CC BY-NC 4.0)

BIODIVERSITY SCIENCE

1,776,749
SPECIES OCCURRENCES

Belgium

Exploring 70 years of wild bee data in Belgium, study describes declines in occupancy and activity, likely driven by changes in land-use

Drivers of global change, including climate warming, urbanization and agricultural intensification, affect abundance, distribution and activity of many species worldwide.

In this study, researchers examined how drivers of global change affect biodiversity from individual species to species assemblages by exploring 70 years of data of more than 200 bee species in Belgium. They discovered that occupancy had decreased on average by 33 per cent and that bees were active earlier in the year. Overall, the

flight period started nine days earlier, but the duration was shortened by 15 days. The distributions of more than 60 per cent of species had decreased.

Turning to traits, including two temperature indices calculated using GBIF-mediated occurrences combined with bioclimatic data, the authors found that species in southern Belgium advanced their flight period more than species in the north. The social behaviour and size of bees were also associated with trends in both occupancy and flight dates.

The study concludes that the main driver behind the decline of bee populations is changes in land use, not climate, with agricultural intensification being the main culprit.

Duchenne F, Thébault E, Michez D, Gérard M, Devaux C, Rasmont P, Vereecken NJ and Fontaine C

France, Belgium

Evaluating lichens as climate change indicators

Punctelia jeckeri (Roum.) Kalb observed in Brunswick, Germany by Jakob Fahr *(CC BY-NC 4.0)*

Europe. Only 17 species, however, had sufficient historic data for modelling.

The resulting models revealed that half the investigated species had substantial fractions of their modern occurrences in areas previously considered unsuitable, while the majority of records for just under half of the species were found in suitable climates.

While data was lacking for many proposed indicator species, the results of modelling for half the species with sufficient data showed that distributional shifts occurred within areas historically considered suitable, indicating that taxa may be responding to other, more local drivers such as shifting pollution.

These results question whether the remaining taxa are indeed strong positive indicators of climate change, and the authors call for more quantitative, evidence-based derivations of indicators.
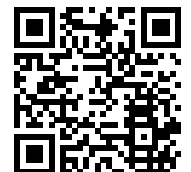

CLIMATE CHANGE

10,855
SPECIES OCCURRENCES

Germany

Study reveals lack of lichen data and suggests that range shifts for some species may be driven by changes in pollution, not climate

Well-known bioindicators of forest health, air and soil quality, lichens are also considered potential indicators of climate change. Drivers of changes to lichen proliferation and distribution, however, may be linked, and disentangling effects is necessary to understand the true impact.

To explore the validity of lichens as indicators of climate change, this study used GBIF-mediated occurrences coupled with Worldclim bioclimatic data to model habitat suitability of 45 designated indicator species in Central

Shade-grown coffee helps preserve avian insectivore richness

36

Ploceus baglafecht (Daudin, 1802) observed in Tanzania by Catarina Lobato *(CC BY-NC 4.0)*

CLIMATE CHANGE

AGRICULTURE

77
SPECIES

Ethiopia, Kenya, Tanzania, United Republic of Uganda, Burundi, Rwanda

Study shows that shade trees on coffee farms are able to mitigate effects of warming corresponding to 50 years of climate change

Coffee is a multibillion-dollar industry and an important export product in many developing countries. Rising temperatures threaten production, but growing coffee among larger shade trees may help not only to mitigate the effects of climate change on cultivation, but also to sustain avian insectivore diversity.

In this study, researchers explored potential distributions of insect-eating birds in coffee-growing regions of East Africa. They used the Maxent algorithm on GBIF-mediated occurrences combined with Worldclim temperature layers to model the current and future distributions of 77 species from 20 families.

To explore the effects of shade, they conducted a field study using temperature sensors at 13 coffee-growing sites with varying shade levels. The results were used to adjust the data from the climatic data layers used in the Maxent models.

Their analysis showed that in 50 years, avian diversity might decrease by 25–62 per cent (depending on the climate scenario) on East African coffee farms. If all shade trees were removed immediately, the effect on bird diversity would be similar to 50 years of climate change.

