Nº 12

Science Review

GBIF

Nº 12

Science Review

GBIF SECRETARIAT

Foreword

JOE MILLER
GBIF Executive Secretary

Welcome to this year's edition of the GBIF Science Review!

Use of GBIF-mediated data in science continues to grow across both disciplines and geography. In the first three months of 2025, we logged an increase of 27 per cent in papers using data compared to the year before. In this Review, we are excited to share with you summaries of 50 studies that all make use of GBIF-mediated data in reaching their conclusions. Covering a wealth of topics, the selection of papers represents only a small fraction of the more than six papers discovered every single day of the year.

While the global COVID pandemic and subsequent lockdowns may seem like a past chapter for many, the One Health approach—with integrated research into animal and human diseases, their sources and vectors—remains more relevant than ever. Our feature section this year highlights 12 human health studies covering topics ranging from mercury poisoning from illegal gold mining—over zoonotic mpox and schistosomiasis—to a clinical study on inflammatory bowel disease.

We hope you enjoy the Science Review!

About the Science Review

DANIEL NOESGAARD
Communications Manager

Evolving from an entirely manual effort, our literature tracking programme that started in 2010 captured maybe a couple of papers per week in the first few years. In 2015, this number had increased to one per day, and ten years later, just as we were getting used to saying "nearly six papers per day", when referring to use of GBIF-mediated data in journal articles, it's now "more than six" or even "close to seven". Will it ever stop?

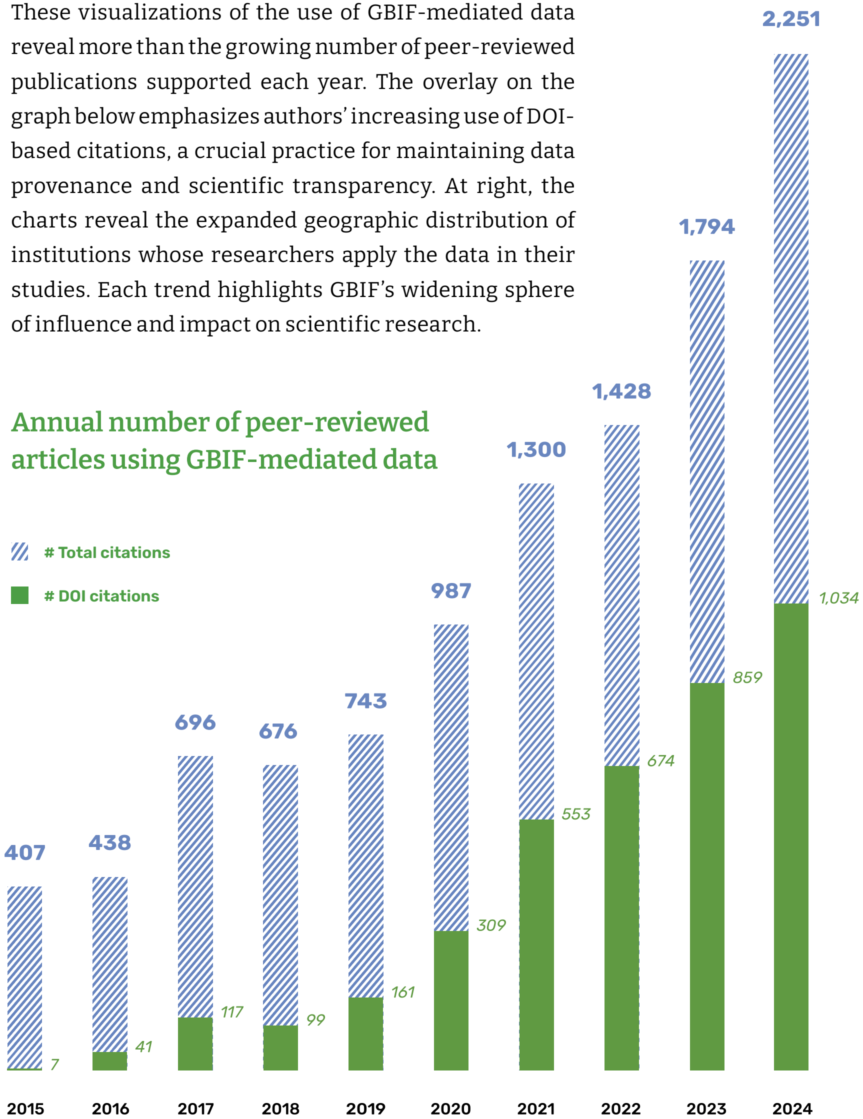
Why don't we just use artificial intelligence (AI) and large language models (LLMs) to do all this work for us? While I do think that "AI" in the form of machine learning will eventually play a role in helping us keep the literature tracking programme sustainable, curating topics and writing summaries is much more than simply stitching words together. It requires scientific understanding, real writing skills and actual intelligence. So far, LLMs only possess the ability to mimic these.

So, for now, please enjoy this selection of hand-picked, human-authored summaries of some of the best and most interesting use of GBIF-mediated data in science.

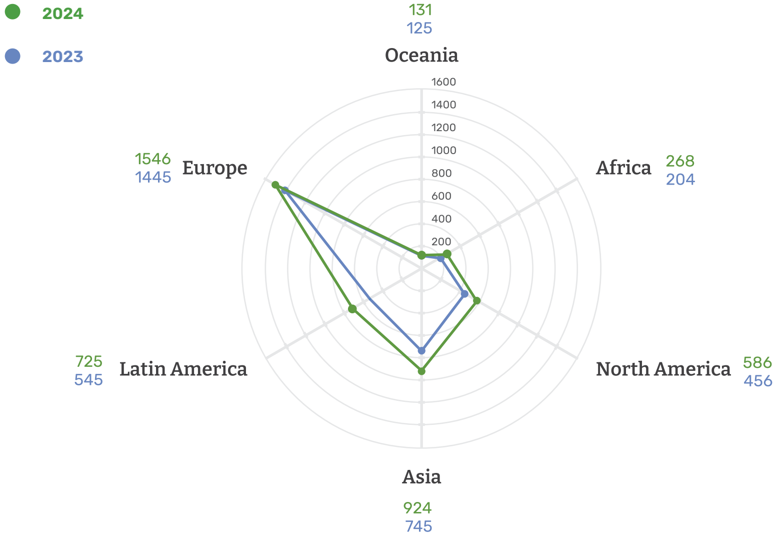
Uses and trends

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 studies. Each trend highlights GBIF's widening sphere of influence and impact on scientific research.

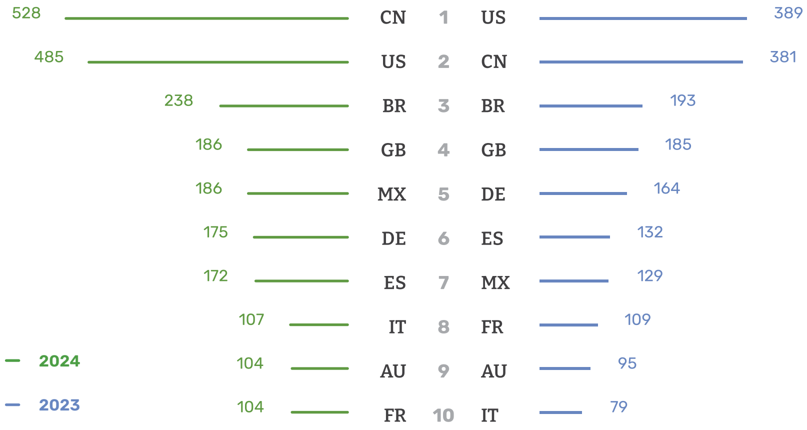
Annual number of peer-reviewed articles using GBIF-mediated data



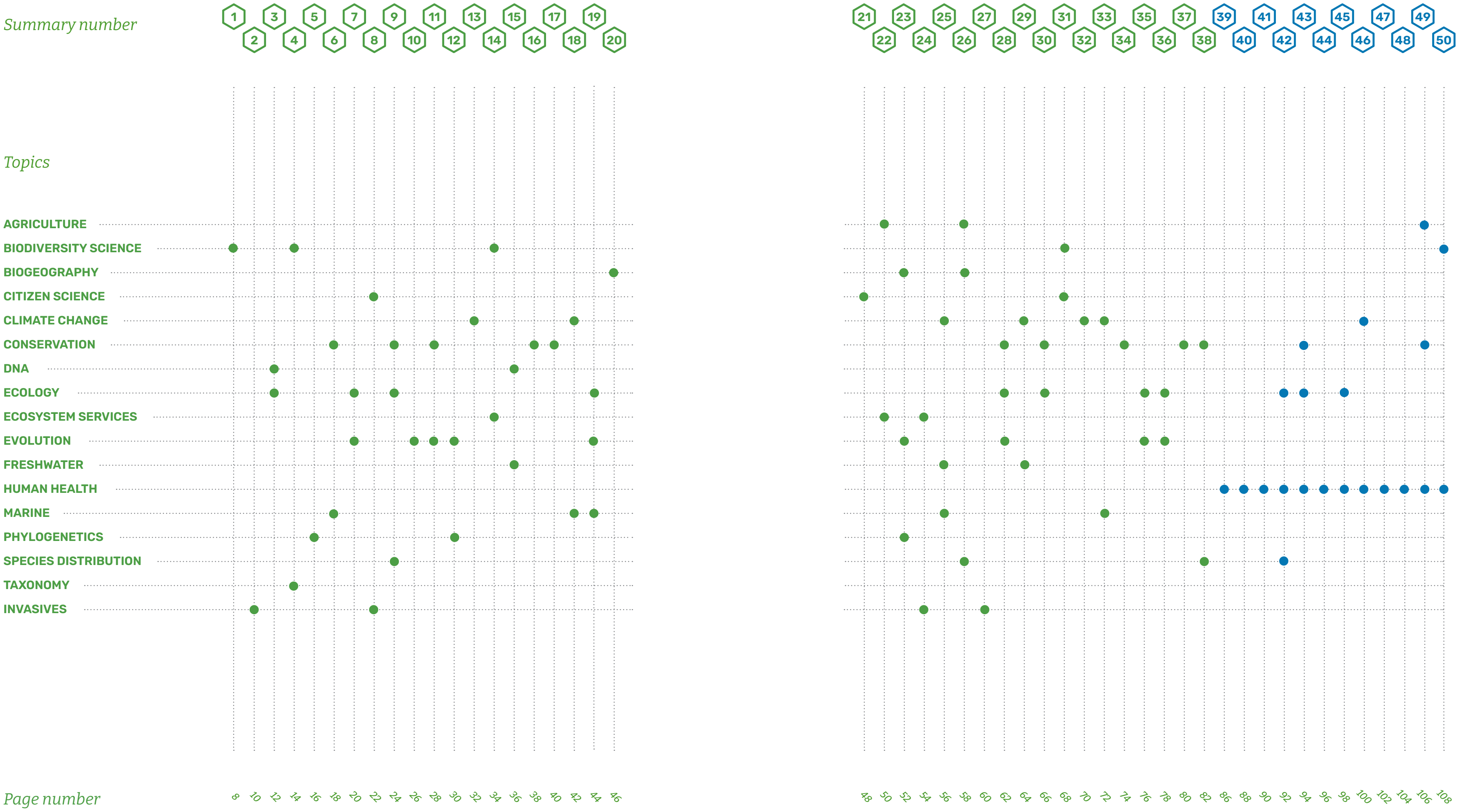
Peer-reviewed articles by region



Peer-reviewed uses by country



Navigation



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CONSERVATION						●			●		●					●	●			
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TAXONOMY				●																
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TAXONOMY																														
INVASIVES				●			●																							

Mapping global vascular plant diversity: identifying hotspots and conservation priorities

1

Cypripedium yunnanense observed in Lijiang, Yunnan, China by Oron Peri (CC BY-NC-ND 4.0)

BIODIVERSITY SCIENCE

402,039,160
SPECIES OCCURRENCES

Massive study by single author uses novel approach to map global vascular plant diversity, revealing previously undetected hotspots and targets for conservation efforts

While GBIF currently provides access to nearly 500 million occurrences of vascular plants, gaps and biases in the data can result in analyses making spurious ecological inferences. Other taxonomic groups, such as tetrapods, tend to be less poorly sampled. Modelling plant diversity alongside knowledge of such taxa with which they are associated, may improve predictions.

In this study of global vascular plant diversity, sole author Daru designed and applied a state-of-the-art distribution modelling framework using GBIF-mediated occurrences to generate high-resolution, species-level range maps of more than 200,000 plant species. Stacking these maps, Daru identified clusters of high species richness which also coincided with areas of high phylogenetic diversity.

When comparing diversity measures of vascular plants with those of tetrapods, the author found a high overlap, suggesting that conservation efforts focused on well-sampled tetrapod groups can likely capture vascular diversity as well. The study, however, did identify unique plant hotspots in the Chaco and Cerrado savannas, Yunnan and DR Congo, which did not align with tetrapod hotspots.

By training a second model assuming globally unbiased sampling to extrapolate vascular plant diversity as a function of tetrapod diversity alongside climatic variables and habitat characteristics, the author also uncovered previously undetected hotspots in, e.g., Yucatan (Mexico), Mato Grosso (Brazil), southern Angola and Sumatra. He also identified novel endemism hotspots in central South America, central Africa and Southeast Asia.

Finally, the author explored how well the identified plant hotspots from both modelling approaches were covered by existing protected areas. He found that less than 40 per cent of extrapolated hotspots were inside protected areas, leaving more than 60 per cent outside and potentially vulnerable, making them ideal candidates for future conservation priorities.

BH Daru

United States

Predicting undetected native vascular plant diversity at a global scale

Proceedings of the National Academy of Sciences

doi.org/10.1073/pnas.2319989121

Bright, big-brained birds boldly breaking boundaries

2

Monk parakeet (Myiopsitta monachus) observed in Cádiz, Spain by Zac Peterson (CC BY-NC 4.0)

INVASIVES

312,708,608
SPECIES OCCURRENCES

Study assessing climatic niche shifts in avian invasions finds success driven by brain size and behavioural innovation

The invasion success of alien species depends on many factors. Species may thrive in new locations with similar climatic conditions, but if incursions take place in climates different from a species' native range, surviving a shift in climatic niche requires the ability and innovation to adapt.

In this study, researchers explored species-level traits of successful alien bird invaders and the effect of these traits on the species' ability to adapt to new environments. Using the Global Avian Invasions Atlas database, the authors identified 117 species with successfully established populations outside their native ranges. They assembled data on brain and body size as well as measures for behavioural innovation for each species from published literature.

They then compiled occurrence data for the birds from GBIF and other sources, dividing their distributions into native and invaded ranges. Coupled with 19 bioclimatic variables they quantified the realized climatic niches of each species, comparing native and invaded niches to assess overlap and potential shifts.

Their analyses revealed a low climatic niche overlap between native and invaded ranges with climatic niche shifts detected in 75 per cent of the studied species. To determine effects of traits, the authors carried out a phylogenetic path analysis, revealing that niche expansion increased with innovation rate and brain size. The combined findings suggest that behavioural innovation of a species is more important than residence time and number of individuals in predicting the success of avian invaders.

