Introduction to Essential Biodiversity Variables

Town Peterson

University of Kansas

What is biological diversity?????

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The Intergovernmental Panel on Climate Change (IPCC) is the United Nations body for assessing the science related to climate change.

SIXTH ASSESSMENT REPORT

IPCC-53 BIS

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Essential Biodiversity Variables

EBVs are defined as the derived measurements required to study, report, and manage biodiversity change, focusing on status and trend in elements of biodiversity.

What are EBVs?

EBVs

What are EBVs?

Working Groups

Ecosystem Services

Indicators

EBVs are the abbreviation for Essential Biodiversity Variables.

These Essential Biodiversity Variables, defined as the derived measurements required to study, report, and manage biodiversity change, focusing on status and trend in elements of biodiversity should play the role of brokers between monitoring initiatives and decision makers. They provide the first level of abstraction between low-level primary observations and high-level indicators of biodiversity.

Criteria for Essential Biodiversity Variables

An ideal EBV should be

- able to capture critical scales and dimensions of biodiversity
- biological
- a state variable (in general)
- sensitive to change
- ecosystem agnostic (to the degree possible)
- technically feasible, economically viable and sustainable in time

BEIJING 2018 CALL

ECOLOGY

Essential Biodiversity Variables

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A global system of harmonized observations is needed to inform scientists and policy-makers.

Reducing the rate of biodiversity loss and averting dangerous biodiversity change are international goals, reasserted by the Aichi Targets for 2020 by Parties to the United Nations (UN) Convention on Biological Diversity (CBD) after failure to meet the 2010 target (*1, 2*). However, there is no global, harmonized observation system for delivering regular, timely data on biodiversity change (*3*). With the first plenary meeting of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES) soon under way, partners from the Group on Earth Observations Biodiversity Observation Network (GEO BON) (*4*) are developing—and seeking con-

Change (UNFCCC) (*8*). EBVs, whose development by GEO BON has been endorsed by the CBD (Decision XI/3), are relevant to derivation of biodiversity indicators for the Aichi Targets (*9*). Although CBD biodiversity indicators are designed to convey messages to policy-makers from existing biodiversity data (*1*), EBVs aim to help observation communities harmonize monitoring, by identifying how variables should be sampled and measured.

Given the complexity of biodiversity change (*3*), the challenge of developing a global observation system can appear insurmountable. Nearly 100 indicators have been proposed for the 2020 CBD targets (ongoing work seeks to identify a more limited subset)
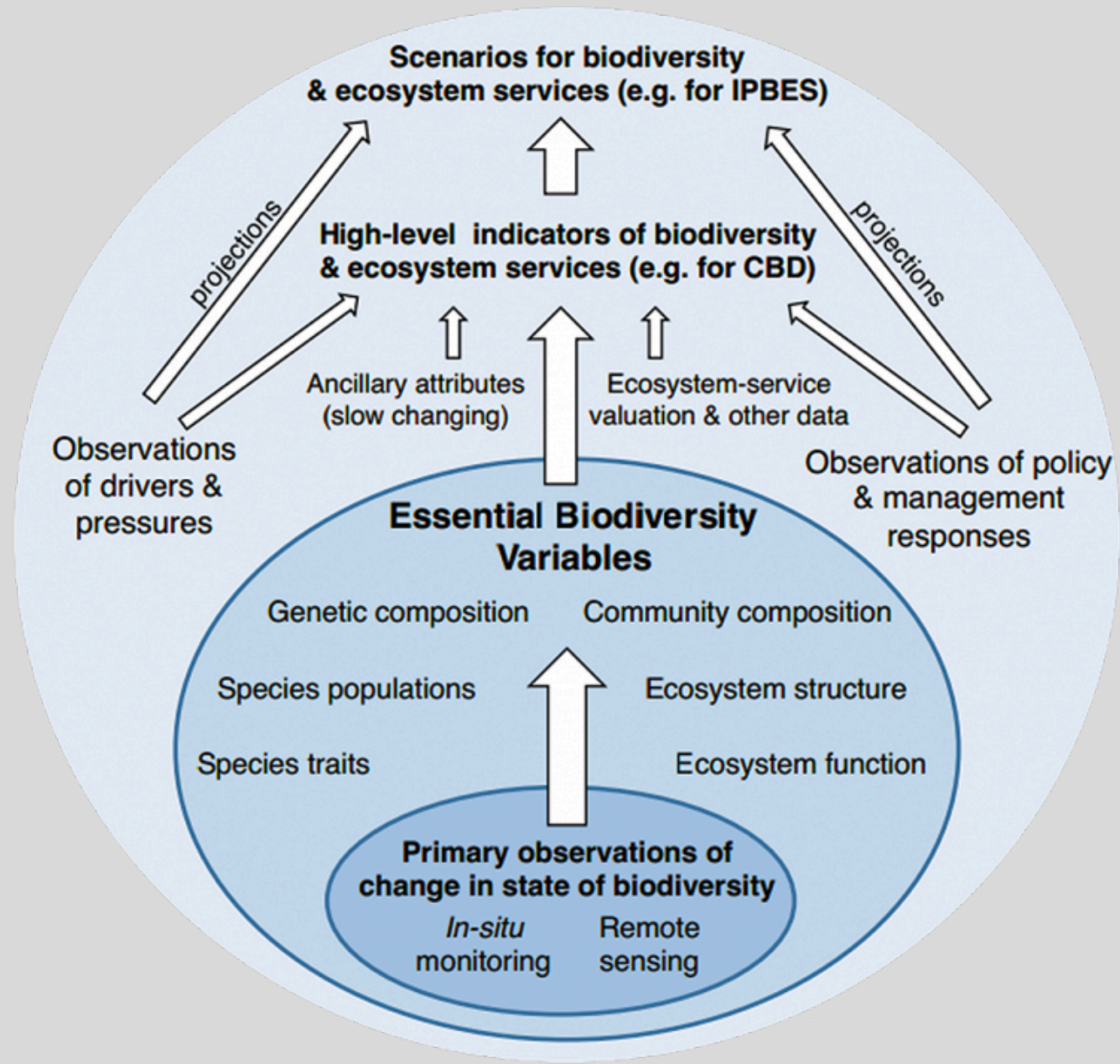
potentially fit this definition. We developed and tested a process, still ongoing, to identify the most essential (*11*). Dozens of biodiversity variables were screened to identify those that fulfill criteria on scalability, temporal sensitivity, feasibility, and relevance. These variables were scored for importance, checked for redundancy, and organized into six classes on the basis of commonalities, general enough for use across taxa and terrestrial, freshwater, and marine realms (see the table).

Often, it is not possible to generalize observations from point locations to the regional scale. Variables selected as EBVs harness remote sensing (RS) to measure continuously across space (e.g., habitat struc-

EBVs

- They provide the first level of abstraction between low-level primary observations and high-level indicators of biodiversity.
- They should be
  - able to capture critical scales and dimensions of biodiversity
  - biological
  - a state variable (in general)
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  - ecosystem agnostic (to the degree possible)
  - technically feasible, economically viable and sustainable in time

Figure showing the framework of Essential Biodiversity Variables linking primary observations to high-level indicators and scenarios.