In the most extreme climate scenario in 2075, with no shade trees, bird diversity on farms would be reduced to about 20 per cent of the current level.
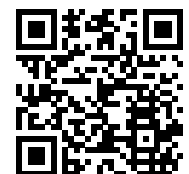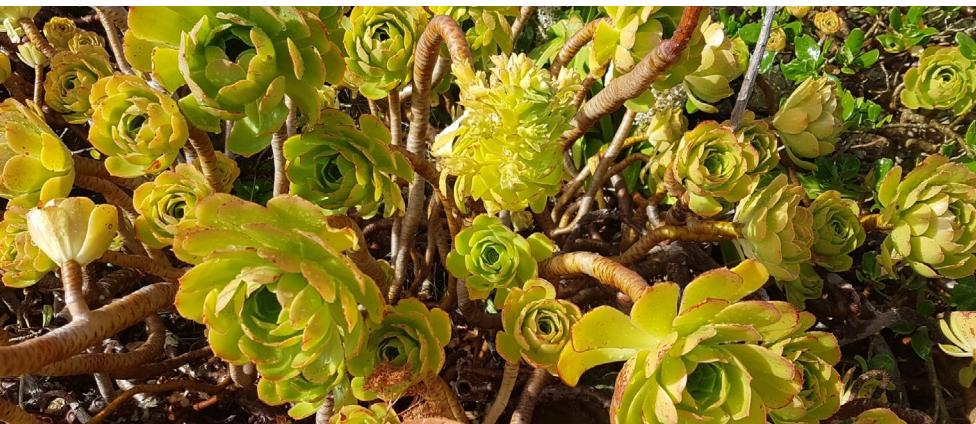
Schooler SL, Johnson MD, Njoroge P and Bean WT

USA

Composition and function of the alien flora of New Zealand

37

Aeonium arboreum (L.) Webb & Berthel. observed in Wellington, New Zealand by weedy1 (CC BY-NC 4.0)

INVASIVES

184,378
SPECIES OCCURRENCES

New Zealand

Study summarizes the current knowledge of traits and distribution of naturalized plants in the Pacific archipelago

Ranked among the world's top 25 biodiversity hotspots, New Zealand is an isolated archipelago in the South Pacific with very high endemism, including more than 80 per cent of reptiles and flowering plants.

The islands, however, have also been "ravaged by biological invasions" (Simberloff, 2008), and today, more than half of the land area consists of ecosystems dominated by non-native plants.

To support a contemporary management strategy of naturalized plants, this study summarizes the current knowledge of traits and distribution of the alien flora of New Zealand.

By mapping GBIF-mediated occurrences of 1,798 naturalized species, the authors showed that alien plants are distributed mainly in larger, more northerly and more populated regions, with Auckland and Canterbury having the highest numbers.

Overall, these plants, currently comprising 43.9 per cent of the vascular flora, add 67 families and 649 genera to the total vascular flora. The naturalized group is more taxonomically diverse than the native population and has a much higher proportion of herbaceous and annual species—but a lower proportion of perennials.

Combined, such knowledge of taxonomic and functional differences between native and alien may guide the management of naturalized species from local to national scale.

Brandt AJ, Bellingham PJ, Duncan RP, Etherington TR, Fridley JD, Howell CJ, Hulme PE, Jo I, McGlone MS, Richardson SJ, Sullivan JJ, Williams PA and Peltzer DA

New Zealand, Australia, USA

Naturalised plants transform the composition and function of the New Zealand flora

Global reliance on agriculture shaped by ecological opportunity and cultural transmission

38

Sus scrofa Linnaeus, 1758 observed in Florida, USA by moliverna (CC BY-NC 4.0)

EVOLUTION

AGRICULTURE

ECOLOGY

116
SPECIES

Ecological forces shaped the geography of agriculture by biasing human movement and the dispersal of domesticates

Agriculture has affected humanity like no other human development, and while food security has improved significantly since the first attempts at plant and animal domestication some 12,000 years ago, the adoption of agriculture as a main mode of subsistence has varied across societies well into the twentieth century.

As an attempt to explain the global patterns of reliance on agriculture, this study used GBIF-derived ecological niche models of the first 116 plant and animal species domesticated by humans to determine the effects of ecological opportunities.

Creating a map of local environments supporting early domesticates, the study found the highest suitability in tropical regions. Coupled with data on location and subsistence techniques of 1,200 traditional cultural groups, the models suggested that early-twentieth-century farming practices were shaped by local species richness, and that reliance on farming continued to be significantly predicted by how suitable the environment was for those early domesticates.

Using proxies for processes of transmission of cultural knowledge, the study also suggested that both population expansion and inter-group contact are likely to have shaped the spread, adoption and continued evolution of agricultural practices.