JIN L, JIANG Y, HAN L, LUAN X, LIU X, LIAO W

China

Big-brained alien birds tend to occur climatic niche shifts through enhanced behavioral innovation

Integrative Zoology

DOI doi.org/10.1111/1749-4877.12861

The Global Spore Sampling Project

3

Pilobolus kleinii *observed in Pretoria, South Africa by tjeerd (CC BY-NC 4.0)*

ECOLOGY

DNA

6,189,602
SPECIES OCCURRENCES

148,209 occurrences shared using the GBIF Metabarcoding Data Toolkit

Novel method for sampling and characterizing airborne fungal spores, capturing samples yielding 27,954 species-level operational taxonomic units from 47 locations worldwide

Infamously hard to sample and characterize, fungi are one of the most unexplored kingdoms of life, despite their diversity and ecological importance. While soil sampling has proven successful to some extent, patterns detected may be substrate-specific. A new approach involving capturing fungal spores from the air could pave the way for global fungal sampling.

In the Global Spore Sampling Project (GSSP), researchers installed so-called cyclone samplers at 47 locations in varying climatic zones and altitudes across all continents except Antarctica. Collecting all particles greater than one µm in size from the air, the units took two 24-hour samples per week for at least one year. Each sample contained particles filtered from 24 m^3 of air.

For DNA sequencing of the more than 2,500 samples, the authors used PCR to amplify a specific region of the fungal genome, known as ITS2, a universal molecular barcode for fungi. From the sequences they derived amplicon variants which could be directly assigned to a known taxon or grouped into approximately species-level operational taxonomic units (OTUs). In total, the pipeline produced 27,954 species-level OTUs and 1,392 sequences that corresponded reliably to known species.

To validate the taxonomic classifications, they compared the distribution of species identified in study based on sampling locations with GBIF-mediated occurrence records. Overall, the distributions of the study data correlated significantly with GBIF occurrences with mismatches for only 1 per cent of species, suggesting valid taxonomic classifications.

Using a generalized linear model of the 485 most frequently occurring OTUs and climate data for the sampling locations, the authors found a strong ecological signal suggesting that most variation in species could be explained by differences in air temperature.

Ovaskainen O, Abrego N, Furneaux B, Hardwick B, Somervuo P, Palorinne I, et al

Australia, Germany, Cameroon, Iceland, China, Benin, Estonia, Finland, Austria, Japan, Greenland, Brazil, Argentina, Denmark, France, Canada, Croatia, Kenya, Madagascar

Global Spore Sampling Project: A global, standardized dataset of airborne fungal DNA

Scientific Data

doi.org/10.1038/s41597-024-03410-0

Global patterns of taxonomic uncertainty and its impacts on biodiversity research

4

Planigale tealei, *recently described* *species from the Pilbara region of Western Australia.*
Photo by L. Umbrello (CC BY-NC 4.0)

TAXONOMY

BIODIVERSITY SCIENCE

12,485,651
SPECIES OCCURRENCES

Study describes temporal trends in taxonomic synonyms and explores drivers of the accumulation of invalid names

While more than 2 million species are known to science, many species still lack formal description. Likewise, many currently recognized species are actually the same species described under more than one name, and these will eventually be synonymized. Failure to identify invalid names can inflate species lists and obscure species attributes, hampering use in biodiversity and conservation science.

This study explored the processes leading to the accumulation of invalid names, while analyzing patterns and identifying potential drivers in synonym counts across terrestrial vertebrates globally. For their analysis, the authors extracted data on synonym counts from the Catalogue of Life, traits from the TetrapodTraits database and specimen occurrences from GBIF.org. In total, they included 33,049 terrestrial vertebrates in the study.

The initial overview counted more than 35,000 unique synonyms, i.e., on average more than one per species. Forty-five per cent had no synonyms, while some had more than 100. Since Linnaeus's seminal work 270 years ago, more than half of all amphibian, mammalian and reptilian names have been invalidated.

Synonym counts varied highly in in realm-specific analyses, ranging from under 10 per cent for Nearctic birds up to 92 per cent for Nearctic amphibians. At the species level, the key predictors of synonym count were year of description, range size, and the number of preserved specimens. In grid-cell assemblages at three spatial resolutions, latitude and median discovery year were the most important and consistent predictors, with higher average numbers of synonyms observed toward the poles and for older assemblages.

The authors demonstrated how measures of diversification increased with synonyms, highlighting that taxonomic uncertainty can influence patterns in phylogenetic studies. This effect was more pronounced at lower latitudes for amphibians, reptiles and birds. Overall, such uncertainties can impact macroecology and conservation biology by reducing the applicability of biodiversity data or biasing model inferences.

Guedes JJM, Moura MR,
Jardim L, Diniz-Filho JAF

Brazil

Global Patterns of Taxonomic
Uncertainty and its Impacts on
Biodiversity Research. Antonelli
A, editor

Systematic Biology

doi.org/10.1093/sysbio/syaf010

Understanding plate tectonics through species diversification in South East Asia

5

Skunk vine (Paederia foetida) observed in Cát Hải, Hai Phong, Viet Nam by Luan Mai Sy (CC BY-NC 4.0)

PHYLOGENETICS

58,239
SPECIES OCCURRENCES

Phylogenetic analysis unravels the dynamic geological history of the extrusion of Indochina

About 55 million years ago, the Indian Plate collided with the Eurasian Plate, setting into motion some of the most significant tectonic events of Earth's history. This ongoing convergence caused the uplift of the Qinghai-Tibet Plateau platform and the Himalayas, and the extrusion of Indochina (Southeast Asia).

As tectonic events affect biotic evolution, diversification of species with limited dispersal ability can reflect geological changes. To better understand the geodynamic processes of the Indochinese extrusion, researchers analysed more than 1,700 species of plants and animals distributed across the Ailao Shan-Red River shear zone (ARSZ) that delineates the geological discontinuity separating South China from Indochina.

The authors created phylogenies for 42 clades and used GBIF-mediated occurrences to model and reconstruct ancestral niches based on six climatic variables. They then analysed divergence events between north and south ARSZ lineages to determine potential associations with variations in climate. Their analysis showed that more than 95 per cent of niche divergences were not associated with differences in climatic variables across the ARSZ, suggesting that phylogenetic separations were most likely caused by geological processes rather than climatic events.

By mapping divergence events through time, the authors showed that the split between northern and southern lineages started ~53 million years ago, indicating that the extrusion of Indochina began much earlier than previously suggested by geological evidence. This analysis also suggested a two-phase model with peaks in divergences taking place ~19 and ~7 million years ago, coinciding with the changes of the India-Asia convergence rate and angle and the uplift of the Qinghai-Tibet Plateau. Around these peaks, Indochina moved at least 25 km southeast at a rate of 5 mm per year.

Li XQ, Peng HW, Xiang KL,
Xiang XG, Jabbour F,
Ortiz R del C, et al

France, China

Phylogenetic evidence clarifies
the history of the extrusion of
Indochina

Proceedings of the National
Academy of Sciences

doi.org/10.1073/
pnas.2322527121

Climate warming leads to variable regional impacts for Arctic marine predators

6

Walrus (Odobenus rosmarus) observed near Svalbard by Morton Ross (CC BY 4.0)

MARINE

CONCONSERVATION

155
SPECIES OCCURRENCES

Study suggests habitat expansion for Arctic apex and mesopredators, particularly evident in northernmost areas

The acceleration of human-driven climate warming in recent decades has had lasting effects across Arctic regions. Ongoing temperature increases and ice loss have substantially altered the physical and biochemical properties of these ecosystems, leading to changes in food availability and nutrient exchange in marine environments. This study examined species richness and distribution trends across eight Artic marine areas between 2000 and 2019 to better understand the impacts of climate warming on Arctic biodiversity.

Authors used data from satellites and biogeochemical models to assess environmental factors including zooplankton, chlorophyll-a concentrations and salinity. They then compiled occurrence records for 69 marine taxa (26 apex predators and 43 mesopredators) accessed through GBIF, OBIS and NOAA databases and used species distribution modelling to analyze biodiversity patterns.

Results showed that changes in temperature and ocean productivity had variable effects on Arctic marine biodiversity across different regions. Species richness and productivity generally increased along inflow and outflow shelves (where different oceans meet) and continental slopes. However, other regions experienced species declines during low sea ice periods. Areas of greatest climate warming were identified in northern areas, where habitat expansion of apex and mesopredators were more evident. These findings demonstrate that Arctic landscapes are rapidly transforming, and highlights the importance of flexible conservation planning that accounts for regional variability and species responses under different climate scenarios.

Alabia ID, García Molinos J, Hirata T, Mueter FJ, David CL

Japan, United States, Netherlands

Pan-Arctic marine biodiversity and species co-occurrence patterns under recent climate

Scientific Reports

doi.org/10.1038/s41598-023-30943-y

Rainbow connection: Colour variety does not expand range size of web-building spiders

7

(*Araneus circulissparsus*) observed near Gold Coast, Australia by hermanmoller (CC BY 4.0)

EVOLUTION

ECOLOGY

724
SPECIES OCCURRENCES

Colour-polymorphic spiders more likely to be found on islands, but overall this trait does not affect niche breadth

Colour polymorphism (variation in colour) has been hypothesized as a factor that could extend the potential niche breadth of species, allowing individuals to be phenotypically specialized to exploit specific resources and habitats while reducing overall predation through visual diversity. This phenomenon has been observed in flowers and some insects. Web-building spiders use colour for multiple purposes, such as thermoregulation and prey attraction, but the relationship between colour polymorphism and range capacity in these lineages has been poorly understood.

To examine whether colour-polymorphic web-building spiders exhibit broader ranges than monomorphic species, a recent study used GBIF-mediated data and other sources to assess 140 spider species across 58 genera. The authors conducted an extensive literature review of colour polymorphism and used geographic measures—such as range size and the number of climatic zones occupied—as proxies for species' niche breadth.

Results showed that North America, Europe and north-eastern Australia had the highest numbers of reported polymorphic species. Colour-polymorphic spiders were more likely to be present on islands compared to monomorphic species, with 19 per cent of polymorphic species found exclusively in these environments. However, the authors found no overall association between colour variation and range size or niche breadth among web-building spiders.

These findings highlight the need for further research to better understand the ecological role of colour in shaping niche breadth, particularly regarding its influence on island colonisation.

Salgado-Roa FC, Stuart-Fox D, White TE, Medina I

Australia

Colour polymorphism is prevalent on islands but shows no association with range size in web-building spiders

Journal of Evolutionary Biology

doi.org/10.1093/jeb/voae118

Citizen science supports improved invasive species detection

8

Feral pigeon (Columba livia var. domestica) observed *in Milan, Italy by zweifwfuerstenburg* (CC BY-NC 4.0)

INVASIVES

CITIZEN SCIENCE

234,627,141
SPECIES OCCURENCES

Widespread biodiversity monitoring detects invasive species faster than official records, but adoption of complementary monitoring methods remains a persistent challenge for invasive species management

Invasive alien species (IAS) incursions are a significant contributor to biodiversity decline and the disruption of ecosystem services globally, but early detection can mitigate these negative impacts. Citizen science—through the use of platforms like eBird and iNaturalist—has emerged as an early warning monitoring strategy to detect new invasions over the past 15 years, supporting traditionally used methods such as published research and government reports; however the effectiveness of citizen science in IAS detection compared to official reporting has not been quantified. To address this, this study compared the time lag of IAS detection of more than 200 million records from citizen science platforms accessed via GBIF and 687 official first records of alien species from 30 European countries between 2010 and 2021. Authors found that citizen science platforms reported IAS earlier than or in the same year as the official databases for 50 per cent of records. Researchers then assessed the impact of covariates including species traits (taxonomic and ecological group and occupied habitat), popularity on citizen science platforms, public and research attention and regulatory status.

They found that species receiving increased attention on citizen science platforms (particularly for vertebrates) were reported much earlier than official records. Likewise greater species popularity in neighbouring countries resulted in faster IAS detection through citizen science. The only factor associated with IAS reporting being faster through official channels than citizen science was if the species was recognized through national or EU legislative priorities; but IAS detection was not affected by overall usage of citizen science platforms per country.

Authors demonstrated that having increased broad-scale species surveillance through citizen science overall benefited IAS detection; however a persistent challenge is increasing the usage and integration of citizen science IAS records by management authorities across all countries.

González-Moreno P, Anđelković AA, Adriaens T, Botella C, Demetriou J, Bastos R, et al

Spain, Serbia, Belgium, South Africa, Cyprus, Portugal, Austria, New Zealand, United Kingdom, Türkiye, Slovenia

Citizen science platforms can effectively support early detection of invasive alien species according to species traits

People and Nature

doi.org/10.1002/pan3.10767

Increased urbanization creates hazards for raptors in Kenya

9

Steppe eagle (Aquila nipalensis) observed near Samburu, Kenya by ckuytz (CC BY 4.0)

ECOLOGY

CONSERVATION

SPECIES DISTRIBUTION

1,340
SPECIES OCCURRENCES

Kenya

Species with overlapping distributions to semi-urban and forest areas most at risk of collision and electrocution

Expanding electrical infrastructure creates a more connected world for humans but often leads to increased physical hazards for biodiversity, particularly raising the risk of electrocutions for avian species. The level of risk to birds associated with powerlines depends on the grid configuration, powerline voltage, overlap of infrastructure with species ranges and species' life history traits (influencing the likelihood of species to actively interact with powerlines).

Using GBIF-mediated occurrence data, a recent study sought to identify the risk of powerline collision and electrocution for 13 species of raptors in Kenya. The authors considered the physical configuration of powerlines, spatial distribution of species and bioclimatic variables including elevation and precipitation in species distribution modelling to identify hotspot areas for collision and electrocution. They also considered foraging behaviour and wingspan in assessing potential hazard risk.

Seven of the 13 surveyed species were deemed to be at high risk of collision and electrocution with powerlines, with Meru and Kiambu Counties identified as the highest hotspots for electrocution. These semi-urban areas are surrounded by forest-covered landscapes and were found to have a high density of low voltage powerlines. The three species most vulnerable to electrocution were the Steppe eagle, Long-crested eagle and Augur buzzard, due to their behavioural ecological traits, spatial distributions and conservation statuses.

The authors indicate that there is significant opportunity for deeper collaboration with policymakers and the energy sector to guide the configuration of new electrical infrastructure in ways that mitigate biodiversity impacts, particularly in developing countries. There is also potential to expand the risk assessment framework developed in this study to include other avian species, especially migratory and wetland birds such as flamingos in evaluating their risk of collision and electrocution to powerlines.

Ngila PM, Chiawo D, Owuor MA, Wasonga VO, Ellwood ER, Mugo D

Kenya, United States

Assessing the susceptibility of raptor species to electrocution: A framework for Kenya

Environmental and Sustainability Indicators

doi.org/10.1016/j.indic.2024.100400

The evolution of brightly coloured truffles in New Zealand

10

Gallacea scleroderma observed in Manapouri, New Zealand by Lukas Phan-huy (CC BY-NC 4.0)

EVOLUTION

32,132
SPECIES OCCURRENCES

New Zealand

Study reveals global patterns of truffle-like fungi colour diversity and suggests adaptation for dispersal by fruit-eating birds

Truffle-like fungi (TLF) hold their spores entirely within their fruiting bodies and rely on being consumed by animals for dispersal. Globally, TLF have dull-coloured, underground fruiting bodies with scents for attracting mammals. In New Zealand, however, many TLF have above-ground, brightly coloured fruiting bodies, speculated to have evolved to mimic fruit and attract birds.

Exploring this phenomenon, researchers hypothesized that colourful TLF developed fruit-like traits to attract avian dispersers, and that the high abundance of this group in New Zealand lead to significantly more colourful TLF here than in the rest of the world. Based on existing literature, the authors compiled a global dataset of 479 TLF, and classified each species according to diameter, colouration and habitat. They used GBIF-mediated occurrences of all fungus species to analyse patterns in distributions and to describe both biotic and abiotic predictors of TLF traits.