Scenarios for biodiversity & ecosystem services (e.g. for IPBES)

projections

High-level indicators of biodiversity & ecosystem services (e.g. for CBD)

projections

Observations of drivers & pressures

Ancillary attributes (slow changing)

Ecosystem-service valuation & other data

Observations of policy & management responses

Essential Biodiversity Variables

Genetic composition   Community composition

Species populations   Ecosystem structure

Species traits   Ecosystem function

Primary observations of change in state of biodiversity

In-situ monitoring   Remote sensing

- **Genetic composition**: Co-ancestry, allelic diversity, population genetic differentiation, breed and variety diversity
- **Species populations**: Species distribution, population abundance, population structure by age/size class
- **Species traits**: Phenology, morphology, reproduction, physiology, movement
- **Community composition**: Taxonomic diversity, species interactions
- **Ecosystem function**: Net primary productivity, secondary productivity, nutrient retention, disturbance regime
- **Ecosystem structure**: Habitat structure, ecosystem extent and fragmentation, ecosystem composition by functional type

Examples of candidate Essential Biodiversity Variables

EBV class	EBV examples	Measurement and scalability	Temporal sensitivity	Feasibility	Relevance for CBD targets and indicators (1,9)
Genetic composition	Allelic diversity	Genotypes of selected species (e.g., endangered, domesticated) at representative locations.	Generation time	Data available for many species and for several locations, but little global systematic sampling.	Targets: 12, 13. Indicators: Trends in genetic diversity of selected species and of domesticated animals and cultivated plants; RLI.
Species populations	Abundances and distributions	Counts or presence surveys for groups of species easy to monitor or important for ES, over an extensive network of sites, complemented with incidental data.	1 to >10 years	Standardized counts under way for some taxa but geographically restricted. Presence data collected for more taxa. Ongoing data integration efforts (Global Biodiversity Information Facility, Map of Life).	Targets: 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15. Indicators: LPI; WBI; RLI; population and extinction risk trends of target species, forest specialists in forests under restoration, and species that provide ES; trends in invasive alien species; trends in climatic impacts on populations.
Species traits	Phenology	Timing of leaf coloration by RS, with in situ validation.	1 year	Several ongoing initiatives (Phenological Eyes Network, PhenoCam, etc.)	Targets: 10, 15. Indicators: Trends in extent and rate of shifts of boundaries of vulnerable ecosystems.
Community composition	Taxonomic diversity	Consistent multitaxa surveys and metagenomics at select locations.	5 to >10 years	Ongoing at intensive monitoring sites (opportunities for expansion). Metagenomics and hyperspectral RS emerging.	Targets: 8, 10, 14. Indicators: Trends in condition and vulnerability of ecosystems; trends in climatic impacts on community composition.
Ecosystem structure	Habitat structure	RS of cover (or biomass) by height (or depth) globally or regionally.	1 to 5 years	Global terrestrial maps available with RS (e.g., Light Detection and Ranging). Marine and freshwater habitats mapped by combining RS and in situ data.	Targets: 5, 11, 14, 15. Indicators: Extent of forest and forest types; mangrove extent; seagrass extent; extent of habitats that provide carbon storage.
Ecosystem function	Nutrient retention	Nutrient output/input ratios measured at select locations. Combine with RS to model regionally.	1 year	Intensive monitoring sites exist for N saturation in acid-deposition areas and P retention in affected rivers.	Targets: 5, 8, 14. Indicators: Trends in delivery of multiple ES; trends in condition and vulnerability of ecosystems.

Data Distribution Centre

IPCC Site

DDC Home
About the DDC
Guidance on the use of data
Scenario process for AR5
Data: Observations
Data: Simulations
Data: Synthesis
Visualisation

Quick links

IPCC Reports
Video tour of the DDC

Centre for Environmental Data Analysis
SCIENCE AND TECHNOLOGY FACILITIES COUNCIL
NATURAL ENVIRONMENT RESEARCH COUNCIL

Department for Business, Energy & Industrial Strategy

DKRZ
DEUTSCHES KLIMARECHENZENTRUM

WDC CLIMATE

Center for International Earth Science Information Network
EARTH INSTITUTE | COLUMBIA UNIVERSITY

NASA

W3C XHTML 1.0

Welcome to the IPCC Data Distribution Centre

Location: DDC Home

Welcome to the Data Distribution Centre (DDC) of the Intergovernmental Panel on Climate Change (IPCC). The DDC provides climate, socio-economic and environmental data, both from the past and also in scenarios projected into the future. Technical guidelines on the selection and use of different types of data and scenarios in research and assessment are also provided.

The DDC is designed primarily for climate change researchers, but materials contained on the site may also be of interest to educators, governmental and non-governmental organisations, and the general public.

The DDC is overseen by the IPCC Task Group on Data Support for Climate Change Assessments (TG-DATA) (formerly the Task Group on Data and Scenario Support for Impact and Climate Analysis - TGICA) and jointly managed by the Centre for Environmental Data Analysis (CEDA) in the United Kingdom, the ICSU World Data Center Climate (WDCC) in Germany, and the Center for International Earth Science Information Network (CIESIN) at Columbia University, New York, USA. The data are provided by co-operating modelling and analysis centres.

| About the DDC | Guidance on use of data | Discover, view and download data |

Introduction to the IPCC Data Distribution Centre (Full page)

The DDC has been established to facilitate the timely distribution of a consistent set of up-to-date scenarios of changes in climate and related environmental and socio-economic factors for use in climate impacts assessments. The intention is that these new assessments can feed into the review process of the IPCC (Full page).

In this section:

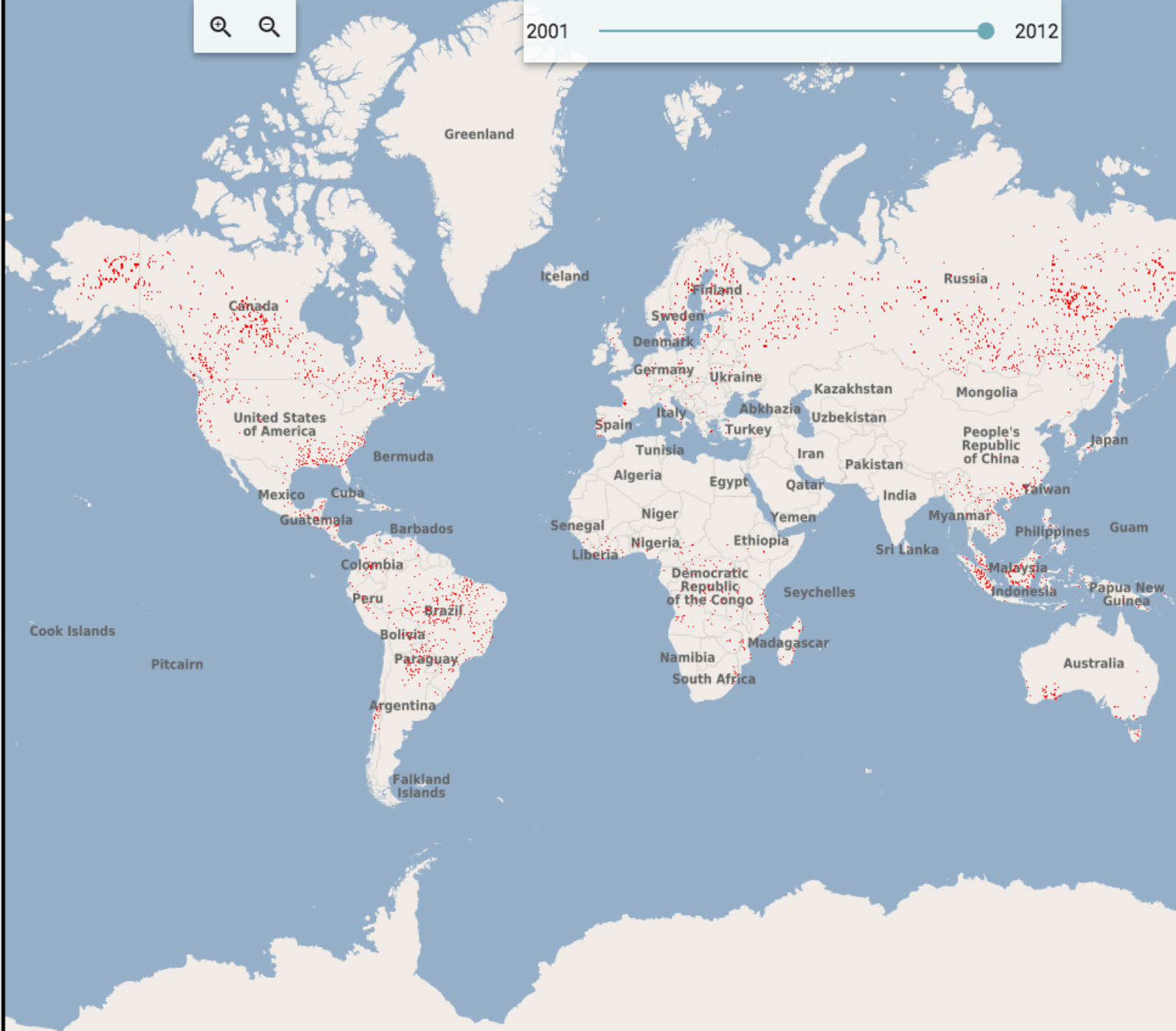- Why the DDC exists
- What the DDC provides
- Who runs the DDC
- User surveys
- How the site is arranged

Highlights

Factsheet on CMIP5 data in the DDC.

Results from the 2015 user survey.

2001 ———————————————●——— 2012

GEO BON
powered by UZT
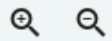
| Forest Cover ▾ | Global forest cover loss ... ▾ |

EBV class: ⛰ Ecosystem Structure
EBV: Ecosystem Extent

Title: Forest cover

Description: Data in this layer were generated using multispectral satellite imagery from the Landsat 7 thematic mapper plus (ETM+) sensor. The clear surface observations from over 600,000 images were analyzed using Google Earth Engine, a cloud platform for earth observation and data analysis, to determine per pixel tree cover using a supervised learning algorithm.

Plot Options

| Country ▾ | 2001 ▾ | 2012 ▾ | sum ▾ |

Calculate

2015

GEO BON
powered by UKZT

Changes in local bird div... ▾   Global species richness ... ▾

EBV class: ♺ Community Composition
EBV: Alpha Diversity

Title: Changes in local bird diversity (cSAR)

Description: Changes in bird diversity at the grid cell level caused by land-use, estimated by the cSAR model (Martins & Pereira, 2017). It reports changes in species number (percentage and absolute), relative to 1900, for all bird species, forest bird species, and non-forest bird species in each cell. Uses the LUH 2.0 projections for land-use, and the PREDICTS coefficients for bird affinities to land-uses.

Plot Options

Country ▾   2001 ▾   2012 ▾   sum ▾
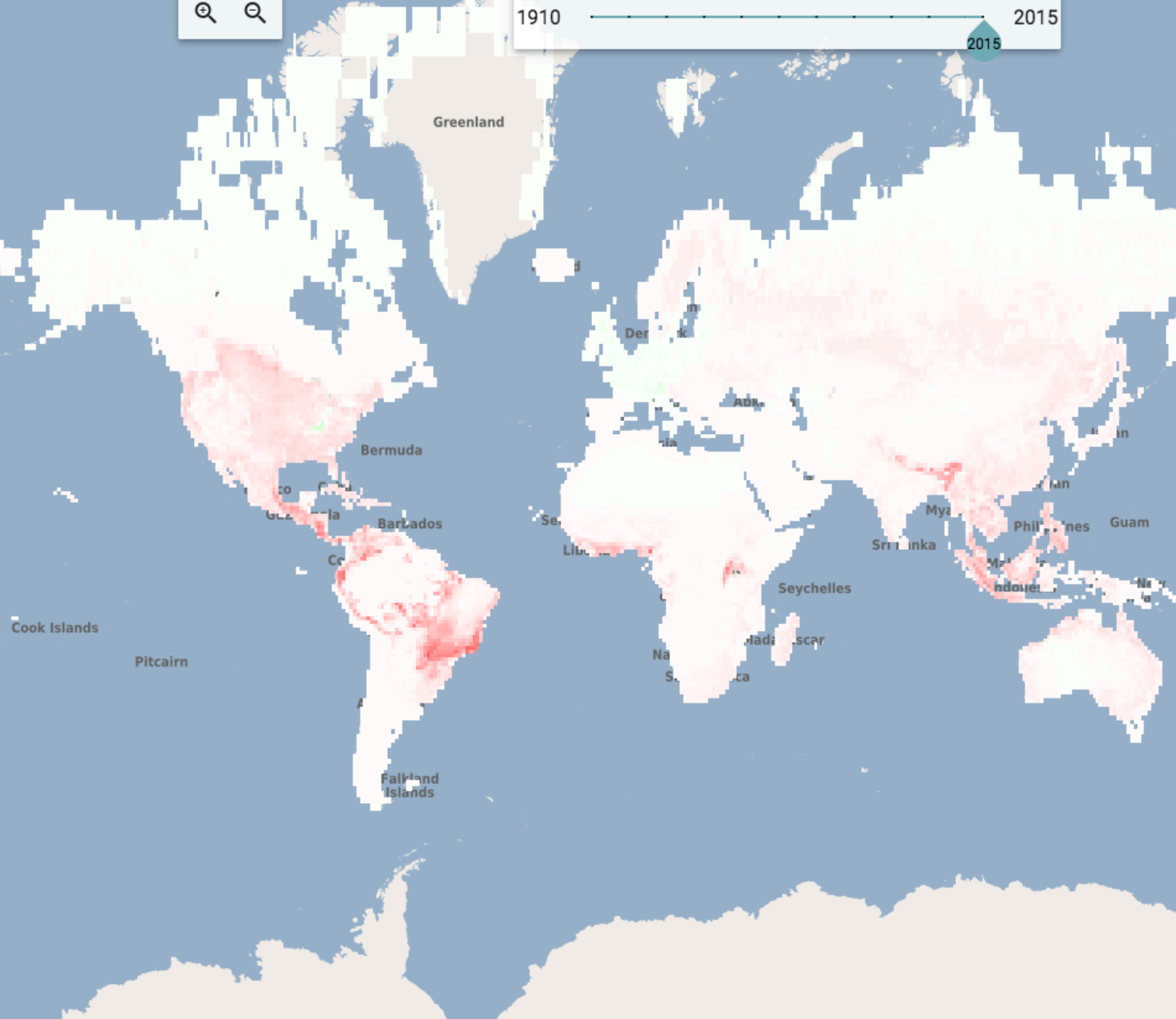
Calculate

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Genetic Composition

Loch Ness monster could be a giant eel, say scientists

Otago University researchers confirm the loch contains no monster – or dinosaur – DNA

Guardian graphic. Source: Otago University, New Zealand

▲ University of Otago geneticist Prof Neil Gemmell at Loch Ness. Photograph: Andy Buchanan/AFP/Getty Images

The Loch Ness monster could be a giant eel, according to a fishy new theory that will keep Highland tourists guessing.