Vilela B, Fristoe T, Tuff T, Kavanagh PH, Haynie HJ, Gray RD, Gavin MC and Botero CA

Brazil, Germany, Canada, USA

Impacts of agriculture on Philippine biodiversity

39

Philippine eagle (Pithecophaga jefferyi) by Sinisa Djordje Majetic (CC BY-SA 2.0 via Flickr)

Ortiz AMD and Torres JNV

UK, Singapore

Assessing the Impacts of Agriculture and Its Trade on Philippine Biodiversity

Land

doi.org/10.3390/
land9110403

CONSERVATION

AGRICULTURE

717,508
SPECIES OCCURRENCES

Philippines

Study assesses interactions between agriculture and biodiversity, finding direct threats to several critically endangered species

One of the world's largest exporters of pineapple and banana, the Philippines has experienced critical declines in biodiversity due to land-use change and agricultural intensification as a result of poor resource management and overexploitation.

In this study, researchers reviewed current Philippine policies while analysing data on agriculture, trade and biodiversity to assess risks to species caused by intensive, export-oriented production of bananas and pineapples.

By combining data on plantations, protected areas (PA), Important Bird Areas (IBA) and GBIF-mediated occurrences of threatened species, the authors mapped the current interactions between agriculture and biodiversity. To account for varying size and spillover effects from intensive agricultural production, the authors added a 10-km buffer to plantations.

The resulting maps revealed many overlaps between plantations, ecologically important areas and threatened species, including direct threats to the critically endangered Philippine eagle, Peregrine falcon and Philippine naked-back fruit bat.

In total, the study identified 83 threatened species of animals and plants at risk of exposure to the impacts of intensive agriculture in the Philippines.
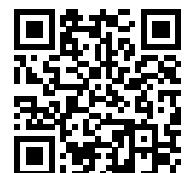
Bryophyte dispersal rates too slow to keep up with changing climates

40

Cyrtomnium hymenophyllum Holmen, 1957 observed in Vågå, Norway by Anders Breili (CC BY-NC-SA 4.0)

CLIMATE CHANGE

174,335
SPECIES OCCURRENCES

Despite their high dispersal capacities, bryophytes may be centuries behind future climate change

In response to warming climates, organisms may adapt by shifting their range, but the extent to which species can mitigate the effects of climate change remains somewhat unexplored. Highly efficient wind-dispersers, bryophytes are potentially excellent candidates for keeping up with shifts in areas of suitable climate.

This study used GBIF-mediated occurrence data of 40 European bryophyte species combined with climatic variables to produce suitability models calibrated under present and projected under future climatic conditions.

The authors used species-specific traits and environmental variables (e.g. spore size, canopy height and wind speed) to build mechanistic dispersal models simulating potential migrations in the future.

The suitability models for 2050 predicted the highest rates of range loss for Arctic-alpine species, while Mediterranean species had the highest range gain. The dispersal simulations showed that less than 30 per cent of species would be able to colonize newly suitable areas fully by 2050.

Simulations beyond 2050 predicted that most species would need up to 500 years to successfully colonize newly suitable areas fully, signifying that even highly dispersive species may not be able to compete with the rates of climate-induced range loss.

Zanatta F, Engler R, Collart F, Broennimann O, Mateo RG, Papp B, Muñoz J, Baurain D, Guisan A and Vanderpoorten A

Belgium, Switzerland, Spain, Hungary

Bryophytes are predicted to lag behind future climate change despite their high dispersal capacities

Climate change: buzzkill for North American tomato pollinators

41

Bombus vosnesenskii Radoszkowski, 1862 on Orange Paruche tomato flowers in San Diego, CA, USA.
Photo by ghazard (CC BY 4.0)

CLIMATE CHANGE

ECOSYSTEM SERVICES

1,245
SPECIES OCCURRENCES

USA

Carrasco L, Papeş M, Lochner EN, Ruiz BC, Williams AG and Wiggins GJ

USA

Potential regional declines in species richness of tomato pollinators in North America under climate change

Ecological Applications

doi.org/10.1002/eap.2259

The authors built ecological niche models based on current climatic conditions at GBIF-mediated occurrences of 15 buzz pollinator species associated with tomato crops. They then used greenhouse gas emission scenarios to project these models into future climates.

All future predictions revealed net losses of pollinator species richness across North America by 2050 and 2080. Losses in 394 identified tomato-producing counties in the US were 80 per cent higher than the continental average of 1.25 species by 2050. The most significant declines in richness were seen in the eastern and northeastern US, with some areas standing to lose up to 11 species.