Their results showed that TLF in most regions of the world are predominantly brown, cream or white coloured with some additional diversity in Australia and South/Central America. In New Zealand, however, the primary TLF colours included red, blue, purple and orange, and the colour diversity was the highest in the world. While the authors found significant relationships between abiotic factors (temperature and precipitation) and colourful TLF, the effects were relatively small. In contrast, they revealed a positive correlation with much larger effects between colourful TLF and the number of trees and fruit-eating birds.

Providing insights into drivers of fungal traits, the study highlights how unique ecosystems can provide novel and fascinating opportunities of exploring how sessile organisms like plants and fungi can take advantage of the sensory systems of animal dispersers.

Brunton-Martin A, Wood J, Gaskett AC

Australia, New Zealand

Evidence for adaptation of colourful truffle-like fungi for birds in Aotearoa-New Zealand.

Scientific Reports

doi.org/10.1038/s41598-024-67333-x

Madagascar: the birthplace of baobabs

11

Grandidier's baobab (Adansonia grandidieri) observed in Menabe, Madagascar by zdeno60 (CC BY-NC 4.0)

EVOLUTION

CONSERVATION

9,346
SPECIES OCCURRENCES

Madagascar

Study unravels the evolutionary history of baobabs, finding Madagascar the most likely location of origin of the 'mother of the forest'

With their outlandish appearance and enormous size, baobabs (*Adansonia* spp.) have intrigued humans for centuries, inspiring arts, folklore and traditions. Among eight extant species, *A. digitata*, is widespread across continental Africa, while *A. gregorii* is restricted to North West Australia. The six remaining species are endemic to Madagascar. To uncover the evolutionary history and inform conservation strategies to ensure the survival of baobabs, a multinational group of researchers performed whole-genome sequencing and built high-quality chromosomal-level genome assemblies for all eight species.

Analysing the genetic landscape of baobabs, they found a base number of 44 chromosomes conserved in all diploid (having two of each) *Adansonia* species, except *A. perrieri* with 42 chromosomes. Phylogenetic analyses suggested a baobab lineage origin about 41 million years ago with the diversification of Malagasy species probably occurring in the last 20. African *A. digitata* and Australian *A. gregorii* formed a sister clade to the Malagasy lineage.

To better understand Malagasy baobab demography and population dynamics, the authors modelled the distribution of the six species using GBIF-mediated occurrences and bioclimatic variables in the present and past. Aside from altitude, which affected all species, temperature was also important for *A. madagascariensis* and *A. rubrostipa*, while the remaining four species were mainly affected by precipitation.

The models suggested that almost all species had larger ranges on the western coast of the island during the last glacial maximum, 22,000 years ago. For two species, *A. suarezensis* and *A. perrieri*, the models revealed past potential for a continuous range rather than fragmented as it is today. Based on all findings, the study finally dissected previous hypotheses on the location of origin of *Adansonia*, dismissing both continental Africa and Australia. Instead the authors suggested that the hypothesis offering the most reasonable explanation of the present data establishes Madagascar as the most likely origin of baobabs.

Wan JN, Wang SW, Leitch AR, Leitch IJ, Jian JB, Wu ZY, et al

Madagascar, Kenya, United, Kingdom, China, Denmark

The rise of baobab trees in Madagascar

Nature

doi.org/10.1038/s41586-024-07447-4

Hitting the high notes: body size shapes song in honeyeaters

12

Blue-faced honeyeater (Entomyzon cyanotis) observed in Nightcliff, NT, Australia by Branden Darlison-Hoskin (CC BY-NC 4.0)

PHYLOGENETICS

EVOLUTION

253,742
SPECIES OCCURRENCES

Phylogenetic analysis assesses constraints of morphology and habitat on honeyeater song patterns, revealing effects of body size on frequency and pace

Birds use song to attract mates, defend territory, alert others of danger and socialize in general. Shaping the evolution of avian diversity, birdsong is a complex trait mediated by both morphology and habitat, but support for hypotheses around their individual contributions remains equivocal.

In this study, researchers employed a suite of phylogenetic comparative methods for assessing the effects of habitat and morphology on bird song at a macroevolutionary scale. The authors focused on honeyeaters (Meliphagidae) due to their immense diversity in song, body size, beak shape and environment, making them ideal for disentangling the factors that shape birdsong.

They collected and analysed song data for 163 honeyeater species, extracting and categorizing each by frequency, bandwidth and pace. To this, they also added data on beak and body size, habitat type and distribution based on GBIF-mediated occurrences.

Using two modelling approaches, the authors revealed several relationships in the compiled birdsong dataset. They found that frequency correlated negatively with body size, meaning that smaller birds produce higher frequency sounds and faster paced songs. Beak shape had no impact on any song variables, but spatial analysis showed that species in warmer areas tend to sing with narrower bandwidths. Finally, the models indicated that habitat types influenced evolution of song in honeyeaters with values of frequency, bandwidth, and pace tending to be lower for closed habitats than for open habitats.

The study firmly establishes body size as the main constraint of song in honeyeaters. Environment appears to play only a secondary role, mediating parameters of song via indirect impact on body size only. Changes in climate, however, may result in reduction in avian body size, subsequently leading to an increase in higher pitched songs.

Hay EM, McGee MD, White CR, Chown SL

Australia

Body size shapes song in honeyeaters

Proceedings of the Royal Society B: Biological Sciences

doi.org/10.1098/rspb.2024.0339

Climate warming driving urban biodiversity shifts in Canada and the United States

13

Opossum (Didelphis virginiana) observed in West Point, MS, USA by Adrian Naveda (CC BY 4.0)

CLIMATE CHANGE

95,917,360
SPECIES OCCURRENCES

Canada, United States

Biodiversity range shifts are likely to increase as temperatures rise

Species that humans interact with on a day-to-day basis are important in shaping community familiarity with biodiversity, delivering ecosystem services such as pollination and providing mental and physical health benefits.

With more than half of the world's population living in cities, anthropogenically driven climate change is causing range shifts for many urban species, leading to disconnects between culturally significant species and current occurrence patterns. For example, the Californian grizzly bear (*Ursus arctos* subsp. *californicus*) is extinct yet appears on the state flag.

In this study, researchers used climate data combined with GBIF-mediated occurrences of more than 2,000 terrestrial animal species across the 60 most populous cities in Canada and the United States to model species distributions now and in the future.

Their models predicted a "great urban shift" as increasing greenhouse gas emissions continues to affect the climate, leading to a large turnover of species in cities by the end of the current century. Some of the largest range changes were expected across birds and insects, with amphibians, canines and loons among the most negatively impacted.

The author noted that impacted species were also likely to be affected by additional factors such as urban noise and light pollution, zoonotic diseases and habitat fragmentation, which may accelerate the rate of range decline.

The impacts of urban wildlife loss are multi-faceted and may alter future generations' relationship with nature. These results highlight the critical need for mitigation strategies to curb the rate of species range shifts from anthropogenically-driven climate change.

Filazzola A, Johnson MTJ, Barrett K, Hayes S, Shrestha N, Timms L, et al

Canada

The great urban shift: Climate change is predicted to drive mass species turnover in cities.

PLoS ONE

doi.org/10.1371/journal.pone.0299217

Animals working hard to reshape the surface of the planet

14

North American beaver (Castor canadensis) observed in Deschutes, OR, USA by David Willingham (CC BY 4.0)

BIODIVERSITY SCIENCE

ECOSYSTEM SERVICES

122,767,752
SPECIES OCCURRENCES

Researchers estimate that animals weighing the equivalent of 53 million beavers shape the Earth's surface, contributing energy equivalent to hundreds of thousands of extreme floods

Ecosystem engineers are animal species that interact with and shape their surroundings in order to create or improve habitat in ways that enhance their survival. Ant mounds can alter soil erosion and beaver dams can change riverine landscapes, but the overall nature and combined significance of animals shaping Earth's surface is largely unknown.

Starting from a large systematic review of scientific literature, authors screened more than 8,000 articles, identifying ~500 papers describing animal species with geomorphological activities. Focusing on terrestrial and freshwater ecosystems, these activities included removal of material, reworking of soil and sediment, production and accumulation of materials and stabilizing or reducing erosion.

Based on a list of 500 animals—330 terrestrial and 170 freshwater—identified at the species level, they downloaded data from GBIF to create global maps of zoogeomorphic distribution and richness, and to estimate and identify patterns in their abundance. The highest richness of geomorphic animals was seen in Western Europe and North America, but bias in both research and data may impact these patterns.

By classifying genera by size, proportion of reported geomorphic agents and taxonomic characteristics, the authors explored the potential for unknown geomorphic species, highlighting a significant potential for undiscovered geomorphic animals within large genera, especially those with small, less-studied species, among, e.g., insects.

Finally, the study estimated the combined biomass of geomorphic animal agents at 200,000 metric tons of carbon (corresponding to roughly 1.33 million tons actual body weight or the equivalent of 53 million beavers or 330 trillion ants). By applying a conservative minimum of one per cent energy contributed to geomorphic activitives, they calculated the combined expenditure of all geomorphic animals to 76,000 GJ (equivalent to the energy of hundreds of thousands of extreme floods).

Harvey GL, Khan Z, Albertson LK, Coombes M, Johnson MF, Rice SP, et al

United Kingdom, United States

Global diversity and energy of animals shaping the Earth's surface

Proceedings of the National Academy of Sciences

DOI doi.org/10.1073/pnas.2415104122

Integrating eDNA with habitat suitability models for freshwater biodiversity monitoring

15

Mystacides azureus observed in Marin-Epagnier, Switzerland by zorille (CC BY-NC 4.0)

FRESHWATER

DNA

~2.5M
SPECIES OCCURRENCES

Switzerland

Study explores combined capacity of eDNA sampling with high-resolution habitat suitability models to provide larger scale and spatially integrative inferences about freshwater biodiversity

Losing species at accelerating rates, freshwater systems are among the most affected by anthropogenic impacts such as pollution and climate change. Monitoring data is crucial for quantifying and mitigating loss, but riverine systems are undersampled and existing data is scattered. In an attempt to overcome this challenge, this study combined high-resolution habitat suitability models with eDNA-based assessments of 127 aquatic insect species across all major river catchments of Switzerland—to assess their individual and combined ability to predict species occurrences.

For the eDNA assessments, researchers sampled 172 sites and extracted DNA to construct libraries for sequencing and species identification. Using species occurrences from the Swiss National Biodiversity Data and Information Centres and GBIF, the authors constructed habitat suitability models for each of the 127 focus species.

The authors found significant correlation between the frequency of suitable habitat and eDNA detection of a given species. However, the models predicted suitable habitat at far more catchments on average than eDNA detected species signals—an observation in line with realized niches being smaller than fundamental niches.

For eDNA detections outside suitable habitat, the authors calculated the minimal distance to upstream suitable habitat patches, indicating possible sources of eDNA signals. They estimated a range of ~1 km, a distance significantly smaller than null model predictions and congruent with previous reported observations.

While eDNA and habitat suitability models gave very different pictures of freshwater species distributions and richness, the study showed how the techniques can complement and validate each other. Their integration could prove especially powerful in remote and hardly accessible landscapes or for elusive species, allowing for larger scale community monitoring.

Brantschen J, Fopp F, Adde A,
Keck F, Guisan A,
Pellissier L, et al

Switzerland

Habitat suitability models reveal the spatial signal of environmental DNA in riverine networks

Ecography

doi.org/10.1111/ecog.07267

Knowledge gaps in Southeast Asian insect conservation

16

Calyptomyrmex beccarii observed in Singapore by Melvyn Yeo (CC BY-NC 4.0)

CONSERVATION

659,490
SPECIES OCCURRENCES

Singapore, Malaysia, Timor-Leste, Thailand, Brunei, Darussalam, Philippines, Cambodia, Lao People's Democratic Republic, Viet Nam, Indonesia, Myanmar

Quantitative review of insect occurrence records, research papers and conservation-related social media posts suggests gaps and biases in knowledge and capacity

While rarely prioritized in biodiversity planning, insects make up most of terrestrial animal biodiversity. Global insect declines are well-documented, but in tropical biodiversity hotspots, such as Southeast Asia, limited data on population dynamics hampers conservation efforts. To identify knowledge gaps in the region, this study carried out a quantitative assessment of insect occurrence data, published studies and global social media content published since 2001. Their analysis relied on more than 650,000 GBIF-mediated species occurrences, 15,000 primary literature records and 1.3 million social media posts, tagged '#conservation'.

Citizen science butterfly records predominated occurrence data with nearly 50 per cent shared through iNaturalist and more than 40 per cent belonging to Lepidoptera—respectively. The authors observed significant gaps in data in Myanmar and parts of Indonesia. Singapore had the highest density of records, while Malaysia accounted for most records overall.

Among published studies on Southeast Asian insects, the authors noted a general increase in numbers in the study period. Local and regional authorship and funding also increased to more than 50 per cent by 2023. Thailand and Timor-Leste had the highest and lowest number of studies, respectively.

Less than three per cent of conservation-related social media posts focused on insects with bees and butterflies being the prevailing topics. World Bee Day (20 May) saw the highest number of conservation-related posts on insects.

Overall, the study shows uneven taxonomic and geographic representation in studies and clear bias towards charismatic insect orders in occurrence data and social media discourse. The authors call for political prioritization and funding to increase engagement initiatives, local biodiversity monitoring and integrative taxonomic approaches to improve insect conservation efforts in the region.

Ong XR, Tan B, Chang CH, Puniamoorthy N, Slade EM

Singapore, United States

Identifying the Knowledge and Capacity Gaps in Southeast Asian Insect Conservation

Ecology Letters

doi.org/10.1111/ele.70038

A mass extinction event that never happened

17

Gasteranthus extinctus *observed* *near El Mirador, Ecuador by Dawson White* (*CC BY-NC 4.0*)

CONSERVATION

4,837,795
SPECIES OCCURRENCES

Ecuador

Newly synthesized checklists based on GBIF-mediated occurrences combined with fieldwork disproves Centinelan extinction hypothesis

After years of surveying the Centinela mountain ridge in Western Ecuador, botanists Calaway Dodson and Al Gentry published results in 1991 reporting a unique flora that included 90 endemic plants. Centinela became a notorious example of instant extinction caused by deforestation of a hyperdiverse cloud forest.

To start testing the hypothesis of the so-called "Centinelan extinction," this large team of authors from Ecuador and the United States assembled a current species checklist for the site. Using GBIF-mediated data along with additional digital collection databases and unpublished checklists, they accumulated more than 2,000 specimens representing 886 unique and taxonomically valid species.

Because Dodson and Gentry's paper didn't include a full list of the presumed endemics, the authors reconstructed the list based on older, unpublished work from the site that focuses on collections with new or undetermined status. This exercise yielded 98 species, aligning well with the 90 plants Dodson and Gentry originally suggested as endemic to the Centinela ridge and suspected to be extinct.

When comparing the new and reconstructed lists, the authors found that only a single species, *Bifrenaria integrilabia*, had not been collected or reported outside Centinela, and none were extinct. In fact, nearly all the supporting collections had already taken place when Dodson and Gentry's paper came out in 1991, although the specimens were not yet digitized. Fieldwork in Centinela by the authors from 2021 to 2023 also revealed numerous small remnants of original forest that harboured several of the alleged microendemics.

While refuting the "Centinelan extinction" hypothesis, this work shows an immense conservation value of the larger region and highlights the importance of well-curated biological collections, digitized and shared openly, to improve understanding of the extinction risks that plants face worldwide.