In one of the biggest DNA studies of its kind, a team of scientists from New Zealand's Otago University found the presence of about 3,000 species in the deep murky waters of the Scottish loch.

Six Shark Species Identified By Sequencing Their DNA From Seawater

ECOLOGY

Environmental DNA illuminates the dark diversity of sharks

Germain Boussarie,[1,2]* Judith Bakker,[3]* Owen S. Wangensteen,[3,4] Stefano Mariani,[3]
Lucas Bonnin,[1,2] Jean-Baptiste Juhel,[1,2] Jeremy J. Kiszka,[5] Michel Kulbicki,[6] Stephanie Manel,[7]
William D. Robbins,[8,9,10] Laurent Vigliola,[1†] David Mouillot[2,11†‡]

In the era of "Anthropocene defaunation," large species are often no longer detected in habitats where they formerly occurred. However, it is unclear whether this apparent missing, or "dark," diversity of megafauna results from local species extirpations or from failure to detect elusive remaining individuals. We find that despite two orders of magnitude less sampling effort, environmental DNA (eDNA) detects 44% more shark species than traditional underwater visual censuses and baited videos across the New Caledonian archipelago (south-western Pacific). Furthermore, eDNA analysis reveals the presence of previously unobserved shark species in human-impacted areas. Overall, our results highlight a greater prevalence of sharks than described by traditional survey methods in both impacted and wilderness areas. This indicates an urgent need for large-scale eDNA assessments to improve monitoring of threatened and elusive megafauna. Finally, our findings emphasize the need for conservation efforts specifically geared toward the protection of elusive, residual populations.