Study reveals regional declines of up to 11 species of tomato pollinators under climate change

Thirty-five per cent of the world's food supply stems from crops dependent on insect pollination. Evidence suggests that diversity and abundance among pollinators are declining globally due to climate change, habitat loss, pathogens and pollution.

Specialized "buzz" pollinators, such as bumblebees, use muscle vibrations to release pollen from flowers. In this study, researchers assessed the potential impacts of climate change on the buzz pollinator communities of tomato crops in the United States.

Mapping Africa's biodiversity: More of the same is just not good enough

42

Otocyon megalotis (Desmarest, 1822) observed in Kenya by Yvonne A. de Jong (CC BY-NC 4.0)

40,457,393
SPECIES OCCURRENCES

Study estimates that using current practices may take up to three centuries to achieve sampling completeness in Africa

Biodiversity data availability is growing, but data is affected by temporal, spatial and taxonomic biases. Understanding these and what causes them is important to preventing future bias and filling data gaps.

In this paper, researchers present a novel approach to quantifying sampling effort in Africa by exploring the influence of existing knowledge about a site on attracting researchers, while estimating the time needed to complete sampling.

Initially, the authors mapped GBIF-mediated occurrences of amphibians, mammals and birds to 100x100 km cells to identify the number of estimated sampling events by taxa and country.

By applying a logistic model between sampling completeness, events and year, they discovered that across most of Africa, previous sampling of amphibians and mammals strongly increased the likelihood of resampling. For bird sampling before 1940, however, there was a higher tendency to visit unsampled areas, indicating a preference for discovering new species.

Modelling sampling rate, the authors predicted that it would take between 171 and 273 years to obtain 90 per cent coverage. To record 50 per cent of species within a cell would take on average 11.5 visits for amphibians, 12.7 visits for mammals and 27 visits for birds.

Farooq H, Azevedo JAR, Soares A, Antonelli A and Faurby S 👤

Sweden, Portugal, Mozambique, Brazil, UK 📍

Crop wild relatives of the United States require urgent conservation action

43

Solanum elaeagnifolium Cav. observed in Texas, USA by moonmist (CC BY-NC 4.0)

CONSERVATION

AGRICULTURE

396,355
SPECIES OCCURRENCES

USA

National inventory of US crop wild relatives find most taxa to be vulnerable or threatened and nearly all urgent or high priorities for ex situ conservation

With important crops being threatened by global change in their current areas of cultivation, food security may depend on the conservation and accessibility of crop wild relatives (CWR) to contribute genetic traits for plant breeding.

In this paper, US researchers present a national inventory of CWR, classifying taxa by relation to agricultural crops and significance as a wild food source.

Using GBIF-mediated occurrences, the authors modeled the potential distributions of more than 500 prioritized CWR taxa—including wild relatives of apples, barley, grapes, onions, potatoes and zucchini—according to bioclimatic and topographic predictors, showing the highest CWR richness in the Northeast, Midwest and Pacific Northwest.

Preliminary threat assessments identified only 23 taxa as of least concern (LC), while more than 500 taxa were near threatened (NT) or worse, including 42 taxa potentially critically endangered (CR).

While 400 institutions hold accessions of at least one US native CWR, 14 per cent of the assessed taxa are completely absent from seed banks and botanic gardens. The study further assessed more than 75 per cent of taxa as urgent collection priorities to address gaps in *ex situ* conservation.
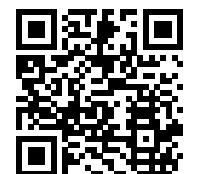
Khoury CK, Carver D, Greene SL, Williams KA, Achicanoy HA, Schori M, León B, Wiersema JH and Frances A

USA, Colombia, Peru

Crop wild relatives of the United States require urgent conservation action

Proceedings of the National Academy of Sciences

doi.org/10.1073/pnas.2007029117

Making species data open and FAIR

44

Aucuba japonica Thunb. observed in Belgium by toftof *(CC BY-NC 4.0)*

Reyserhove L, Desmet P, Oldoni
D, Adriaens T, Strubbe D, Davis
AJS, Vanderhoeven S, Verloove F
and Groom Q

Belgium

A checklist recipe: making
species data open and FAIR

Database

**doi.org/10.1093/
database/baaa084**   DOI

DATA MANAGEMENT

396,355
SPECIES OCCURRENCES

Paper proposes a reproducible and semi-automatic workflow for turning traditional checklists into FAIR datasets discoverable through GBIF

Lists of taxa typically sharing a geographic or temporal distribution, checklists are important sources of information for use in research and policy. Publishing checklists to GBIF allows for open and FAIR (Findable, Accessible, Interoperable and Reproducible) sharing of data about species.