White DM, Pitman NCA, Feeley KJ, Rivas-Torres G, Bravo-Sánchez S, Sánchez-Parrales F et al

Ecuador, France, United States

Refuting the hypothesis of Centinelan extinction at its place of origin

Nature Plants

doi.org/10.1038/s41477-024-01832-7

Rough seas ahead: Climate change unlikely to expand habitat ranges of commercial squid

18

Longfin inshore squid (Doryteuthis pealeii) observed near Rockport, MA, USA by alex_shure (CC BY-NC 4.0)

MARINE

CLIMATE CHANGE

271,819
SPECIES OCCURRENCES

Squid in the Southern Hemisphere stand to be most negatively affected under future climate scenarios

Greenhouse gases are predicted to alter the physiochemical properties of oceans globally over the coming decades. However, under different climate scenarios these effects may have varying impacts on biodiversity.

Squids and other cephalopods play a crucial role in global food webs, accounting for up to one quarter of mollusc biomass. Squids in particular, comprise approximately 70 per cent of cephalopods used for human consumption.

In this study, researchers tested the hypothesis that climate change may have positive effects on 12 commercially harvested squid species, as some species have been observed to expand their ranges and abundances poleward as a response to changing climates over the past 60 years. Researchers hypothesized that these changes were the result of adaptative capacity of squid to cope with environmental shifts, and therefore amplified pressures from climate change may lead to increased ranges and abundances for cephalopods.

Using species distribution models based on occurrence records from GBIF and OBIS, and climate models for the periods 2000–2014 and 2050–2100 under different emission scenarios, the authors found that habitat suitability (interpreted as a proxy for squid abundance) varied by region and species.

They primarily observed increases in habitat suitability for species found north of 50°N (e.g. near North America), whereas tropical regions showed a projected decrease. These effects were more pronounced under high-emission scenarios, with Southern Hemisphere regions being the most negatively impacted. Overall, the results of this study contradicted the original hypothesis, indicating that commercially important squid species are unlikely to benefit from amplified effects of climate change, with the majority of the studied species unlikely to experience increased habitat suitability.

Guerreiro MF, Borges FO, Santos CP, Xavier JC, Hoving HJ, Rosa R

Germany, United Kingdom, Portugal

Impact of climate change on the distribution and habitat suitability of the world's main commercial squids

Marine Biology

doi.org/10.1007/s00227-023-04261-w

Sea spiders more connected in colder and deeper Antarctic waters

19

Decolopoda australis observed near Southern Ocean, Antarctica by davidcothran (CC BY 4.0)

MARINE

EVOLUTION

ECOLOGY

44,979
SPECIES OCCURRENCES

Antarctica

Study uses pycnogonids as a case study to investigate how species richness varies across the Antarctic Polar Front

The seafloor south of the Antarctic Polar Front is the coldest marine habitat on Earth, and is thought to act as a biological barrier, with species diversity and distribution differing on either side. Although marine Antarctic conditions are harsh, these deep-sea waters have given rise to uniquely adapted benthic species such as sea spiders (Pycnogonida), largely due to nutrient-rich and stable conditions.

Twenty per cent of all known sea spider species are found in the Southern Ocean which is the only place where all pycnogonid families are represented. This has led to the hypothesis that the Southern Ocean may be the evolutionary centre for extant lineages.

A recent study used pycnogonids as a case study to investigate species distribution across the Antarctic Polar Front as they are slow moving benthic animals with limited dispersal capacity. Researchers applied spatial mapping using occurrence data from GBIF and OBIS covering 254 sea spider species from 2,187 sampling locations to identify patterns in species richness and diversity hotspots.

They found that sea spider communities north and south of the Polar Front were distinct at depths shallower than 1000 m. However, below this depth, communities became more mixed with the highest species richness observed below 2000 m. Authors concluded that the Polar Front appears to act as a semipermeable barrier to species exchange, with pycnogonids likely being better adapted to colder, deeper waters. Despite their apparent high diversity and competitive advantage in extreme environments in the Southern Ocean, pycnogonids may be particularly vulnerable to the impacts of ongoing ocean warming.

Maxwell J, Griffiths H, Allcock AL

Ireland, United Kingdom

Antarctica is less isolated with increasing depth - evidence from pycnogonids

Biodiversity and Conservation

doi.org/10.1007/s10531-024-02876-z

Oldest trick in the book: Analysing distributions of trickster species in folklore

20

Raccoon (Procyon lotor) observed in Atlanta, GA, USA by Isabelle Cormier (CC BY-NC 4.0)

BIOGEOGRAPHY

93,090,848
SPECIES OCCURRENCES

Study of interactions between ecology and culture shows that animals in folklore are bound by nearly same distributional constraints as in real life

Folklore incorporates themes beyond time and space, and stories often include anthropomorphic representations of animals and creatures that do not exist in the real world. While such myths may seem limited by imagination only, not all themes are universal and cognitive constraints still apply.

In a fantastical study of mythical creatures, researchers focused on a specific character in zoological folklore: the trickster, a character type that performs tricks and deceptions or exhibits mischievous behaviours, such as stealing and cheating. Using a global database of myths that includes 3,000 unique motifs categorized by properties and indexed by geographic coordinates, researchers identified 16 potential trickster animals (e.g., badgers, mice, raccoons and rabbits) which they included in their analysis.

The authors downloaded GBIF-mediated occurrences of trickster-matched taxa and created a global hexagonal grid of 842 cells that coded the presence of both real-life and mythical tricksters. By applying data on annual mean temperature and precipitation, they also assigned a biome class to each hex cell.

Initial analysis showed that the distributions of 12 of the 16 real animals were constrained by climate, constraints that were less evident for trickster animals' distributions. But by calculating distribution probabilities, the authors showed that the presence of real animals was an almost necessary condition for the presence of trickster animals.

The study demonstrates how ecological and climatic conditions have dominant effects on contents in folklore. While rabbits and raccoons may lie and steal, their presence in myths somehow remains limited to their local distributional ranges.

Shibasaki S, Nakadai R, Nakawake Y.

Japan

Biogeographical distributions of trickster animals

Royal Society Open Science

doi.org/10.1098/rsos.231577

Citizen science data reveals the world's "lost" birds

21

Long-billed bush warbler (Locustella major) observed in Northern Areas, Pakistan by James Eaton (CC0)

CITIZEN SCIENCE

11,689,362
SPECIES OCCURRENCES

With nearly complete coverage of global avifauna, citizen science derived data has potential to reveal meaningful absences signifying species lost to science and possibly extinct

With immense quantities of data of broad spatial, temporal and taxonomic scale, citizen science offers one of the only practical solutions to filling remaining gaps in biodiversity knowledge. Projects such as eBird, Xeno-Canto and iNaturalist have become so popular that bird datasets now make up more than half of all species occurrences in GBIF.

In this study, researchers evaluated the potential of citizen science data to reveal meaningful absences and establish bird taxa "lost" to science. The authors combined all occurrences from Macaulay Library and Xeno-canto with "research-grade" iNaturalist observations—mediated by GBIF—representing the most complete databases of media-supported bird observations.

Analysing more than 42 million vouchered observations between 2012 and 2021, the authors identified evidence of more than 98.8 per cent of the almost 12,000 examined bird species. Only 144 species did not have any supporting media for the 10-year period, meeting the authors' criteria for being lost. The median time since last documented occurrence for lost species was 54 years.

Most lost species were tropical residents with small island or montane distributions in Oceania (56 species), Africa (31 species), Asia (27 species) and South America (19 species). The lost birds spanned the full spectrum of IUCN Red List categories from Data Deficient (12 per cent) to Critically Endangered (41 per cent), but twenty-six per cent of the lost species were not considered threatened.

Nine lost species were documented following the study's 10-year timeframe (including the long-billed bush warbler shown above from 2022). When compared with previous global bird inventories, the current study found recent evidence of 24 species, while adding 67 new species to the list of lost species. Focused studies will determine whether these are secure within uninhabited, wilderness terrain seldom visited by citizen scientists or truly lost.

Rutt CL, Miller ET, Berryman AJ, Safford RJ, Biggs C, Mittermeier JC

United Kingdom

Global gaps in citizen-science data reveal the world's "lost" birds

Frontiers in Ecology and the Environment

doi.org/10.1002/fee.2778

GBIF-mediated weeds: a proxy for agricultural intensification in the EU

22

Spiny cocklebur (Xanthium spinosum) observed in Vácrátót, Hungary by Attila Lengyel (CC BY-NC 4.0)

AGRICULTURE

ECOSYSTEM SERVICES

2,082,796
SPECIES OCCURRENCES

Study explores the use of maize-associated weed occurrences across the European Union to identify potential indicator species for agricultural intensification

Agricultural intensification is a multivariate process acting at multiple spatial scales influencing the composition and structure of wild species communities in farmlands. It is a major driver of direct and indirect species loss of both plants and animals, and the ecosystem services these provide to agriculture.

Protecting farmland biodiversity and reversing agroecosystems degradation requires robust monitoring frameworks. In addition to formal survey and monitoring schemes, data from citizen science initiatives may help the development of relevant indicators. In this study, authors explored the feasibility of GBIF-mediated weed occurrences as indicators of agricultural intensification, focusing on maize and associated species as a case study.

The authors used a fine-scale map of crops in Europe based on satellite data, from which they derived levels of agricultural intensification based on proportion of maize within each 1 km grid cell. They compiled an exhaustive list of 204 weeds associated with maize crops in Europe and downloaded GBIF-mediated occurrences to assess species richness and identify potential indicator species.

Their analysis demonstrated how species richness decreased as the share of maize increased. By exploring the species only present in cells with the lowest maize share, the authors identified a group of 12 species sensitive to agricultural intensification and thus potential indicator species.

To validate the approach, the authors compared the 12 sensitive species with 25 non-sensitive species in terms of growth in number of occurrences on arable land vs non-arable land. In the latter, occurrences grew significantly along the time series, whereas arable lands showed no growth. These results combined suggest an overall negative effect of agriculture on the most sensitive species of the community and highlights the potential role of GBIF-mediated data in assessing agricultural intensification.

Rotllan-Puig X, Guerrero I, d'Andrimont R, van der Velde M

Spain

Can open access weeds occurrences across the European Union become a proxy for agricultural intensification?

Ecological Indicators

doi.org/10.1016/j.ecolind.2024.112664

On the origin of crocodiles

23

Nile crocodile (Crocodylus niloticus) observed in Kruger National Park, South Africa by Chris Rehberg (CC BY-NC 4.0)

BIOGEOGRAPHY
EVOLUTION
PHYLOGENETICS

183,512
SPECIES OCCURRENCES

Biogeographical study reveals the likely area where crocodile ancestors evolved and links saltwater tolerance to transoceanic dispersal events

With the exception of Europe and Antarctica, crocodiles occur on every continent of the planet in humid, tropical regions. All modern crocodilian species including alligators, caimans, crocodiles and gharials belong to the Neosuchia clade. Despite progress in evolutionary studies, many aspects of neosuchian biogeography remain disputed, including where neosuchians first evolved.

Relying on state-of-the-art phylogenetic approaches, this study attempts to fill some of the gaps in our knowledge of neosuchian crocodiles. Using two different sets of phylogenies combined with occurrence data from the Paleobiology Database for fossils and GBIF for extant taxa, authors carried out biogeographical analyses to estimate the ancestral ranges of the studied taxa.

Their results place the origin of Neosuchia in northwestern parts of the Pangaean supercontinent around 200 million years ago with subsequent radiations into Gondwana. Eusuchia, the earliest common ancestor of modern crocodilians, likely emerged in Europe 145 million years ago and later dispersed into the North American and Asian landmasses.

The study finally explored whether transoceanic dispersal events could be linked to saltwater tolerance in crocodilian taxa. This analysis showed that such events were less likely to have taken place for alligatoroids, which is consistent with the saltwater intolerant physiology of modern alligators.

Groh SS, Upchurch P, Day JJ, Barrett PM

United Kingdom

The biogeographic history of neosuchian crocodiles and the impact of saltwater tolerance variability

Royal Society Open Science

doi.org/10.1098/rsos.230725

Future threat of invasive species to European ecosystem services

24

Coypu (Myocastor coypus) observed in Saintes-Maries-de-la-Mer, France by David Torres (CC BY-NC 4.0)

INVASIVES

ECOSYSTEM SERVICES

8,829,830
SPECIES OCCURRENCES

Continental-scale analysis of invasive species and their adverse impacts on ecosystem services reveal widespread potential risks, but notes highest exposure in areas with lower provision of services

Invasive alien species threaten not only native biodiversity, but also pose risks to the provision of ecosystem services. While effects on species are well-documented, large-scale assessments of impact of invasive species on specific ecosystem services are largely absent.

Leveraging recent growth in the availability of species risk assessments, occurrence data and mapping of ecosystem services, this study provides a spatial evaluation of risks posed by 94 invasive species on seven ecosystem services in Europe. Based on European Union data, the list of species covered terrestrial and freshwater plants and animals, including 81 continental invaders and 13 species currently under assessment.

The researchers first obtained GBIF-mediated occurrences for their target species, gridding the data to a map at 10-arc minute resolution. They added spatial data on ecosystem services from the European Environmental Agency, selecting services with reported adverse impacts by the target species.

Assessing 658 combinations of invasive species and ecosystem services, the authors identified 269 potential impacts. Outdoor recreation, habitat maintenance and crop provision had most impacts, while timber provision and flood control had the fewest. They found the highest exposure to invasive species of concern in Western Europe where ecosystem contributions to crop provision and nitrogen retention were at their highest.

To predict the future impact of the invaders, they created species distribution models using 21 variables. By assigning risk categories based on both provision of services and future favourability of invasion, they revealed a substantial increase in risk, particularly along coastal areas. While the overall area suitable for invasion increased by 77 per cent, most areas with high ecosystem service provisioning, however, had low accessibility and climatic suitability for invasive species, thereby limiting exposure.

Gallardo B, Bacher S, Barbosa AM, Gallien L, González-Moreno P, Martínez-Bolea V, et al

Spain, Portugal, France, Switzerland, United Kingdom, United States

Risks posed by invasive species to the provision of ecosystem services in Europe

Nature Communications

doi.org/10.1038/s41467-024-46818-3

Seagrass mediates effects of climate change on future distribution of manatees

25

West Indian manatee (Trichechus manatus) observed in Belize by Rob Van Epps (CC BY-NC 4.0)

MARINE

FRESHWATER

CLIMATE CHANGE

35,072
SPECIES OCCURRENCES

Study finds proximity to freshwater and seagrass availability most important predictors of manatee distribution under climate change

Climate change may shift the ecological niches of species, forcing them to migrate poleward to track their optimal climatic conditions. For mobile species this might be simple, but if the dispersal ability of their essential foods is limited, migrations may be futile.

In this study, researchers employed species distribution modelling to better understand the ecology of the vulnerable West Indian manatee (*Trichechus manatus*) under climate change and thus inform conservation efforts.

For the models, the authors used GBIF-mediated manatee occurrences combined with climatic and physiographic variables, but also important data on consumer-resource interactions. As fully aquatic herbivores consuming nearly 10 per cent of their total body weight each day in aquatic plants, manatees rely on seagrasses for their survival. To account for this, the models included layers representing availability of seagrass and freshwater for hydration.

The models showed that 94 per cent of the manatee distribution overlapped with seagrass distribution. Seagrass and freshwater availability were the most important factors for manatee distribution with a combined contribution of 78 per cent. When projected into future climate scenarios, the models suggested marked declines in manatee ranges, mediated not only by direct effects of climate changes but especially by diminishing habitat suitability for seagrass.