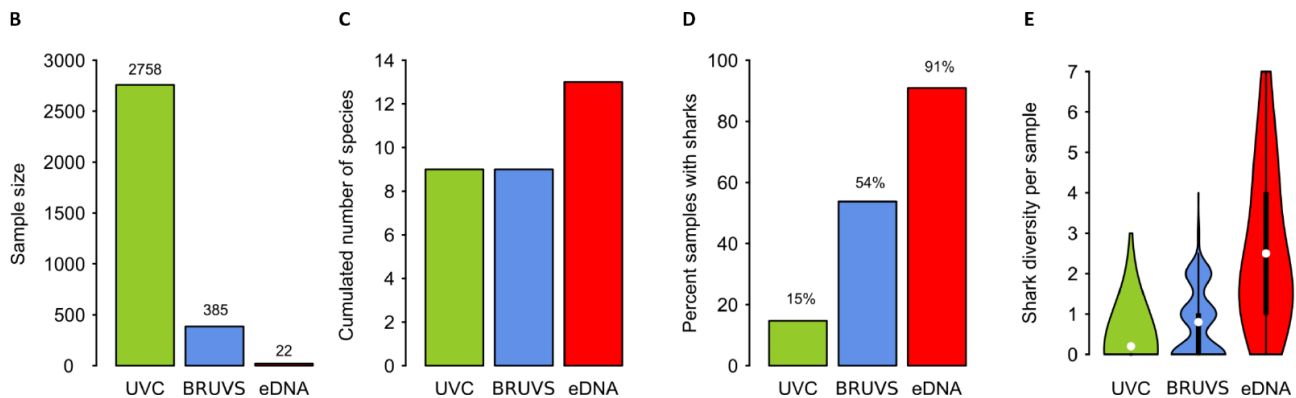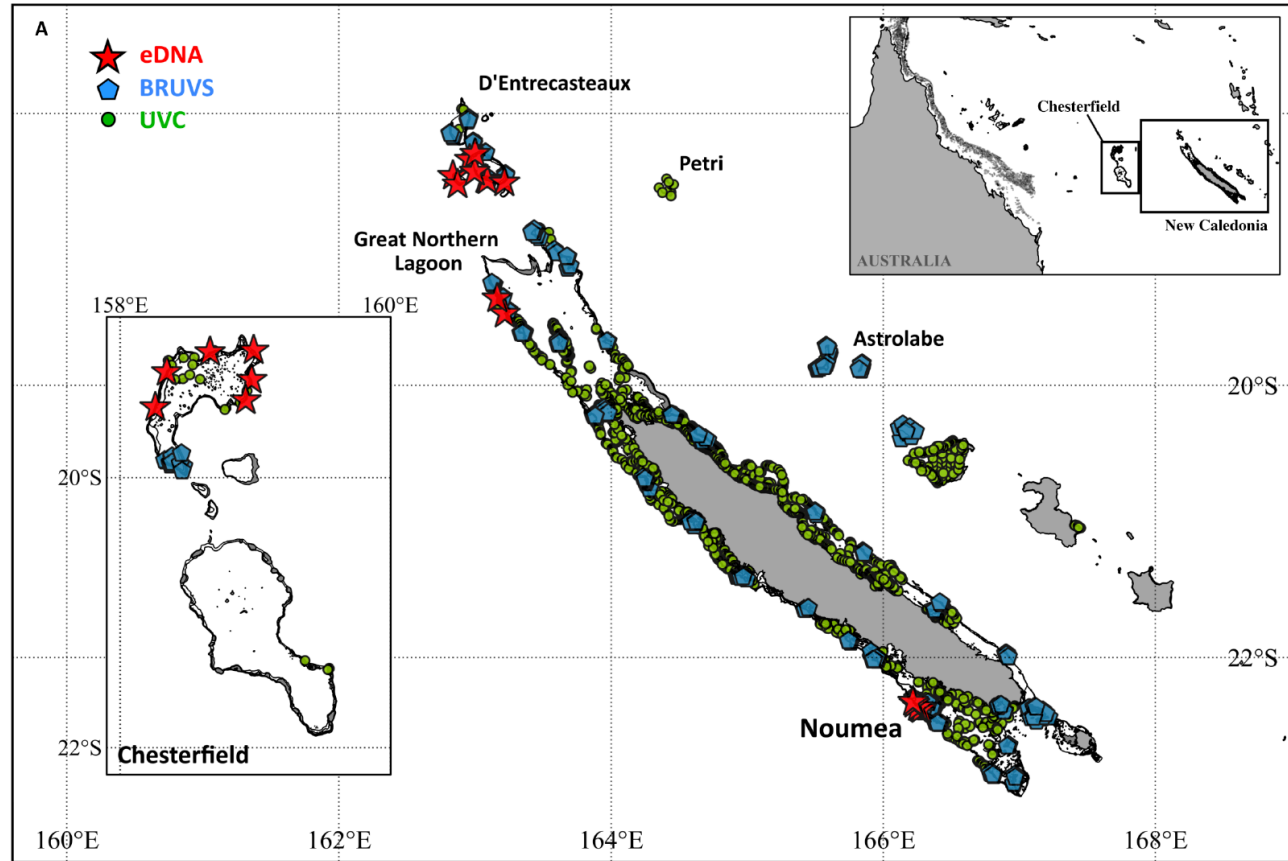
Fig. 1. Sampling design and analyses of surveys across the New Caledonian archipelago, southwestern Pacific. (**A**) Sampling design in the New Caledonian archipelago (red stars, eDNA; blue pentagons, BRUVS; green dots, UVC). (**B**) Sample size (UVC, $n = 2758$; BRUVS, $n = 385$; eDNA, $n = 22$). (**C**) Cumulated number of shark species detected. (**D**) Frequency of samples with sharks detected. (**E**) Violin plot showing detected shark species richness, significantly different between techniques ($P < 0.001$, Kruskal-Wallis test), with eDNA detecting more shark species (2.5 ± 1.9) compared to BRUVS (0.8 ± 0.8) and UVC (0.2 ± 0.5) ($P < 0.001$, Dunn's tests). White dots are mean values; thick black bars correspond to interquartile ranges; thin black lines are 95% confidence intervals.
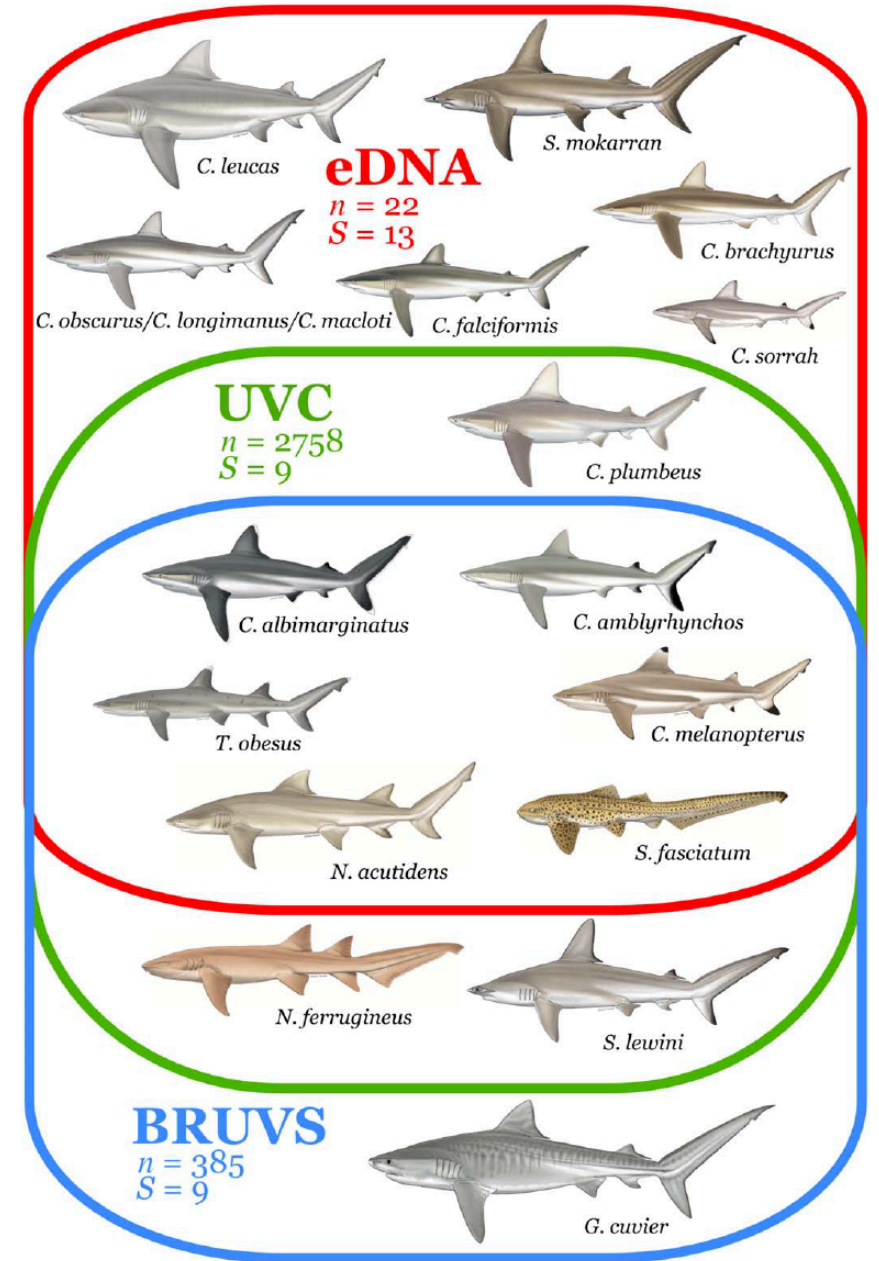
Fig. 2. Detection of shark species with different sampling methods. Venn diagram showing the species detected by eDNA ($n = 22$ samples, $S = 13$ species), UVC ($n = 2758$ samples, $S = 9$ species), and BRUVS ($n = 385$ samples, $S = 9$ species). Scientific drawings courtesy of M. Dando.
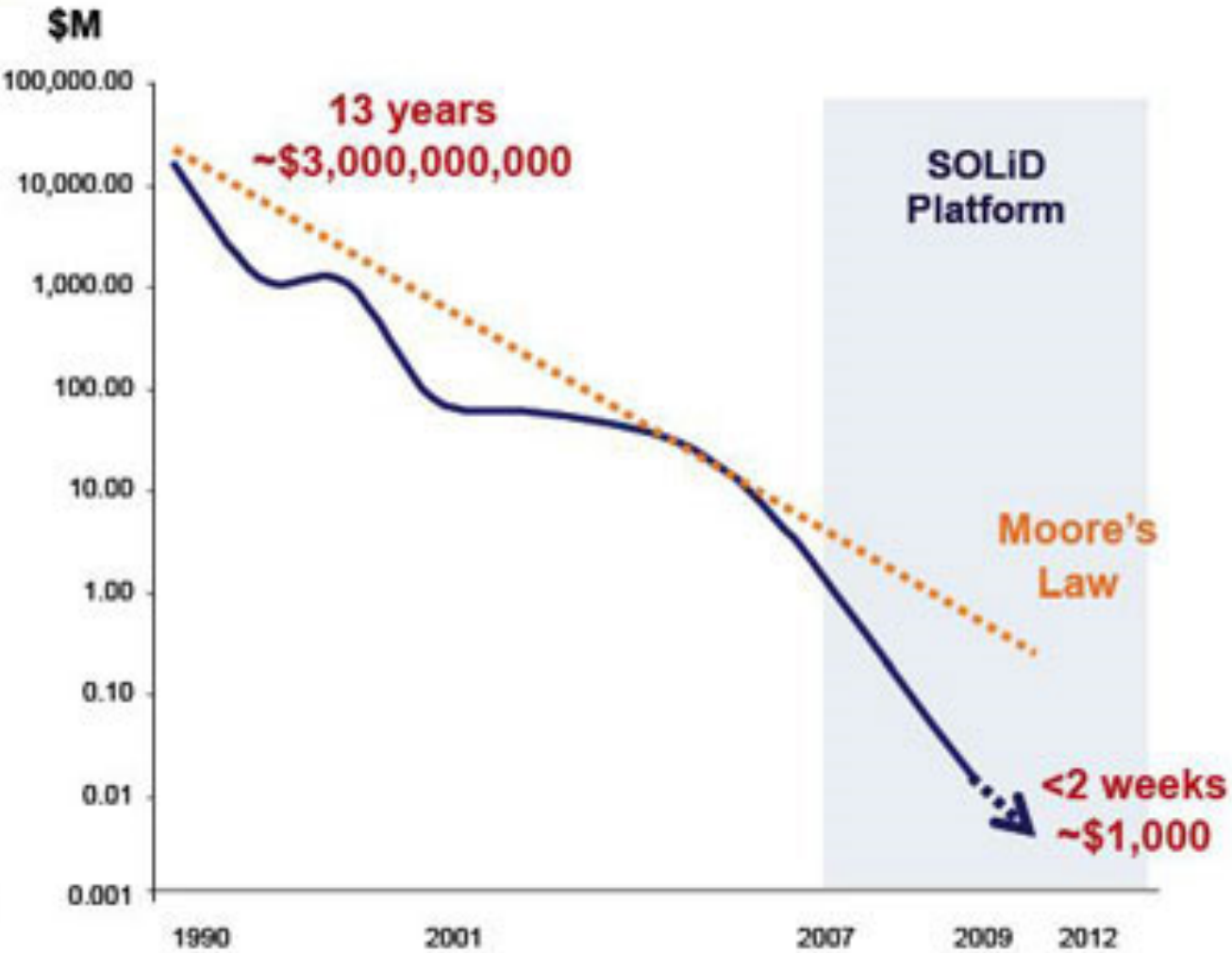
This and succeeding slides were borrowed (with thanks) from lecture slides generously put online by MCB7300 Bioinformatics Lecture, Ohio State University