This paper proposes a reproducible and semi-automatic workflow for transforming traditional checklist data

into FAIR data to be ingested and shared through GBIF. Combining source data management, reproducible data transformation according to accepted standards, version control, and data documentation, the approach provides a holistic solution to FAIR checklist publication.

Taking advantage of collaborative platforms for managing content, code and metadata, such as Google Docs, GitHub, and the Integrated Publishing Toolkit (IPT), the authors provide proof of concept by employing the proposed workflow to publish the Manual of the Alien Plants of Belgium containing all invaders in the country since 1800, thoroughly documenting each step of the process.

The code and examples described in the paper are freely available for anyone to copy, modify, use and distribute as they see fit, provided the copyright and license notices are preserved.

M A R I N E

About this special section

KYLE COPAS
Communications Manager

The summaries included here only hint at the full range of cross-cutting marine science studies enabled by open data from the GBIF network. While emerging and projected impacts of climate change provide a common thread in this corpus, the analyses in such studies often extend into specific applied questions like food security, invasive species, conservation and biogeography.

Likewise, authors frequently highlight—explicitly or implicitly—the critical importance of cross-network collaboration between GBIF and OBIS, the Ocean Biodiversity Information System. Through the renewal of a second multi-year agreement, GBIF and OBIS remain committed to exchanging data, knowledge and skills between their networks and improving the usability, interoperability and overall fitness-for-use of FAIR and open data on marine biodiversity available through both infrastructures.

Bryozoan hitch-hikers launching invasions on Antarctic islands

45

Membranipora membranacea observed in Malibu, CA, USA by Andrea Kreuzhage (CC BY-NC 4.0)

passenger organisms, including the non-native and ecologically harmful bryozoan *Membranipora membranacea*.

Using GBIF-mediated occurrences, the authors mapped the distributions of the passenger species found on kelp rafts at Deception Island to assess the potential of these species for becoming established. *M. membranacea* is found as far north as northern Scandinavia in the Arctic, where other studies have found algal substrate may be more important than temperature in limiting its spread. With widespread macroalgal substrates, the risk of invasion in the Southern Ocean may be high.

Avila C, Angulo-Preckler C, Martín-Martín RP, Figuerola B, Griffiths HJ and Waller CL

Spain, UK

INVASIVES

MARINE

20,128
SPECIES OCCURRENCES

Antarctica

Invasive marine species discovered on non–native kelp rafts in the warmest Antarctic island

Remote and isolated ecosystems in the Southern Ocean and Antarctica have been thought to be relatively protected from invasive species carried in ballast water, due to the strong circumpolar winds and currents. A new study, however, finds evidence of a non-anthropogenic mechanism for introduction to the continent.

Seventy million kelp rafts are estimated to be afloat in the Southern Ocean at any one time. Making its way onto an Antarctic beach inside the flooded caldera of a small, relatively warm volcanic island—Deception Island—one such raft was found by researchers to carry "hitch-hiking"

Climate change increases the extent and richness of invasion hotspots in the Arctic

46

Sargassum muticum (Yendo) Fensholt observed in West Sussex, England by Jarvo (CC BY-NC 4.0)

INVASIVES

CLIMATE CHANGE

MARINE

63,923
SPECIES OCCURRENCES

Canada

Study in the Canadian Arctic identifies 23 high-risk invasive species and four invasion hotspots, predicted to increase significantly in future climates

Considered one of the main drivers of biodiversity loss and recent extinctions, invasive species are a global threat with great ecological, economic and even human health impacts. Invasion risks are believed to increase with global warming, particularly in high latitude regions.

In the Arctic, shipping activities are responsible for almost half of all known marine invasions, and with predicted future ice-free conditions, more shipping corridors will open. In this study, researchers aimed to identify potential high-risk species and predict current and future invasion hotspots in the Canadian Arctic.

Through a stepwise vetting process, the authors identified 23 known marine invasive or harmful species for which they gathered occurrences mediated by GBIF and OBIS for use in MaxEnt modelling of current and future distributions. The models identified four hotspots in the region with overlapping suitability for up to 20 species: Hudson Bay, Northern Grand Banks/Labrador, Chuckchi/Eastern Bering seas and Barents and White seas.