These results call for comprehensive conservation efforts to secure a sustainable future for West Indian manatees. With climate change affecting all species, the study highlights the importance of considering biotic interactions in large scale distribution modelling.

Deeks E, Kratina P, Normande I, Da Silva Cerqueira A, Dawson T

United Kingdom, Brazil

Proximity to freshwater and seagrass availability mediate the impacts of climate change on the distribution of the West Indian manatee

Latin American Journal of Aquatic Mammals

doi.org/10.5597/lajam00321

Reevaluating cacao’s native range: Insights from genetic and biogeographic evidence

26

Cacao (Theobroma cacao) collected in Tobago. Photo via Royal Botanic Gardens, Kew. (CC BY 4.0)

BIOGEOGRAPHY

AGRICULTURE

SPECIES DISTRIBUTIONS

15,849
SPECIES OCCURRENCES

Human interference likely the biggest driver of cacao range expansion, challenging assumptions of natural occurrences

Cacao (*Theobroma cacao*) is a globally significant agricultural crop, primarily harvested for its seeds which are fermented and used for chocolate production. Thought to originate approximately 10 million years ago, the role of human intervention in shaping the distribution of the crop is not clear.

Previous studies suggested that cacao’s domestication involved introduction of Ecuadorian varieties into Mesoamerica, likely aided by Indigenous populations. In contrast, the distribution of cacao in Amazonian regions indicates historical ranges were more restricted due to limited dispersal by wildlife such as mammals and birds. This study sought to investigate the impact of human influence on the distribution of cacao by comparing areas identified as native ranges with introduced areas.

The authors conducted an extensive literature review to assess the origin, distribution and dispersal of cacao prior to human influence. They then analyzed over 15,000 GBIF-mediated occurrence records of preserved specimens, along with remote sensing images and land-use profiles to differentiate between native and introduced ranges.

Results revealed a strong association between human-impacted areas and the presence of cacao specimens, potentially challenging conventional perceptions of the species’ native range. For example, evidence from archaeological sites indicates that Amazonian Indigenous peoples actively domesticated cacao. However, genetic and biogeographic data suggest that cacao’s true native range is likely limited to parts of Ecuador, Colombia, Peru and the westernmost region of Brazil, which overlap with areas of the high genetic diversity.

The study provides evidence that cacao’s present-day distribution is largely the result of human activity, while wild populations are restricted to a smaller native range. These findings may have significant scientific, conservation and legal implications for genetic resource ownership and biodiversity policy concerning cacao.

Colli-Silva M, Richardson JE, Figueira A, Pirani JR

United Kingdom, Brazil, Ireland, Colombia

Human influence on the distribution of cacao: insights from remote sensing and biogeography

Biodiversity and Conservation

dx.doi.org/10.1007/s10531-023-02777-7

Fewer species invade Indigenous peoples' lands than other lands

27

Red fox (*Vulpes vulpes*) observed in Melbourne, Australia by andrewk (CC BY-NC 4.0)

INVASIVES

866,977,420
SPECIES OCCURRENCES

Quantifying invasions on Indigenous-held lands, study finds less than one third as many invasive species as on other lands, suggesting potential importance of sustainable management practices

While colonization by European empires before 1900 resulted in the spread of uncountable species, the current level of biological invasions in Indigenous peoples' lands (IPLs) compared to other lands is unknown. Covering at least 28 per cent of Earth's terrestrial surface worldwide, IPLs play an important role in biodiversity conservation through land stewardship and management practices.

By integrating comprehensive global spatial layers of IPLs, a cross-taxonomic collection of regional alien species, and species occurrences from GBIF and OBIS, this study quantified the level of invasions on IPLs. The initial analysis revealed 128,515 records of 6,192 alien species on IPLs worldwide.

The number of alien species on IPLs correlated significantly with the total number of alien species in a given country. Overall, however, IPLs had less than one-third of the number of alien species found on other lands. Other metrics of human impact appeared to follow this trend with higher forest cover, less cultivated land, lower road density and less night-time light on IPLs versus other lands. But the number of alien species remained significantly lower on IPLs than on other lands even after accounting for variation in sampling, human infrastructure, population size and land cover.

Australia stood out with both disproportionately high and low alien species numbers on IPLs in the country. This difference more likely resulted from an interplay of regional factors, with IPLs close to large urban areas having high alien species numbers while numbers in remote IPLs in central and northwestern Australia are low.

Overall, the study show that IPLs are more resistant to biological invasions and highlights the role of Indigenous peoples in protecting nature and providing refuges for threatened native species. To explain the prevalence of biological invasions on other sites, the authors suggest that Indigenous peoples often apply land management practices that are more sustainable than most modern methods.

Seebens H, Niamir A, Essl F, Garnett ST, Kumagai JA, Molnár Z, et al

Hungary, Germany, Austria, Australia, United States

Biological invasions on Indigenous peoples' lands

Nature Sustainability

doi.org/10.1038/s41893-024-01361-3

Drivers of species invasions in new territories

28

Hong Y, Yuan Z, Liu X
China
Global drivers of the conservation–invasion paradox
Conservation Biology
doi.org/10.1111/cobi.14290

Japanese macaque (Macaca fuscata) observed near Nagano, Japan by Reflectitur Photons (CC BY-NC 4.0)

EVOLUTION

CONSERVATION

ECOLOGY

2,580,377
SPECIES OCCURRENCES

Exploring the conservation-invasion paradox on a global scale

Species may become threatened in their native ranges for a variety of reasons including competition, resource availability, climatic changes and lack of genetic diversity. The conservation-invasion paradox (CIP) is a phenomenon observed when species threatened in their native ranges are able to successfully sustain viable populations when introduced to other regions. This has been observed across a range of taxa including mammals, birds, insects, reptiles and plants; however there is currently limited understanding of factors driving CIP introductions globally.

To better understand this process, this study assessed potential factors affecting CIP events by compiling a global database of 1,071 threatened terrestrial vertebrate introduction events (based on IUCN Red List assessments) across 174 species. The authors quantified and tested the importance of factors such as location, event and species levels using data accessed through GBIF and generalized linear mixed models.

Authors identified three main threat factors that determined the occurrence of CIP events. These were the greater the introduction event, the more likely a successful establishment event is to occur, increased chance of success when species are phylogenetically closely related to native species in a new region and lack of natural enemies in non-native ranges.

They concluded that CIP events were most likely to succeed in Australia, the eastern hemisphere and in areas with fewer native threats, especially with less climate warming. Although this study provides a basis for informing threatened species conservation and invasive species mitigation strategies, caution must be taken when considering species introductions to non-native ranges due to their impact to local ecological communities.

Some like it hot: latitudinal range predicts response to warming for freshwater fish

29

European eel (*Anguilla anguilla*) observed in Lombardy, Italy by Mattia (CC BY-NC 4.0)

FRESHWATER

CLIMATE CHANGE

20,609,971
SPECIES OCCURRENCES

Population time-series analysis coupled with GBIF-mediated ranges shows warming leads to declines towards the equator but increases towards the poles

Distributional range shifts caused by climate change are well-documented for both marine and terrestrial organisms. For freshwater species, particularly fish, higher water temperature means less dissolved oxygen and increased metabolism and thus food requirements, however, our understanding of actual responses of freshwater fish to climate warming is limited.

Using more than 90,000 species-specific abundance records from the RivFishTime database, researchers in this study analysed time series of community data of 632 riverine fish species worldwide from 1958 to 2019. They estimated water temperature at each location from terrestrial surface temperature to model the species' responses to warming.

To determine the relative location of a species' abundance record in its entire range, the authors used more than 20 million GBIF-mediated occurrences of the species of interest. This allowed them to test for climate change-driven poleward increases and declines around the equator in freshwater fish populations.

Their results showed significant surface temperature warming of 0.21°C per decade on average across survey locations and consistent patterns of population change since the 1950s. Changes in abundance were most evident in larger species with higher trophic levels and more widespread distributions.

Overall, their models suggested a dichotomous response to warming as increasing temperatures in poleward populations were correlated with increases in abundance, while equatorward populations saw decreases in abundance with increasing temperatures.

Brown TM, O'Connor J, Genner MJ

United Kingdom

Climate warming drives population trajectories of freshwater fish

Proceedings of the National Academy of Sciences

doi.org/10.1073/pnas.2410355121

Restoring cactus habitat in the Sonoran Desert

30

Saguaro (Carnegiea gigantea) observed in Peoria, AZ, USA by Eric Hough (CC BY-NC 4.0)

ECOLOGY

CONSERVATION

10,655,658
SPECIES OCCURRENCES

United States, Mexico

Study combines habitat suitability, biotic interactions and fire disturbance data to identify high-value restoration areas for the giant saguaro cactus

The Sonoran Desert is North America's most diverse desert, home to more than 500 vertebrate species and over 2,000 native plant species, including the iconic saguaro cactus (*Carnegiea gigantea*). Reaching up to 16 meters in height, saguaros can live for up to 250 years, taking up to 50 years to reach reproductive maturity.

Widespread desert wildfires have increased significantly over the last few years, and, despite its abundance, saguaro cacti are particularly vulnerable to fire damage. In this study, researchers set out to identify high-value restoration areas for the saguaro by exploring habitat suitability of the cactus itself alongside associated species known to promote saguaro growth, dispersion and germination.

The authors relied on GBIF-mediated occurrences combined with high-resolution environmental data to predict the geographic range of the saguaro, four nurse-plants and 63 associated animals. By locating hotspots of combined high suitability for the cactus and its helper species and overlaying these with wildfire burn data, they identified several high-value restoration areas, concentrated in the northeast portion of the Sonoran Desert.

Providing valuable information about the ecological restoration of the saguaro, these findings represent opportunities for protecting highly suitable habitat for the cactus and its associated species. The study suggests targeting unburned saguaro hotspots throughout the region to prioritize fire prevention, management of invasive species and other conservation efforts.

Albuquerque FS de, Rowe H, Búrquez A, Rey Benayas JM

United States, Mexico, Spain

Integrating habitat suitability, disturbance, and biotic interactions into the ecological restoration of the saguaro (Carnegiea gigantea) in drylands of the southwest of the United States and northern Mexico

Restoration Ecology

doi.org/10.1111/rec.14357

Digitizing natural history collections maximizes biodiversity data coverage in Canada

31

Red maple (Acer saccharinum) collected in Papineau, Canada by Marie-Victorin Herbarium, Université de Montréal Biodiversity Centre. (CC BY 4.0)

BIODIVERSITY SCIENCE

CITIZEN SCIENCE

7,519,260
SPECIES OCCURRENCES

Canada

Natural history collections contain less biased records than citizen science-derived observations

Since 2010, citizen science initiatives have generated more biodiversity records than what was collected through traditional scientific methods over the previous century. Advances in digital technologies have accelerated data collection and broadened public participation in biodiversity research. However, platforms like iNaturalist tend to favor conspicuous, charismatic species in urban areas, introducing taxonomic and spatial biases. Natural history collections are instead thought to be less biased and more representative of rare and rural species, though much of this information remains locked in undigitized, irreplaceable physical specimens.

To evaluate this claim, the authors analyzed all available vascular plant records in GBIF in Canada since 1900, totaling over 7.5 million records. Of these, 23 per cent were herbarium specimens, 72 per cent originated from iNaturalist, and fewer than five per cent originated from other sources. Researchers used ecological and environmental modeling to assess taxonomic, phylogenetic, functional and ecological niche coverage to understand data biases between herbarium specimens and citizen science records.

Herbarium records exhibited substantially less bias than iNaturalist data across nearly all metrics and were more effective in representing both plant biodiversity and species' environmental niches. Although individual plant species were on average represented 4.8 times more in iNaturalist observations than herbarium records, this oversampling disproportionately represented a small subset of taxa, with over half of all iNaturalist observations representing just four per cent of Canadian plant species.

The authors identified that digitizing existing natural history collections—estimated at three Canadian dollars per specimen—was the most effective strategy for expanding biodiversity coverage in Canada. By contrast, the study estimated that achieving equivalent benefits through iNaturalist would require approximately 27 million additional observations.

Eckert I, Bruneau A, Metsger DA, Joly S, Dickinson TA, Pollock LJ

Canada

Herbarium collections remain essential in the age of community science

Nature Communications

doi.org/10.1038/s41467-024-51899-1

Brown bears help mitigate effects of climate change on wild cherries

32

Cantabrian brown bear (Ursus arctos subsp. arctos) observed in Somiedo, Asturias, Spain by Martin Costechareire (CC BY-NC 4.0)

CLIMATE CHANGE

62
SPECIES OCCURRENCES

Spain

Climate change will decrease habitat suitability of wild cherry, but brown bears may facilitate dispersal to more suitable areas

Ecological interactions are important when considering the effects of climate change. When changing temperature and precipitation alter the climatic suitability for one species, it will affect any other species that depend on it.

In this study, researchers studied the potential effects of climate change on wild cherry and subsequent consequences for brown bear populations in the Cantabrian Mountains in northern Spain. With rising temperatures in the area, previous studies have shown that cherries have become an increasingly important part of the diet of brown bears in recent years.

Based on field sampling, forest inventories, Google Street View inspections and GBIF-mediated data, the authors built an extensive database of wild cherry occurrences, which coupled with relevant climatic predictors formed the basis of a distribution model. To assess the extent of berry consumption and potential seed dispersal, they used georeferenced data on bear faeces collected through regional bear-monitoring projects and classified by cherry seed presence.

Their results showed that cherry habitat suitability was very sensitive to predictors related to water, especially soil water volume and seasonality of precipitation. Climate change was predicted to decrease overall habitat suitability, shifting climatic optimums in a south-eastern direction and towards higher elevations.

The models, however, also suggested high availability of cherries for Cantabrian brown bears regardless of climate change scenario. The analysis of seed-containing bear droppings also showed a potential for long-distance dispersal, which may facilitate the expansion of wild cherry to higher altitudes within both current and future bear ranges.

Pérez-Girón JC, Álvarez-Álvarez P, Ballesteros F, López-Bao JV

Spain

Potential impacts of climate change on wild cherry distribution and associated consequences on brown bears

Biological Conservation

doi.org/10.1016/j.biocon.2023.110390

Shark attack: hammerheads threatened by climate-induced shifts in habitat suitability

33

Scalloped hammerheads (Sphyrna lewini) observed near Galápagos, Ecuador by R Lai (CC BY-NC 4.0)

CLIMATE CHANGE

MARINE

4,454
SPECIES OCCURRENCES

Modelling habitats of three hammerhead shark species, study predict future reductions in suitability and range shifts with increased exposure to fisheries

Known for their unique adaptations, in particular the peculiar head shape, hammerhead sharks (family Sphyrnidae) represent one of the youngest shark lineages, but also one of the most threatened phylogenetic branches. Global hammerhead populations are rapidly declining, especially due to bycatch mortality, and climate change may exacerbate this by forcing sharks closer to fisheries worldwide.

In this study of three species—great hammerhead (*Sphyrna mokarran*), scalloped hammerhead (*S. lewini*) and smooth hammerhead (*S. zygaena*)—researchers explored how future oceanographic conditions will likely affect the global patterns of habitat suitability for large hammerhead sharks.

Using GBIF-mediated occurrences coupled with environmental data on sea surface temperature, salinity, chlorophyll, current velocity, and bathymetry (depth of the seafloor), the authors built habitat suitability models for each species at current conditions, as well as mid- and end of the century. Considering four future scenarios of emissions severity, they created a total of nine models for each hammerhead shark.