DNA (nucleotide sequences) databases

- They are big databases and searching either one should produce similar results because they exchange information routinely.

-GenBank (NCBI): *http://www.ncbi.nlm.nih.gov*

-Ensembl: http://useast.ensembl.org/index.html

-DDBJ (DNA DataBase of Japan): *http://www.ddbj.nig.ac.jp*

-TIGR: *http://tigr.org/tdb/tgi*

-Yeast: *http://yeastgenome.org*

-Microbes: *http://img.jgi.doe.gov/cgi-bin/pub/main.cgi*

GenBank FREE

Eric W Sayers ✉, Mark Cavanaugh, Karen Clark, James Ostell, Kim D Pruitt,
Ilene Karsch-Mizrachi

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Abstract

GenBank® (www.ncbi.nlm.nih.gov/genbank/) is a comprehensive database that contains publicly available nucleotide sequences for 420 000 formally described species. Most GenBank submissions are made using BankIt, the NCBI Submission Portal, or the tool *tbl2asn*, and are obtained from individual laboratories and batch submissions from large-scale sequencing projects, including whole genome shotgun (WGS) and environmental sampling projects. Daily data exchange with the European Nucleotide Archive (ENA) and the DNA Data Bank of Japan (DDBJ) ensures worldwide coverage. GenBank is accessible through the NCBI Nucleotide database, which links to related information such as taxonomy, genomes, protein sequences and structures, and biomedical journal literature in PubMed. BLAST provides sequence similarity searches of GenBank and other sequence databases. Complete bimonthly releases and daily updates of the GenBank database are available by FTP. Recent updates include an expansion of sequence identifier formats to accommodate expected database growth, submission wizards for ribosomal RNA, and the transfer of Expressed Sequence Tag (EST) and Genome Survey Sequence (GSS) data into the Nucleotide database.

Table 1.

Growth of GenBank divisions (nucleotide base-pairs)

Division	Description	Release 227 (August 2018)	Annual increase (%)[a]
MAM	Other mammals	6 214 774 850	60.47%
WGS	Whole genome shotgun data	3 204 855 013 281	42.93%
UNA	Unannotated	296 706	42.25%
PLN	Plants	23 027 832 426	37.21%
BCT	Bacteria	53 541 127 504	36.93%
TSA	Transcriptome shotgun data	225 520 004 678	35.01%
PHG	Phages	463 029 085	34.38%
VRL	Viruses	4 073 816 676	16.99%
PAT	Patent sequences	22 019 723 131	14.57%
VRT	Other vertebrates	10 441 689 546	12.90%
ENV	Environmental samples	5 818 999 756	4.09%
HTC	High-throughput cDNA	721 454 983	3.57%
PRI	Primates	8 262 441 252	2.96%
SYN	Synthetic	1 192 279 390	1.62%
GSS	Genome survey sequences	26 339 143 098	1.40%
EST	Expressed sequence tags	42 988 632 150	0.82%
HTG	High-throughput genomic	27 770 730 435	0.45%
ROD	Rodents	4 534 815 151	0.31%
STS	Sequence tagged sites	640 879 986	0.00%
INV	Invertebrates[b]	8 597 126 159	−50.09%
TOTAL	All GenBank sequences	3 677 023 810 243	39.52%

Table 2.

Top organisms in GenBank (Release 227)

Organism	Base pairs[a]
Homo sapiens	19 752 523 722
Mus musculus	10 246 475 076
Rattus norvegicus	6 530 046 440
Bos taurus	5 431 692 037
Zea mays	5 245 788 885
Sus scrofa	5 075 446 882
Hordeum vulgare	3 237 283 130
Escherichia coli	3 220 757 391
Danio rerio	3 191 415 637
Oryzias latipes	2 836 938 628
Arachis hypogaea	2 682 391 941
Triticum aestivum	2 636 490 116
Ovis canadensis	2 590 574 434
Solanum lycopersicum	2 572 291 998
Bos mutus	2 290 216 303
Cyprinus carpio	1 836 731 087
Oryza sativa	1 727 115 789
Apteryx australis	1 595 510 956
Bordetella pertussis	1 456 386 736
Strongylocentrotus purpuratus	1 436 247 256
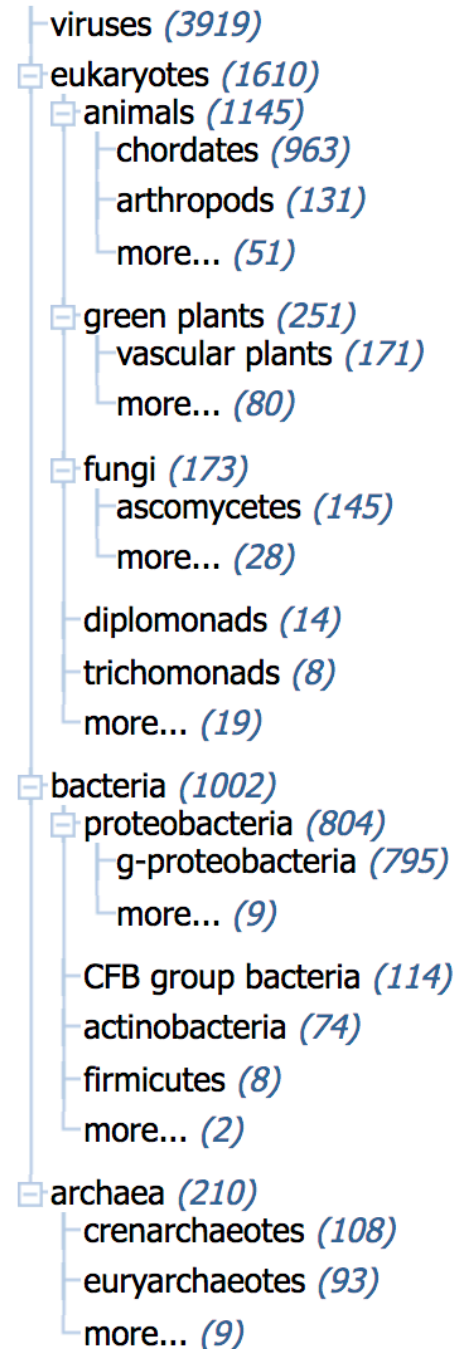
Nucleotide