In future projections for 2050 and 2100, both the geographic extent of hotspots and the potential richness of invasive species in the Arctic are predicted to increase—and at a much larger scale than globally.
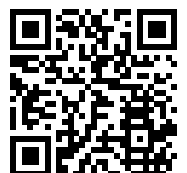
Zanatta F, Engler R, Collart F, Broennimann O, Mateo RG, Papp B, Muñoz J, Baurain D, Guisan A and Vanderpoorten A

Canada

Climate-driven shifts to alter both living resources and lives in the Eastern Tropical Pacific

47

Holacanthus passer Valenciennes, 1846 observed near Marietas Islands, Mexico by Ricardo Arredondo T. (CC BY-NC 4.0)

CLIMATE CHANGE

MARINE

718,202
SPECIES OCCURRENCES

Mexico, Guatemala, El Salvador, Nicaragua, Costa Rica, Panama, Colombia, Ecuador, Peru

Small-scale fisheries likely face the most severe local losses of species and suitable habitat

Wind-driven ocean upwelling systems along the coast of the Eastern Tropical Pacific (ETP) enrich the warmer surface waters with nutrients from cooler depths. The complex dynamics and cycles of these highly productive environments support several key fisheries for the human communities that extend from the Gulf of California to northern Peru.

To understand how future impacts of climate change might alter both the marine biogeography of and food security within the ETP, the authors used GBIF-mediated occurrence data to create environmental niche models

for 505 fishes and invertebrates commonly caught in the region's shrimp trawl, small-scale, small pelagic and large pelagic fisheries.

The results showed similar geographic trends across each fishery, though changes in direction and depth varied more widely. Variables with the greatest impact on shifts in suitable habitats turn out to be rising temperatures and falling oxygen levels, as many species seem likely to shoal in shallower and more oxygen-rich waters, rather than departing for deeper ones.

The Central American coast and small-scale fisheries likely face the most severe local losses of species and suitable habitat, though colonization by range-shifting species from elsewhere may in part compensate in areas of high species turnover. In such a complex region, even positive outcomes like gains for shrimp fisheries may signal deprivation elsewhere, as increased pressures on bycatch species exert higher economic and social costs in a region of underreported catches, employment and incomes.

Measuring the effectiveness of protecting Southern Ocean sea floors with Antarctic sea urchins

48

*Ctenocidaris perrieri Koehler, 1912 collected east of Smith Island, Antarctica
photo via National Museum of Natural History, Smithsonian Institution*

CONSERVATION

MARINE

Antarctica

Study offers approach for preserving Antarctica's most unique marine environments from impacts of climate change

Challenges abound in understanding, much less anticipating, the impacts of climate change on inhabitants of the Antarctic seafloor. But with implementation of a network of marine protected areas (MPAs) underway, this study applies nearly 7,000 Antarctic sea urchin records from the GBIF network as the basis for assessing the new conservation system's potential to protect the unique ecosystems and species of the Southern Ocean through the changes detailed in scenarios from the Intergovernmental Panel on Climate Change (IPCC).

The seabeds of Antarctica are home to more than 40 highly diversified and widely distributed species of sea urchins. This richness provides the foundation for this study, as the authors combined environmental niche models for each individual echinoid species with climate scenarios to generate a set of 12 Antarctic and sub-Antarctic benthic ecoregions.

The resulting first-ever dynamic ecoregional map of the Southern Ocean's entire seafloor reveals the likelihood of far-reaching environmental changes in East Antarctica, on the Antarctic Peninsula and sub-Antarctic islands—each surpassed in severity by the prospect of the possible disappearance of the Campbell Plateau ecoregion. The future-facing findings also highlight the underrepresentation of the current Antarctic ecoregions from the MPA network.

By offering a flexible multidecadal framework for regional conservation and monitoring, this study offers a useful and responsive approach for preserving Antarctica's most unique marine environments from the changes ahead.

Fabri-Ruiz S, Danis B, Navarro N, Koubbi P, Laffont R and Saucède T

France, Belgium

Warming seas power the shifting abundance of marine species from the equator to the poles

49

CONSERVATION

MARINE

4,567,028
SPECIES OCCURRENCES

Study confirms that adaptation alone cannot buffer the negative effects of warming oceans on species abundance

The average temperature of the world's oceans has risen by 1°C since the start of the Industrial Revolution. To assess the impact of this incessant heat wave on marine species abundance, the British author team marshalled the evidence (including more than 4 million GBIF-mediated occurrence records) on how 304 relatively common marine species from nine taxonomic groups have adapted to warmer seas.