Across the models, bathymetry, temperature and salinity were the most important predictors of shark habitat suitability. Regardless of emission scenario and timeframe, the models predicted significant declines in global habitat suitability for *S. lewini* and *S. zygaena*, while projections for *S. mokarran* suggested a modest mid-century expansion, however, insubstantial by the end of the century under the most severe emission scenario.

As a consequence of future projections, the models predicted poleward range shift for all three species with the scale increasing over time and with emission scenario severity. These shifts as well as regional shifts may affect population connectivity and increase exposure to other anthropogenic pressures, such as fisheries. The combined results highlight the importance of considering climate change as a factor when assessing species' extinction risks.

Santos CP, Borges FO, Guerreiro M, Pissarra V, Varela J, Frazão-Santos C, et al

Germany, Portugal, United Kingdom

Shifts in the habitat suitability for large hammerhead sharks under climate change

Marine Biology

doi.org/10.1007/s00227-024-04512-4

Underestimated threats to global tree biodiversity

34

Betula pubescens var. pumila observed *near Lake Nakomyaken, Russia by Игорь Поспелов* (CC BY-NC 4.0)

CONSERVATION

18,612,197
SPECIES OCCURRENCES

Data-driven study suggests more than 17,000 tree species are at risk from rapid global change

Trees provide habitat to half of the world's known terrestrial biodiversity and are undeniably important to both nature and humans, who gain significant economical, cultural and spiritual value from them. While extinction risk assessments have been completed for more than 92 per cent of trees, that leaves 7,700 species whose conservation status remains unassessed due to data deficiency.

To prioritize tree species for (re-)assessment, this study used a data-driven approach that analyses the exposure of 32,000 species to change in six anthropogenic threats over the last two decades. For each species, authors obtained occurrence records from open-access aggregators (including both the Atlas of Living Australia and GBIF) to define the extent of occurrence based on minimum convex polygons covering 95 per cent of available records.

They then added layers representing threats—agricultural expansion, overexploitation, urban expansion, deforestation, fire and climate change—for the period 2000–2020, calculating the recent rate of change per threat for each species. They finally downloaded the latest available IUCN assessments, linking these to the studied species.

Their analysis revealed that, while more than half the species in this study have been exposed to increasing threats over the past two decades, less than 10 per cent are currently considered threatened according to the IUCN Red List. Many of these remain unevaluated, and about half the candidates are listed as Near Threatened or Least Concern. In addition, the Red List assessments of 35 per cent of trees are older than 25 years.

Most species exposed to high rates of recent change were found in South America, sub-Saharan Africa and tropical Southeast Asia, but relative to overall number of species present, threat hotspots occurred in Arctic regions of North America and Eurasia. Combined, the results of the study suggests a substantial underestimation of threats and associated extinction risk for trees.

Boonman CCF, Serra-Diaz JM, Hoeks S, Guo WY, Enquist BJ, Maitner B, et al

France, Netherlands, United States, United Kingdom, China, Denmark

More than 17,000 tree species are at risk from rapid global change

Nature Communications

doi.org/10.1038/s41467-023-44321-9

Human-controlled fire drives colour divergence in gecko lineages

35

Moorish gecko (Tarentola mauritanica) observed near Castilla-La Mancha, Spain by Goro Saber Animal (CC BY-NC 4.0)

EVOLUTION

ECOLOGY

70,639
SPECIES OCCURRENCES

Arthropods attracted to human-controlled fire create untapped foraging niches for geckoes

Fire has been an important tool used by humans for cooking, warmth, repelling predators and cultural interactions since the Pleistocene era. These actions have contributed to "daylight extension" in which humans continue peak activities late into evening hours, a behaviour uncommonly observed in mammals other than primates.

Although fire has historically been used as a deterrent to surrounding biodiversity in human-populated areas, a recent study investigated the possibility that the use of fire at night creates previously untapped foraging niches suitable for insectivorous vertebrates.

Authors used Moorish geckos (*Tarentola mauritanica*) as a case study to investigate whether human-controlled fire has historically influenced temporal niche partitioning between dark-diurnal and pale-nocturnal lineages.

They assessed melanophore density in historical skin samples of light and dark specimens and applied species distribution modelling using GBIF-mediated records combined with phylogenetic analyses to determine the likelihood of human–gecko coexistence and approximate period of lineage divergence. Arthropod attraction to fire was also evaluated by recording the class and volume of insects on the inside walls of controlled light and dark firepits.

Genomic analyses indicated that pale and dark gecko lineages diverged approximately 6,600 years ago, coinciding with the transition of modern humans from nomadic hunter-gatherers to settled agricultural communities. Authors additionally demonstrated fire did attract phototactic arthropods, creating a new prey resource for vertebrates like geckos.

Findings imply that human-controlled fire may have created a novel foraging niche for pale-nocturnal geckos, likely driving the divergence of the gecko variants.

Fulgione D, Russo D, Rivieccio E,
Maselli V, Avallone B,
Mondanaro A, et al

Flame-forged divergence?
Ancient human fires and
the evolution of diurnal and
nocturnal lineages in
moorish geckos

iScience

doi.org/10.1016/j.isci.2024.111715

Successful evolutionary tactics attract birds to disperse mimetic seeds

36

Gang-gang cockatoo (Callocephalon fimbriatum) observed in Victoria, Australia. Photo by hone (CC BY 4.0)

EVOLUTION

ECOLOGY

167,561
SPECIES OCCURRENCES

Mimetic seeds were found to trade-off visual appeal over nutritional value to appeal to bird dispersers

Seed dispersal is crucial for flowering plants to pass on genetic material, with some species resorting to using deceptive tactics to maximize their disperal potential. Mimetic seed species have evolved to display a variety of traits to visually attract bird dispersers. While this strategy has been observed in seed species across the world, it has historically been poorly understood.

This study reviewed the global distribution and traits of mimetic seed species and their interactions with birds. Using GBIF-mediated occurrence records, researchers found that mimetic species are mainly clustered in tropical regions, especially along coasts and islands. Through field observations and comparative analyses, the authors found commonalities in traits displayed by mimetic seeds such as mimicking fleshy-fruiting bodies and often being red and/or black in colour, thought to increase visibility and attractiveness to birds. Likewise, authors observed that many species had hard coats and waxy surfaces, likely as an adaptation to survive digestion and promote long-distance dispersal by birds.

To explain these traits, authors suggest that mimetic seed dispersal may follow an "energy-reallocation strategy," whereby seeds invest in visual signals rather than nutrition for dispersers. In comparison, fleshy-fruited plants typically use a "reward strategy" to attract dispersers through actual nutritional offerings. Authors noted that if mimetic strategies become too common, bird fitness may decline due to reduced food value, potentially leading to shifts in bird foraging behaviour that impact both mimetic and non-mimetic plant species.

Findings concluded that deeper genetic and chemistry research into secondary evolutionary traits responsible for imitative features is needed to better understand co-evolutionary pressures between mimetic seeds and dispersers. Authors proposed using game theory to understand this co-evolutionary process under different scenarios and amongst different dispersers other than birds.

Jin MF, Cai XH, Chen G

China

Seed dispersal by deception: A game between mimetic seeds and their bird dispersers

Plant Diversity

doi.org/10.1016/j.pld.2024.07.006

Can big data accurately quantify vertebrate diversity in protected areas?

37

Delacour's langur (Trachypithecus delacouri) observed near Ninh Binh, Viet Nam by billyschofield (CC BY-NC 4.0)

CONSERVATION

18,164,161
SPECIES OCCURRENCES

Study compares GBIF and IUCN, assessing their ability to accurately predict species richness in protected areas worldwide, finding significant bias in both

Protected areas (PAs) can be a valuable tool in mitigating the current global biodiversity crisis. As the Kunming–Montreal Global Biodiversity Framework mandates protection of at least 30 per cent of the global surface by 2030, optimizing and prioritizing areas for protection is crucial.

Assessing the effectiveness of PAs at scale requires large datasets, and researchers often use data from GBIF and/or IUCN to support their findings. This study sought to evaluate differences and biases between the two repositories in describing the patterns of threatened vertebrates in the global system of PAs.

The authors first compiled a list of all terrestrial vertebrates from any threatened category according to the IUCN Red List. For each of the 7,188 species, they gathered map polygons from IUCN and occurrence records from GBIF, which they combined with geographical data on more than 120,000 PAs worldwide.

For each source, they summarized the number of threatened vertebrates present, finding at least one species in each PA. Overall, the average species richness per PA reported was 150 per cent higher for IUCN than GBIF. To assess the accuracy of both sources, the authors conducted an extensive literature review—of studies quantifying threatened species in PAs—to establish an independent baseline.

When considering GBIF and IUCN combined, this exercise revealed notable disparities across continents with low bias in Europe and North America and substantial bias in South America, Africa and Asia. Overall, on average IUCN data overestimated predictions of species richness by 575 per cent while GBIF underestimated species richness by 63 per cent.

Cordier JM, Osorio-Olvera L,
Huais PY, Tomba AN,
Villalobos F, Nori J

Argentina, Mexico

Capability of big data to capture
threatened vertebrate diversity
in protected areas

Conservation Biology

doi.org/10.1111/cobi.14371

Pollinator distribution analyses provide insight into extinction risk in India

38

Indian giant squirrel (Ratufa indica) observed near Kerala, India by Vijay Anand Ismavel (CC BY-NC 4.0)

CONSERVATION

SPECIES DISTRIBUTION

869,447
SPECIES OCCURRENCES

India

IUCN Red List category was found to be biased towards mammalian pollinators, however, study suggests that both birds and mammal pollinators are in decline

Pollinators are essential to sustaining life on Earth, valued both for their economic importance and their role in regulating ecosystems. Historically, insect species have been the main focus of pollinator research, with vertebrates comparatively poorly represented. To better understand the role of pollinators in a megabiodiverse country with major anthropogenic impacts, authors in this study sought to quantify the macroecological patterns of species richness and extinction risk of bird and mammal pollinators in India.

Researchers compiled a database of vertebrate pollinators (birds and mammals) in India by reviewing nearly 4,000 studies, identifying 85 key species (67 birds, 18 mammals). IUCN Red List data was used to assess extinction risk and population trends, and species locations were mapped using GBIF-mediated datasets to show species richness, threat status and population trends. Range size was estimated and used to predict extinction risk based on traits like body size and reproduction using phylogenetic models.

Results revealed that mammalian pollinator diversity was more concentrated in particular regions (specifically around the Western Ghats), whereas bird pollinator diversity was found more broadly across the country. IUCN Red List category data indicated a quarter of mammalian species are currently threatened with extinction, however, this study suggests that one in four bird and one in two mammal species are in decline.

The authors determined that species traits were unlikely to be the main drivers of these results, instead threats such as agricultural land use, logging and hunting practices were all significant drivers of population declines. They proposed increased research and public education measures as key factors needed to curb the rate of pollinator species decline.

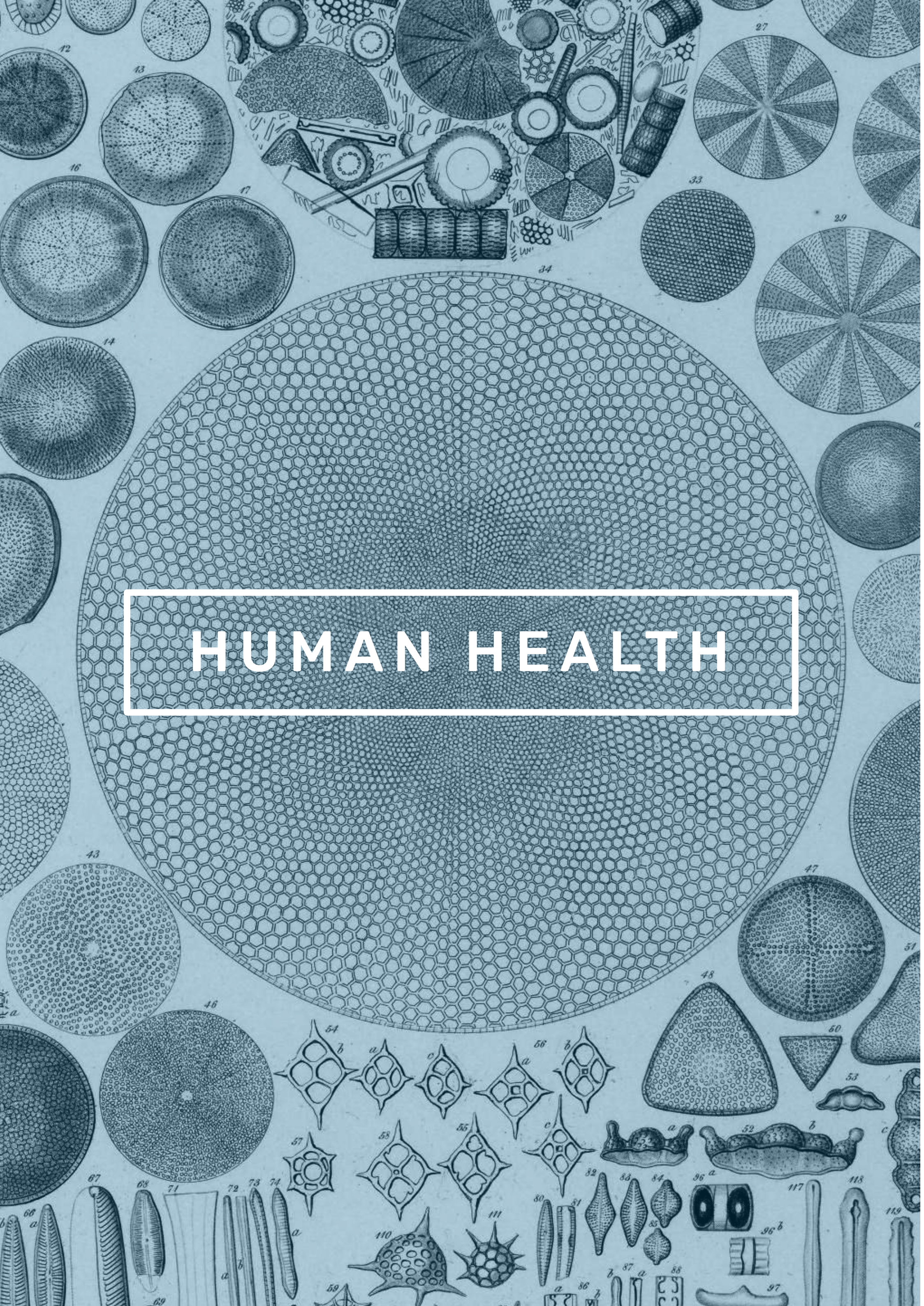
Kallivalappil R, Grattarola F,
de Alwis Pitts D, Cotter SC,
Pincheira-Donoso D

Czechia, United Kingdom,
United Arab Emirates

Species diversity and extinction
risk of vertebrate pollinators
in India

Biodiversity and Conservation

doi.org/10.1007/s10531-024-02848-3



HUMAN HEALTH

About this special section

PALOMA SHIMABUKURO

GBIF contractor - Data on disease vectors

In an era marked by escalating environmental pressures and emerging global health threats, understanding the intricate ties between biodiversity and human health has never been more urgent. This special section on health in the GBIF Science Review brings together research that illuminates the complex interplay between ecosystems and public health outcomes, illustrating aspects of the One Health concept, in which human, animal and environmental health are deeply connected. From modelling the risk of zoonotic diseases like monkeypox and relapsing fever to tracing the ecological dynamics of pathogens in wild birds and plague reservoirs, these studies exemplify the transformative potential of biodiversity data in predicting and mitigating health risks.