Create alert   Advanced   Help

Species
Animals (1,145)
Plants (251)
Fungi (173)
Protists (41)
Bacteria (1,002)
Archaea (210)
Viruses (3,919)
Customize ...

Molecule types
genomic DNA/RNA (6,049)
mRNA (691)
Customize ...

Source databases
INSDC (GenBank) (6,377)
RefSeq (364)
Customize ...

Sequence Type
Nucleotide (6,741)

Genetic compartments
Chloroplast (134)
Mitochondrion (582)
Plasmid (14)
Plastid (138)

Sequence length
Custom range...

Release date
Custom range...

Revision date
Custom range...

Clear all

Show additional filters

Summary ▾   20 per page ▾   Sort by Default order ▾   Send to: ▾

Items: 1 to 20 of 6741

<< First   < Prev   Page [1] of 338   Next >   Last >>

☐ 1. **Banana bunchy top virus isolate Rwanda 138 segment DNA-N, complete sequence**
1,089 bp circular DNA
Accession: JQ820464.1 GI: 394326307
Assembly   Protein   Taxonomy
GenBank   FASTA   Graphics

☐ 2. **Banana bunchy top virus isolate Rwanda 138 segment DNA-C, complete sequence**
1,018 bp circular DNA
Accession: JQ820463.1 GI: 394326301
Assembly   Protein   Taxonomy
GenBank   FASTA   Graphics

☐ 3. **Banana bunchy top virus isolate Rwanda 138 segment DNA-M, complete sequence**
1,047 bp circular DNA
Accession: JQ820462.1 GI: 394326296
Assembly   Protein   Taxonomy
GenBank   FASTA   Graphics

☐ 4. **Banana bunchy top virus isolate Rwanda 138 segment DNA-S, complete sequence**
1,075 bp circular DNA
Accession: JQ820461.1 GI: 394326290
Assembly   Protein   Taxonomy
GenBank   FASTA   Graphics

☐ 5. **Banana bunchy top virus isolate Rwanda 138 segment DNA-U3, complete sequence**
1,062 bp circular DNA
Accession: JQ820460.1 GI: 394326285
Assembly   Taxonomy
GenBank   FASTA   Graphics

Filters: **Manage Filters**

Results by taxon
Top Organisms [Tree]
Human immunodeficiency virus 1 (3392)
Homo sapiens (599)
Xanthomonas cannabis pv. phaseoli (293)
Xanthomonas vasicola (158)
Pantoea rwandensis (140)
All other taxa (2159)
More...

Find related data
Database: Select ▾
Find items

Search details
Rwanda[All Fields]

Search   See more...

Recent activity
Turn Off   Clear

🔍 Rwanda (6741)
                        Nucleotide

📄 GenBank

                        See more...
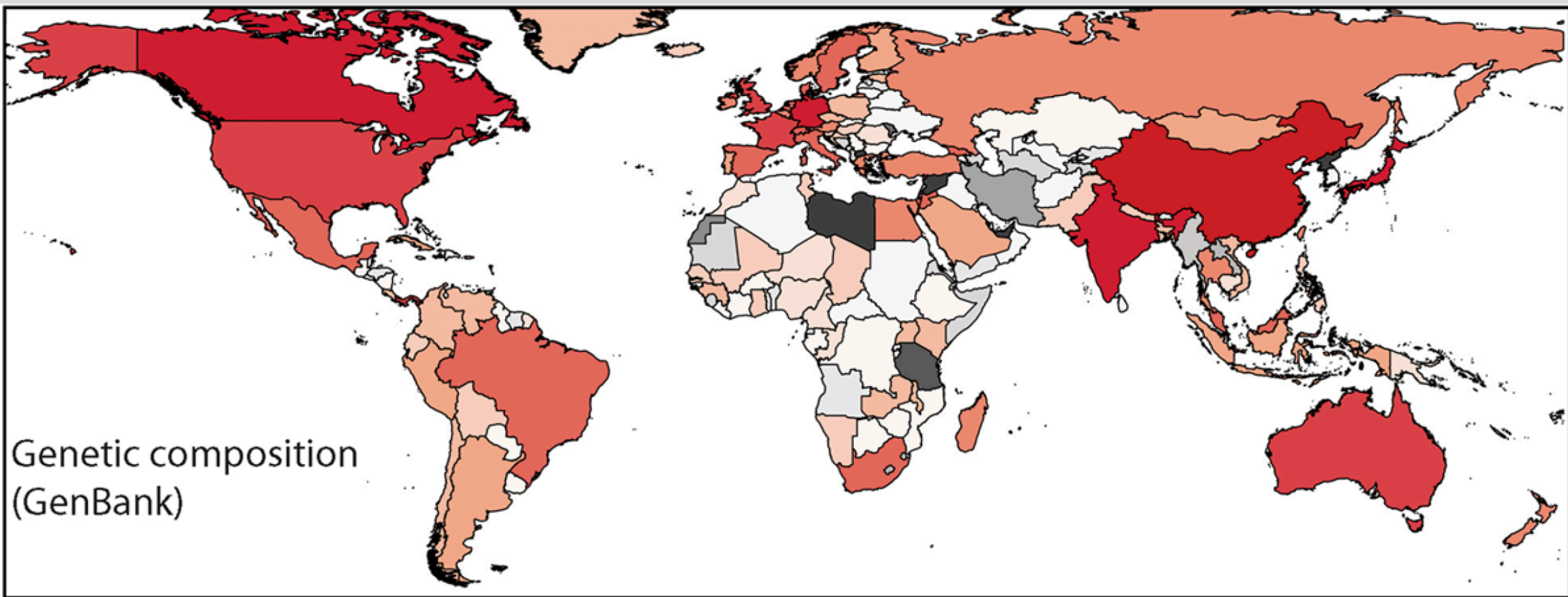
Taxonomic Groups [List]

viruses (3919)
⊟ eukaryotes (1610)
⊟ animals (1145)
  chordates (963)
  arthropods (131)
  more... (51)
⊟ green plants (251)
  vascular plants (171)
  more... (80)
⊟ fungi (173)
  ascomycetes (145)
  more... (28)
diplomonads (14)
trichomonads (8)
more... (19)
⊟ bacteria (1002)
⊟ proteobacteria (804)
  g-proteobacteria (795)
  more... (9)
CFB group bacteria (114)
actinobacteria (74)
firmicutes (8)
more... (2)
⊟ archaea (210)
crenarchaeotes (108)
euryarchaeotes (93)
more... (9)

Genetic composition
(GenBank)

DNA (nucleotide sequences) databases

● They are big databases and searching either one should produce similar results because they exchange information routinely.