Recognizing that temperature is not the only factor for determining the abundance of marine organisms, the study examined impacts of other critical variables affecting species ranges, including oxygen levels, salinity, storminess and food availability. The use of widely distributed species enabled a hemisphere-wide analysis of latitudinal range shifts across a quarter century, from 1991 to 2016.

Despite some variation in the resulting models as well as variability in the connection between thermal and latitudinal gradients, the results reveal that a species' physiological thermal niche is the strongest predictor of recent changes in abundance.

With populations declining at the equatorward edge of species' ranges and increasing on the poleward side, the study highlights the fact that adaptation alone cannot buffer the negative effects of warmer equatorial seas on species abundance, with major implications for local marine resources and the coastal industries that depend upon them.

Mariculture on the move: climate change impacts on species diversity and richness of salt-water farming

50

Fish farming near Amarynthos, Euboea, Greece. Photo by Jebulon via Wikimedia Commons.

MARINE

681,878
SPECIES OCCURRENCES

Study of 85 important mariculture species suggest varied and regional effects of climate change with major declines in diversity for tropical and subtropical farming locations

In recent decades, marine aquaculture has played an increasingly important role in supplying nutrition and food security, particularly to the 3.2 billion people who rely on seafood for at least 20 per cent of their protein intake.

To understand the impacts of climate change on these critical yet undervalued resources, a Canadian author team examined the potential reduction and redistribution of 85 species commonly farmed in the world's fjords, inshore and open waters, and saline inland seas. These 55 chordates and 30 mollusks are economically and nutritionally important, accounting for 70 per cent of all taxa used in mariculture.

Using multispecies distribution models that leveraged more than 680,000 GBIF-mediated occurrences with records from OBIS, FishBase and IUCN, the study calculated likely changes to the cultivated species' suitable habitat under both strong and no mitigation policy emissions scenarios across the 2000s, 2050s and 2090s.

While models suggest the expansion of suitable areas in some locations and relatively modest overall reductions in a global-scale index of "marine species richness potential," direct effects of climate change will be much more varied and stronger regionally. For example, changes to the conditions needed for optimal growth in current tropical and subtropical farming locations could see 10 to 40 per cent declines in the number of suitable species. Likewise, suitable marine areas for top-producing countries of Atlantic salmon, cobia and European bass may be lost.

With such changes ahead, this study provides a basis for informing planned adaptation and minimizing potential local-scale environmental impacts and cross-sectoral conflicts.

Nature and nurture: considering the ecological and evolutionary origins of fish migration

51

Oncorhynchus tshawytscha (Walbaum, 1792) observed in Chico, CA, USA, by sujiar (CC BY-NC 4.0)

MARINE

EVOLUTION

ECOLOGY

33,096
SPECIES

Study of migratory fishes reveals the deep history of genetic predispositions in shaping and informing migratory species richness

Why do some fish migrate? This complex adaptive behaviour is uncommon—migratory fishes are unevenly distributed around the world and represent less than seven per cent of all species—and, as for humans, it can come with heavy costs on the individual.

Describing migratory strategies is itself a challenge. Organized with reference to feeding and reproduction and the environments in which they occur, the life histories characterized within the five accepted categories (amphidromy, anadromy, catadromy, oceanodromy and potamodromy) defy clear and precise distinctions. As a result, revealing possible explanations for migration demands a holistic approach—such as the one delivered by the Chilean authors of this study.

To review current understanding of patterns of migratory fish diversity, they developed a set of global species richness matrices relying on all available native-range records from OBIS and GBIF for migratory species in the class Actinopterygii. The decision to limit their analysis to ray-finned fishes equipped them to include evolutionary data, in the form of an extensive phylogeny for Actinopterygii, alongside climate and environmental data.

Testing for direct relationships between migration and productivity (provisioning, scarcity and precipitation), the study found links between dynamic, resource-rich settings and migratory species richness, except for anadromous species that ascend rivers to breed and potamodromous freshwater migrants. Meanwhile, temperature appears less important when considered with other variables. And while no single factor can explain the "migratoriness" of a given species, the authors' inclusion of evolutionary signals from phylogenetic data reveals how critical the deep history of genetic predispositions is in shaping and informing migratory species richness.