By harnessing GBIF-mediated data, researchers are deploying tools—such as species distribution modelling, climate-informed risk mapping, and integrative ecological analyses—to explore the environmental determinants of disease and health. These efforts span diverse contexts: the impact of gold mining on ecosystem services, the overlooked biodiversity within the human microbiome, and the habitat shifts of species during COVID-19 lockdowns. Collectively, they reveal how shifts in land use, climate and wildlife interactions ripple across human health systems. By framing biodiversity as foundational to global health, these contributions reinforce a vital truth: sustainable health outcomes are deeply rooted in ecological understanding. This section invites readers to explore the frontiers where biodiversity science meets human health, research and planetary sustainability.

Global distribution and diversity of wild-bird-associated pathogens

39

Indian spot-billed duck (Anas poecilorhyncha) observed in Bangalore, India by vipin_biodiversity (CC BY-NC 4.0)

HUMAN HEALTH

320,159,643
SPECIES OCCURRENCES

Study compiles knowledge on zoonotic and emerging pathogens carried by wild birds, revealing distributional hotspots, particularly in tropical regions of the world

While direct transmission of diseases to humans is rare, wild birds play a crucial role in indirect transmission, serving as natural hosts and reservoirs of numerous zoonotic pathogens, including avian influenza virus and West Nile virus. Knowledge on the global diversity and distribution of wild-bird-associated pathogens (WBAPs), however, remains limited. In this study, researchers compiled and integrated data from literature and biodiversity databases in order to provide a scientific foundation for future surveillance and prevention strategies. They searched all available literature for verified infections of WBAPs, extracting spatial, taxonomic and temporal data on bird species and the prevalence of pathogens. From 1,834 publications, the authors identified 760 WBAPs from 1,438 species of wild birds across 38 orders, totalling more than 17,000 pathogen occurrences. Viruses were predominant, representing more than 40 per cent of infections. More than half of identified WBAPs were considered emerging, i.e., discovered after 1980 while nearly a third classified as zoonotic pathogens. When grouped into six ecological bird groups, waterfowl had the highest number of WBAPs, accounting for more than 60 per cent of all pathogen species.

To explore potential drivers of WBAP distribution, the authors modelled the habitat suitability index (HSI) of representative species across all ecological groups—60 wild birds in total—using GBIF-mediated occurrences coupled with climatic, environmental and socioeconomic variables. When HSI was included in a model of WBAPs, areas with high HSI for waterfowl and raptors correlated with zoonotic WBAPs, while HSI of shorebirds was associated with emerging WBAPs.

Overall, the authors found widely distributed hotspots for WBAPs across most continents, with particular overlaps of both zoonotic and emerging pathogens in entire tropical regions such as India, southeast Asia and parts of South America. There were also widespread localized hotspots on the southeastern coast of North America and in the Black Sea-Mediterranean regions.

Qiu Y, Lv C, Chen J, Sun Y, Tang T, Zhang Y, et al

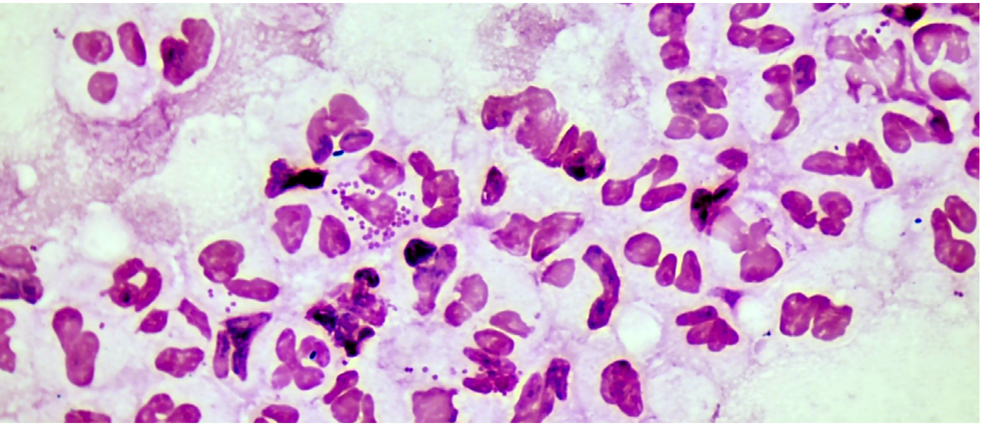
China, United States

The global distribution and diversity of wild-bird-associated pathogens: An integrated data analysis and modeling study

Med

doi.org/10.1016/j.medj.2024.11.006

Invisible biodiversity: absence of human-hosted bacterial occurrences



Neisseria gonorrhoeae observed at Columbia University Medical Center, NY, USA by Ansel Oommen (CC BY-NC 4.0)

HUMAN HEALTH

53,236
SPECIES OCCURRENCES

Despite vast diversity and crucial relevance to human health, bacteria make up less than one per cent of available species occurrence data in GBIF

Bacteria are estimated to make up between 58 and 88 per cent of all living species, and more than 35 per cent of these are dependent on animal hosts, including humans. Microbes are crucial for our well-being, but also responsible for numerous infectious diseases. Despite this relevance for human health, data on bacterial occurrences is remarkably scarce.

To explore this phenomenon, researchers in this study obtained GBIF-mediated occurrences of three common bacteria, *Chlamydia trachomatis*, *Neisseria gonorrhoeae* and *Treponema pallidum*—the causal agents for the sexually transmitted infections chlamydia, gonorrhoea, and syphilis, respectively. At the time of the study, the authors were only able to access 250 occurrences combined.

As a comparison, they mapped the bacterial distributions alongside a rather inconspicuous springtail, *Entomobrya nivalis*, belonging to a taxonomic group with limited studies worldwide. This clearly demonstrated the lack of bacterial data globally, with Benin being the only visible exception, thanks to systematic collection efforts by the Menontin District Hospital in Cotonou, currently responsible for more than 35 per cent of global data on the three pathogens.

The study suggests that infrastructure for systematic collection of data on infectious bacteria already exists, highlighting as an example the solutions provided through the French Natural Heritage Inventory Information System (SINP) framework. With proper mechanisms in place to ensure patient privacy, these workflows could easily be adopted to allow health services staff to log infections according to biodiversity data standards for host and pathogen—all within less than two minutes per record.

The authors estimate that if implemented in France with dedicated resources equivalent to just eight working hours per year, hospitals and biological laboratories could contribute more than 800,000 bacterial species occurrence records annually.

40

Poncet R, Gargominy O

France

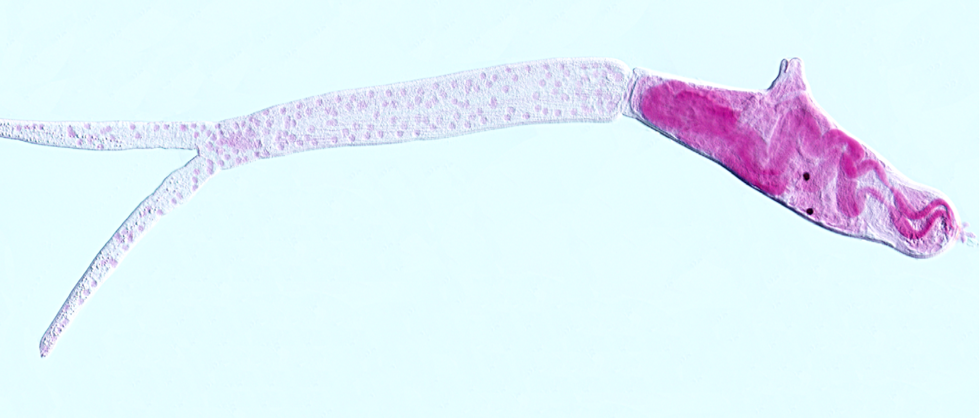
In the Shadow of Medicine: The Glaring Absence of Occurrence Records of Human-Hosted Biodiversity

Online Journal of Public Health Informatics

doi.org/10.2196/60140

Ulcerative colitis associated with hepatitis B viral protein

41



Trichobilharzia szidati by Tomas Machacek, CC BY-SA 4.0, via Wikimedia Commons

HUMAN HEALTH

27,569
SPECIES OCCURRENCES

Biomedical study links viral protein from hepatitis B to chronic inflammatory bowel disease in humans, speculating potential zoonotic source of virus

Ulcerative colitis (UC) is a chronic inflammatory bowel disease among humans with no known cause. Viral proteins have been suspected to play a role in the disease's onset and progression, and previous studies have found increased levels of hepatitis B viral (HBV) protein X (HBx) from *Orthohepadnavirus* in early diagnosed UC patients.

To explore the role of the HBV protein in UC, researchers performed transcriptomic analysis of healthy donor-derived biopsies of soft tissues infected with HBx, which revealed enriched biological processes related to pro-inflammatory pathways.

In mice infected with HBx, the researchers found clear clinical symptoms of colitis. They proceeded to treat the HBx-induced colitic mice with RNA molecules that targeted and silenced HBx, leading to a prompt reduction of the inflammatory symptoms.

In UC patients, though, the presence of HBx in the gut was not related to any ongoing or former infections with human HBV, leading the authors to speculate that the source of the HBx might be non-human and the result of a zoonotic spillover. When searching a high-throughput sequencing data for hits for HBx, they found a majority in samples from *Trichobilharzia*, a genus of trematode parasites, and in *Isatis tinctoria*, a plant in the mustard family, also known as dyer's woad.

Using GBIF-mediated occurrences, the authors observed the overlap between the UC global burden and the geographical distributions of *Trichobilharzia* spp. and *Isatis tinctoria*, which suggests a potential connection. They highlight the need for further studies aiming at the discovery of the real source of HBx to test this association more robustly.

Massimino L, Palmieri O,
Facoetti A, Fuggetta D, Spanò S,
Lamparelli LA, et al

France, Canada

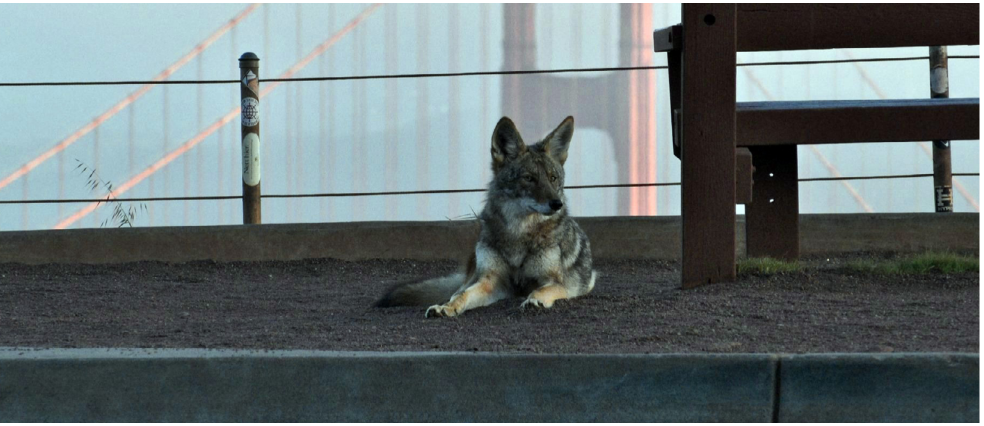
Gut virome-colonising
Orthohepadnavirus genus is
associated with ulcerative colitis
pathogenesis and induces
intestinal inflammation *in vivo*

Gut

doi.org/10.1136/
gutjnl-2022-328375

Species habitat suitability increased during COVID-19 lockdowns

42



Coyote (Canis latrans) observed near San Francisco, CA, USA by Nathanael Aff.

ECOLOGY

HUMAN HEALTH

SPECIES DISTRIBUTIONS

637,526
SPECIES OCCURRENCES

Spain, Portugal

Iberian study links decline in human activity during lockdowns to improved air quality and increased habitat suitability

Reduction in traffic and industrial activities during the COVID-19 lockdowns led to improved air and water quality worldwide. During this so-called "anthropause," some species may have shifted their distributions, as exemplified in numerous anecdotal reports of wildlife appearing in the middle of major cities suddenly devoid of usual human activity.

In this study, researchers explored whether habitat suitability in the Iberian Peninsula increased during the 2020 and 2021 lockdowns. Using GBIF-mediated occurrences of 381 native species of vascular plants, amphibians, reptiles, birds and mammals, the authors created ecological niche models based on five environmental variables from remote sensing before, during, and after the pandemic restrictions came into force.

Overall, the models showed that habitat suitability fluctuated over time, showing a seasonal pattern; however, during both lockdowns, habitat suitability was at its highest of the entire study period running from July 2017 to August 2022. The authors compared these results with air quality and mobility data, finding a clear correlation between decreased air pollution when people stayed at home and the resulting positive effects on species' habitat quality.

As a public health measure, the COVID-19 lockdowns were implemented to prevent uncontrolled spread of the SARS-CoV-2 virus. As challenging as these periods were to both individuals and society, the results of the study highlight a unique opportunity to improve understanding of the true extent of human disturbances on biodiversity and the environment.

Sillero N, Campos JC, Arenas-Castro S & Alírio J

Portugal

Species habitat suitability increased during COVID-19 lockdowns

Global Ecology and Conservation

doi.org/10.1016/j.gecco.2024.e02977

No chill for flying foxes roosting in Queensland

43

Black flying fox (Pteropus alecto) observed near Pine Creek, Australia by Philip Griffin (CC BY-NC 4.0)

HUMAN HEALTH

ECOLOGY

CONSERVATION

88,838
SPECIES OCCURRENCES

Australia

Black flying fox roosting behaviour unaffected by food availability or weather patterns

Anthropogenic changes such as altered land use and the introduction of non-native plants have significant effects on the diversity and availability of food across ecological landscapes. The Hendra virus—an infectious bat-borne pathogen—can infect horses and occasionally humans and is present across Australia. Incidence of Hendra virus 'spillover' is known to spike in winter, researchers hypothesized that bats may have less access to natural food resources and therefore may come into greater contact with humans through increased urban foraging.

In this study, researchers investigated the impact of different environmental factors on winter roosting locations in black flying foxes (a species of megabat) across Queensland between 2007 and 2020.

Using data accessed through GBIF and vegetation maps from the Queensland Herbarium, authors identified locations of typical and atypical winter diet tree species for black flying foxes. Distribution of native and non-native plants within 20km foraging areas of bat roosts were considered to determine whether the density, location or consistency of food sources affected where bats chose to roost in winter. Using data accessed from the Australian Bureau of Meteorology, they assessed the impact of monthly precipitation and temperature pattern using environmental mixed-effects modelling.

Findings indicate that neither food availability nor diet strongly predicted whether bats would be present. Even though roosts were occasionally linked to consistent native food sources, this was not a reliably observed pattern. No interaction between the average past weather conditions and winter habitat attributes were found to influence winter roost occupancy.

Deeper analyses are required to better understand bat movements across winter to increase preparedness and response to future Hendra virus outbreaks in both bats, as well as spillover effects to horses and humans.

Baranowski K, Bharti N

United States

Native and non-native winter foraging resources do not explain Pteropus alecto winter roost occupancy in Queensland, Australia

Frontiers in Ecology and Evolution

doi.org/10.3389/fevo.2024.1483865

Plague and precipitation: the role of reservoir species in mediating disease response to climate

44

Steppe polecat (Mustela eversmanii) observed near Yushu, Qinghai, China by yaoyaoo (CC BY-NC 4.0)

HUMAN HEALTH

341,161
SPECIES OCCURRENCES

China

Retrospective study of plague in Qing-dynasty China suggests a limited role of precipitation; differences in disease intensity cannot be explained by response of reservoir species

During the third bubonic plague pandemic (1772–1964 CE) in China, disease incidence correlated with precipitation levels, but with different responses in northern and southern regions of the country. Prior research has attributed this discrepancy to differences in some reservoir species and their climatic niches.