Alò D, Lacy SN, Castillo A, Samaniego HA and Marquet PA

Chile

The depths of life: assessing 3D model performance for circumpolar marine species

Electrona antarctica (Günther, 1878) collected in Antarctica by Karsten E. Hartel, R/V Polar Duke S-011. Photo via Museum of Comparative Zoology, Harvard University (CC BY-NC-SA 3.0)

MARINE

ECOLOGY

2,918
SPECIES OCCURRENCES

Study of Southern Ocean lanternfish explores potential of using depth as a third dimension for modelling ecological niches

From lightless depths to sunlit surfaces, the species that inhabit Earth's oceans display preferences for different segments of the water column. But most studies of marine species distribution fail to consider these subsurface variations in the seas' vertical ecology.

Seeking to understand potential benefits and tradeoffs from integrating depth as a third dimension in environmental niche models, this research team developed the results of two- and three-dimensional models for 10 species of lanternfish, the most diverse and abundant family (Myctophidae) of offshore fish in the Southern Ocean. Using a total of 2,918 GBIF-mediated occurrences aligned to environmental baseline data for the period 1960–2010, the authors produced three models for comparison across each myctophid species.

Two "simplistic" 2D models stick to the surface, processing both the full dataset and the subset containing depth information while omitting consideration of depth. The third "depth-integrated" 3D model enriched the analysis of the latter subset by retaining the biological bathymetry to place occurrences in one of seven layers of vertical habitat.

After accounting for differences in the sample size of data for each species, the study found considerable overlap between 2D and 3D models across all depth predictions, particularly for depths less than 200 metres. 3D models may be more useful in revealing unrecognized suitable habitat and latitudinal changes in habitat, as species appear to move between shallower waters in the south and deeper ones equatorward. The conclusion echoes a call for well-designed surveys that collect high-quality data, including depth of catch, particularly for species of the middle depths.

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Estimating circumpolar distributions of lanternfish using 2D and 3D ecological niche models
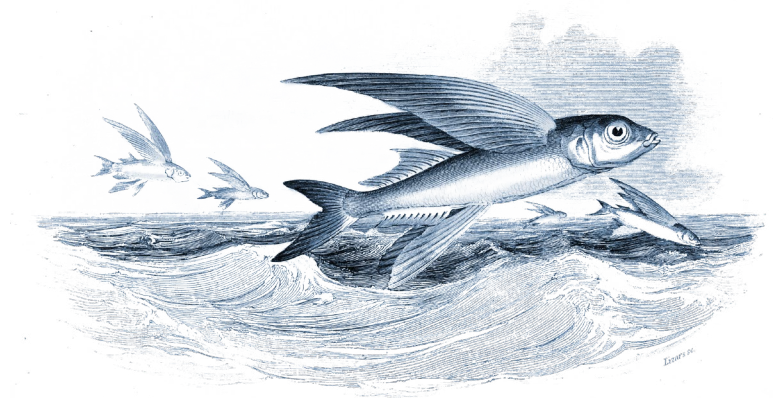
Cover illustration: blue flying fish, Exocoetus volitans Linnaeus, 1758, by James Forbes and Sir Willian Jackson Hooker, included in Oriental memoirs: selected and abridged from a series of familiar letters written during seventeen years residence in India. Via Biodiversity Heritage Library.

Back cover illustration: spotted sea hare, Aplysia depilans Gmelin, 1791, From The royal natural history. Edited by Richard Lydekker, 1896. Via the Internet Archive Book Images.

Marine background illustration: The sea-monster, as Mr. C. Renard supposed to have seen it. From The great sea-serpent, an historical and critical tratise by A. C. Oudemans, 1832. Via Biodiversity Heritage Library

Inner cover illustration: humpback whale, Megaptera novaeangliae (Borowski, 1781), by Charles M. Scammon, included in The marine mammals of the North-western coast of North America, 1874. Via Biodiversity Heritage Library.

Back flap illustration: horsefish, Hippocampus hippocampus (Linnaeus, 1758), by Gottlieb August Lange, included in Gemeinnüzzige Naturgeschichte des Thierreichs, 1873. Via Biodiversity Heritage Library.

Last page illustration: common flying fish by W.H. Lizars, included in The natural history of fishes, particularly their structure and economical uses, 1840. Via Biodiversity Heritage Library.