To test the hypothesis, this study used environmental niche modelling based on GBIF-mediated species occurrences of 33 known mammal reservoir species and a single flea vector (*Ctenocephalides felis*) combined with climate data. The authors constructed models for each species in current climate and hindcast these into historic climate scenarios of the 18th and 19th century.

Comparing the reservoir species in northern and southern regions of the country, they found minimal evidence to support the hypothesis that the response of plague incidence to precipitation was mediated by differences in reservoir species' responses. In fact, precipitation did not appear to be an important predictor in the models at all—with no consistent response to precipitation in either region, respectively.

While the results of the study cannot rule out that precipitation influenced plague intensity during the third pandemic, it is unlikely to have been caused by a uniform response of reservoir species. These findings highlight the complexity of reservoir-vector-disease systems and the dangers of making inferences about ecological mechanisms based on a single or few species.

Fell HG, Jones M, Atkinson S, Stenseth NC, Algar AC

Canada, United Kingdom, Norway, China

The role of reservoir species in mediating plague's dynamic response to climate

Royal Society Open Science

doi.org/10.1098/rsos.230021

Modelling disease ecology: Schistosomiasis host snails in Brazil

45

Schistosoma mansoni specimen *from the Naturalis Biodiversity Center (CC0)*

HUMAN HEALTH

ECOLOGY

77,785
SPECIES OCCURRENCES

Brazil

Rigorous study assesses effects of different modelling algorithms, sources of occurrence data and geographical scale using Brazilian freshwater snails as a case study

Species distribution modelling (SDM) has become a powerful tool in the field of disease ecology used to profile transmission risk for vector-borne, zoonotic diseases. With rapidly evolving SDM methodologies, rigid analyses of various algorithms, data sources and scale are important for securing consistent and sound results.

In this study, researchers compared multiple SDM methods to assess their performance and output, while using a biologically and epidemiologically relevant study system to make significant contributions to knowledge on schistosomiasis risk in Brazil. This debilitating disease is caused by the parasite, *Schistosoma mansoni*, transmitted to humans upon contact with *Biomphalaria* freshwater snails.

The methodological analysis included occurrence data of three snail species from expert sampling regimes and GBIF, respectively, coupled with high-resolution data on climate, hydrology, soil and land-use. The authors created models with varying spatial extent from state to national level using three different modelling algorithms.

While models generally performed well, the predictions at the national scale varied remarkably depending on type. When presented with resulting distribution maps, experts consistently picked the Boosted Regression Tree type as a best match for known snail habitat. At smaller scales, model accuracy was more consistent across the three algorithms.

To compare effects of the data source, the authors created separate models based on expert field data and GBIF-mediated occurrences, respectively. While both models performed well, prediction maps showed substantial variation, but ultimately experts judged that maps from combined models were better representations of snail distributions.

Singleton AL, Glidden CK, Chamberlin AJ, Tuan R, Palasio RGS, Pinter A, et al

Brazil, United States

Species distribution modeling for disease ecology: A multi-scale case study for schistosomiasis host snails in Brazil

PLOS Global Public Health

doi.org/10.1371/journal.pgph.0002224

Effects of climate change on medically relevant viper in the Sahara-Sahel region

46

White-bellied saw-scaled viper (*Echis leucogaster*) observed in Assa-Zag, Morocco by Samuel GUIRAUDOU (CC BY 4.0)

HUMAN HEALTH

CLIMATE CHANGE

478
SPECIES OCCURRENCES

Modelling of suitable climate for the white-bellied saw-scaled viper shows overall stability with substantial increases towards the end of the century and potential risk for more snakebites

Responsible for more fatalities than all other African snakes combined, saw-scaled vipers (*Echis* spp.) are arguably some of the most medically significant serpents in the world. Among 12 recognized species, the white-bellied saw-scaled viper (*E. leucogaster*) occurs in the western half of the Sahel and further north into the Sahara Desert with scattered isolated populations along the northern edge of its range. In order to increase knowledge about the distribution of *E. leucogaster* now and in the future, this study employed ecological niche modelling using GBIF-mediated occurrences, literature records and specimen data from unpublished museum collections. Combining occurrence data with bioclimatic variables on temperature and precipitation, the authors modelled the potential distributions of the viper presently, around 2050 and towards the end of the century based on two greenhouse gas emission scenarios.

The area predicted as currently suitable for *E. leucogaster* fitted well with the known distribution of the viper. Most suitable area was found within the Sahelian acacia savanna and North and West Saharan xeric steppe and woodlands. The models predicted continuous distributions between north-eastern Algeria and central Tunisia, suggesting areas to prioritize for future systematic surveys to verify these findings.

All models of future climates predicted net increases in suitable areas, ranging from 12 per cent at mid-century to 85 per cent towards 2100. Eighty-eight percent of currently suitable areas would remain stable under future scenarios with a slight shift (50-100 km) of the centroid in a south-east direction. While this may be good news for vipers with limited dispersal abilities and a slow life history, urban development and agricultural expansion may lead to increased risk for human encounters and snakebites.

Bouam I, Khelfaoui F, Saoudi M

Algeria

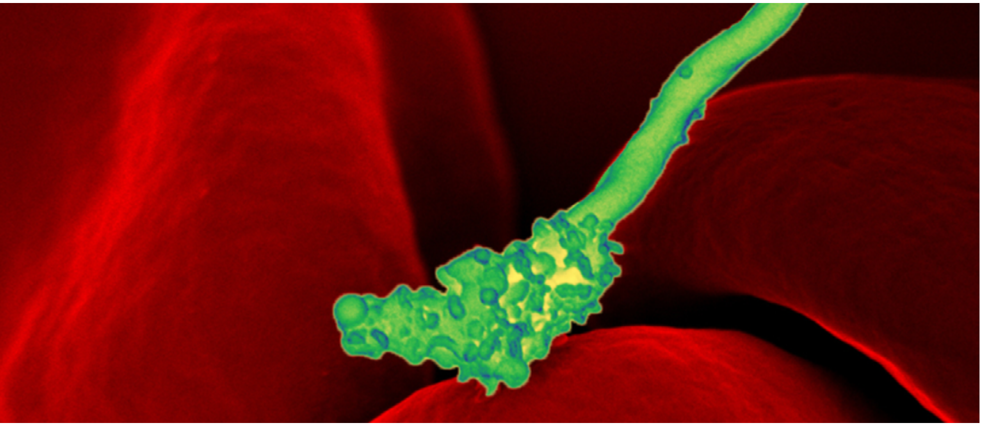
Inferring probable distributional gaps and climate change impacts on the medically important viper Echis leucogaster in the western Sahara-Sahel: An ecological niche modeling approach

Biodiversitas Journal of Biological Diversity

doi.org/10.13057/biodiv/d231025

Borrelia beyond borders: broad distribution of pathogens and vectors

47



Genus Borrelia (CC0)

HUMAN HEALTH

454,405
SPECIES OCCURRENCES

Study indicates greater need for identification, surveillance, and diagnosis of RFGB infections globally

Relapsing fever group *Borrelia* (RFGB) pathogens are bacteria known to cause the disease relapsing fever. The disease is transmitted to animals or humans by arthropod vectors, usually ticks or lice. RFGB currently poses a growing public health risk and is difficult to diagnose due to their relatively broad symptom presentation.

To better understand the global distribution and associated health risk of the disease, a recent study investigated the diversity and distribution and potential infection risk of RFGB. Authors reviewed 13,959 unique scientific studies from 1874 to 2022 that referenced RFGB, of which 697 were used for data extraction where four main *Borrelia* species were identified. They then used data accessed through GBIF and VectorMap to map occurrences for each of the four species on a global grid map. Machine learning algorithms were used to assess 44 environmental, ecoclimatic, biological and socioeconomic variables to to determine potential associations with RFGB infection.

The authors found that 29 RFGB species were recorded worldwide, with 16 of these pathogens causing 26,538 human infections. Findings challenge previously held assumptions that RFGB can be found only in particular hosts and vectors within a given geographical range. Instead, the authors found that multiple tick pathogens from different geographical areas were carrying the same RFGB species, indicating that 'high-risk' geographic regions are likely considerably larger than previously reported.

Tang T, Zhu Y, Zhang YY, Chen JJ, Tian JB, Xu Q, et al

China

The global distribution and the risk prediction of relapsing fever group Borrelia: a data review with modelling analysis

The Lancet Microbe

doi.org/10.1016/s2666-5247(23)00396-8

Mapping global zoonotic and interregional transmission of mpox

48

Lorrain dormouse (Graphiurus lorraineus) observed near Nouamou, Côte d'Ivoire by dalempijevic1 (CC BY-NC 4.0)

HUMAN HEALTH

1,225
SPECIES OCCURRENCES

Study assesses risk of zoonotic transmission of monkeypox virus using GBIF-mediated occurrences of known rodent vectors

Mpox is a zoonotic disease that infects humans and other animals with the monkeypox virus (MPXV) endemic to Western and Central Africa. In 2022 and 2023, an outbreak of human mpox in more than 100 non-endemic countries led to 127 deaths. More recently, at least 450 people have died during another, more severe outbreak caused by a different MPXV variant.

This retrospective observational study has gathered all available historical case reports, outbreak investigations and surveillance studies to assemble a worldwide database of MPXV infections. The authors have documented a total of nearly 50,000 human mpox cases from 78 countries.

Using 525 full-genome sequences of MPXV obtained from GenBank, assembled and aligned to a reference genome, they created a phylogenetic tree, revealing two major viral clades associated with human infection: the Congo Basin clade (I) and the West African clade (II). The 2022-23 global outbreak of mpox was caused by a clade II variant, while a clade I variant is responsible for the recent upsurge in Central and East Africa.

To create a zoonotic transmission risk model, the authors used GBIF-mediated occurrences to map rodent richness and distribution for two reservoir species, *Graphiurus lorraineus* and *Graphiurus crassicaudatus*, then combined them with four climatic variables. The model predicted high risks of human MPXV infection in 28 African countries, highlighting the Democratic Republic of Congo as home to the largest at-risk area and population.

By analyzing global airline travel patterns, the authors predict that cross-border mpox cases are most likely to arise from endemic countries such as Nigeria, Ghana and Côte d'Ivoire, while Western European countries—in particular, the United Kingdom, Spain and Germany—face the highest likelihood of importing human mpox cases.

Sun YQ, Chen JJ, Liu MC, Zhang YY, Wang T, Che TL, et al

China

Mapping global zoonotic niche and interregional transmission risk of monkeypox: a retrospective observational study

Globalization and Health

doi.org/10.1186/s12992-023-00959-0

Tobacco: bad for your health and for biodiversity

49

Tobacco cultivation in Lijiang, Yunnan, China. Photo by Brian Sterling, via Flickr (CC BY-SA 2.0)

HUMAN HEALTH

AGRICULTURE

CONSERVATION

34,880
SPECIES OCCURRENCES

China

Study of impacts of tobacco industry in Yunnan Province, China reveals significant correlations between farming intensity and biodiversity risks

Yunnan is China's most biodiverse province and the world's largest tobacco-producing region with total production areas reaching 473,000 hectares. Despite tobacco's well-documented carcinogenicity and overall adverse effects on human health, areas covered by tobacco farms in Yunnan grew by more than 30 per cent from 2010 to 2020.

In this study, researchers explored a potential relationship between tobacco (*Nicotiana tabacum L.*) cultivation and decreased plant diversity at the county level in Yunnan Province. While other agricultural products grown in the region, such as coffee and tea, often rely on sustainable practices preserving soil health, tobacco farming involve intensive pesticides and chemical fertilizers leading to soil degradation and contamination of water sources.

By gathering GBIF-mediated species occurrences of all higher plants and combining them with climate data, the authors modelled the habitat suitability and potential distribution of threatened flora in the region. They added geospatial information on tobacco farming intensity and tree cover to assess relationships between agricultural activities and biodiversity consequences.

Integrating distribution probabilities with tree loss data, the authors constructed a biodiversity risk index, from which they observed a substantial degree of overlap between areas of intensive tobacco farming and hotspots of biodiversity risks. Areas of very high conservation priority were identified in nearly all counties of the southern prefectures of Honghe and Wenshan.

Overall, the study estimated that one per cent increase in tobacco cultivation corresponded to a 0.1 per cent decrease in plant species richness across Yunnan province.

Shao J, Zhang Q, Wang J

China

Mapping and modelling impacts of tobacco farming on local higher plant diversity: A case study in Yunnan Province, China

Geography and Sustainability

doi.org/10.1016/j.geosus.2024.06.009

Not worth its weight in gold: impacts of illegal gold mining in the Amazon

50

Golden-white bare-ear marmoset (Mico leucippe) observed near Novo Progresso, Pará, Brazil by feelthewildtusk (CC BY-NC 4.0)

BIODIVERSITY SCIENCE

HUMAN HEALTH

550,000
SPECIES OCCURRENCES

Brazil

Study assessed combined environmental and health impacts of illegal, small-scale gold mining, finding societal costs more than double the potential value

Due to increases in gold prices, illegal small-scale mining have intensified in the Brazilian Amazon in the last few years. With significant environmental and health impacts associated with mining, the socio-economic repercussions are complex and thus difficult to assess.

In this study, researchers present a framework for assessing the costs associated with impacts of small-scale gold mining. They created a value transfer formula based on the extent of mining activities and impacts from deforestation, erosion and mercury contamination, and presented a case study applying the framework to mining activities in the Tapajós Basin in the Brazilian Amazon.

First, they estimated the productivity of the mines to derive the total area of impact. From this they assessed the impacts of deforestation both in terms of restoration costs and value of ecosystem services including forest products, climate regulation and species richness. To quantify the latter, the authors used GBIF-mediated occurrences of plants, mammals, reptiles and birds in the municipality of each mining site. They finally considered costs associated with land degradation and mercury contamination.

In non-monetary values, mining activities in the Tapajós Basin impacted more than 4,500 hectares in order to produce ~7,800 kg of gold, requiring 20 kg of pure mercury for the extraction. They estimated that 370,000 people were at risk for mercury ingestion, resulting in 700 heart attacks and 32 children born with intellectual disability every year.

For the year 2020, the total socioeconomic costs of illegal gold mining in the region was USD 1 billion, equivalent to USD 136,000 per kilo of extracted gold. With an average gold price of USD 56,800 per kg, the societal costs are more than double the benefits illegal miners may derive from its extraction.

Gasparinnetti P, Bakker LB, Queiroz JM, Vilela T

Brazil, United States

Economic valuation of artisanal small-scale gold mining impacts: A framework for value transfer application

Resources Policy

doi.org/10.1016/j.resourpol.2023.104259

KYOTO PROTOCOL
2
No. 001
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Cover illustration: *Pteropus vampyrus*, The mammals of Australia. London, 1863. Via Biodiversity Heritage Library.

Back cover illustration: From Esperienze intorno alla generazione degl' insetti. 1668. Via Biodiversity Heritage library.

Special section background illustration: Mikrogeologie: das Erden und Felsen schaffende Wirken des unsichtbar kleinen selbständigen Lebens auf der Erde: atlas. Leipzig: L. Voss, 1854-1856. Via Biodiversity Heritage Library.

Inner cover illustration: Blossom Bat (*Syconycteris australis* (Peters, 1867), Die Fledermäuse des Berliner Museums für Naturkunde. Berlin, 1899. Via Biodiversity Heritage Library.

GBIF Secretariat (2025) GBIF Science Review N° 12

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GBIF

Science Review

Nº 12