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-Ensembl: http://useast.ensembl.org/index.html

-DDBJ (DNA DataBase of Japan): *http://www.ddbj.nig.ac.jp*

-TIGR: *http://tigr.org/tdb/tgi*

-Yeast: *http://yeastgenome.org*

-Microbes: *http://img.jgi.doe.gov/cgi-bin/pub/main.cgi*

Community Composition

Rebuilding Global Fisheries

Boris Worm,[1]* Ray Hilborn,[2]* Julia K. Baum,[3] Trevor A. Branch,[2] Jeremy S. Collie,[4] Christopher Costello,[5] Michael J. Fogarty,[6] Elizabeth A. Fulton,[7] Jeffrey A. Hutchings,[1] Simon Jennings,[8,9] Olaf P. Jensen,[2] Heike K. Lotze,[1] Pamela M. Mace,[10] Tim R. McClanahan,[11] Cóilín Minto,[1] Stephen R. Palumbi,[12] Ana M. Parma,[13] Daniel Ricard,[1] Andrew A. Rosenberg,[14] Reg Watson,[15] Dirk Zeller[15]

After a long history of overexploitation, increasing efforts to restore marine ecosystems and rebuild fisheries are under way. Here, we analyze current trends from a fisheries and conservation perspective. In 5 of 10 well-studied ecosystems, the average exploitation rate has recently declined and is now at or below the rate predicted to achieve maximum sustainable yield for seven systems. Yet 63% of assessed fish stocks worldwide still require rebuilding, and even lower exploitation rates are needed to reverse the collapse of vulnerable species. Combined fisheries and conservation objectives can be achieved by merging diverse management actions, including catch restrictions, gear modification, and closed areas, depending on local context. Impacts of international fleets and the lack of alternatives to fishing complicate prospects for rebuilding fisheries in many poorer regions, highlighting the need for a global perspective on rebuilding marine resources.

Fig. 1. Data sources used to evaluate global fisheries. (**A**) Global catch data; colors refer to the natural logarithm of the average reported catch (metric ton km^{-2} year^{-1}) from 1950 to 2004). (**B**) Other data: Stock assessments quantify the status of exploited populations; research trawl surveys are used to estimate fish community trends; ecosystem models are used to assess responses to fishing. Ecosystems that were analyzed in some detail are highlighted in green (not overfished), yellow (low exploitation rate, biomass rebuilding from overfishing), orange (low to moderate exploitation rate, not yet rebuilding), or red (high exploitation rate).
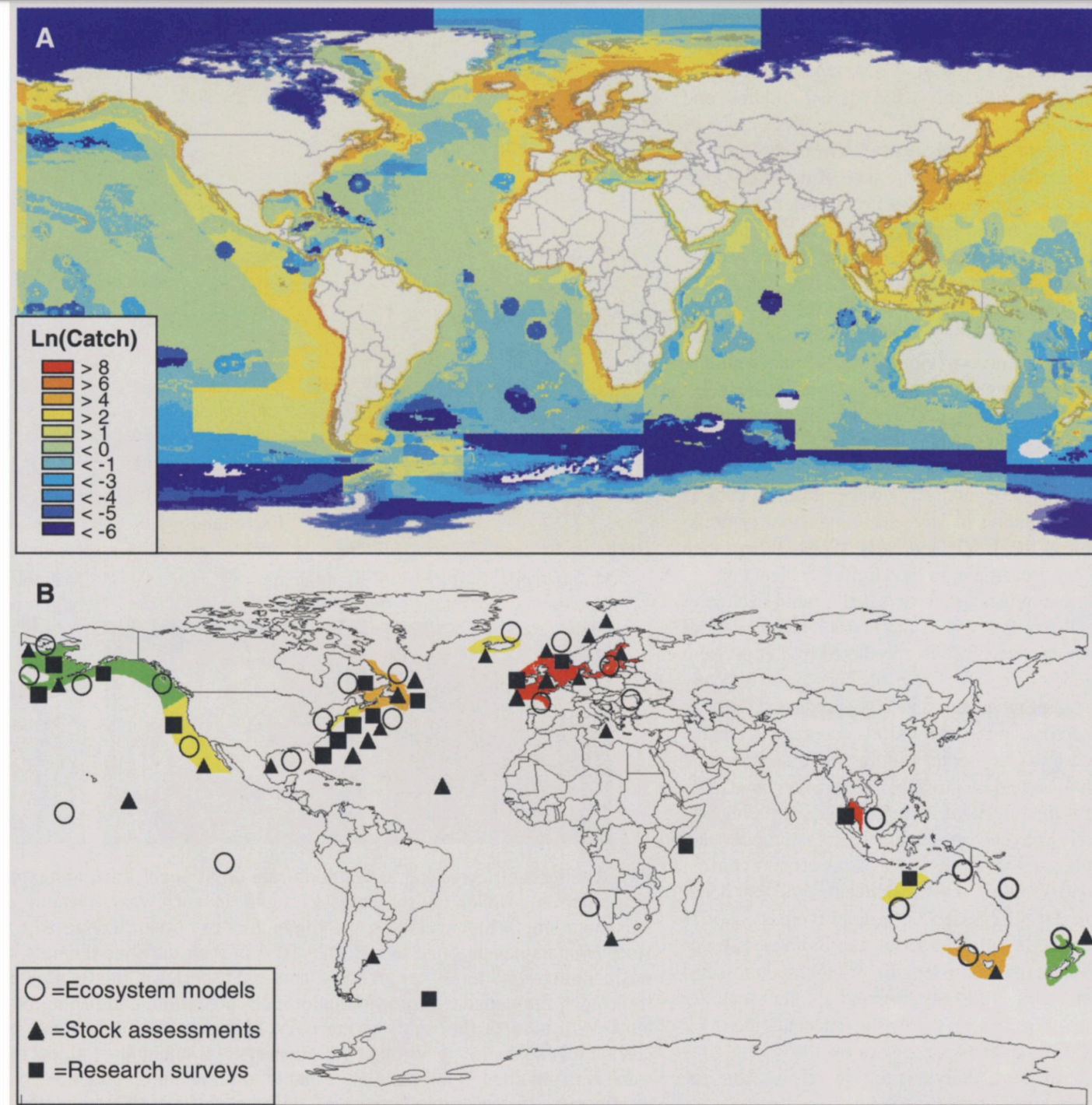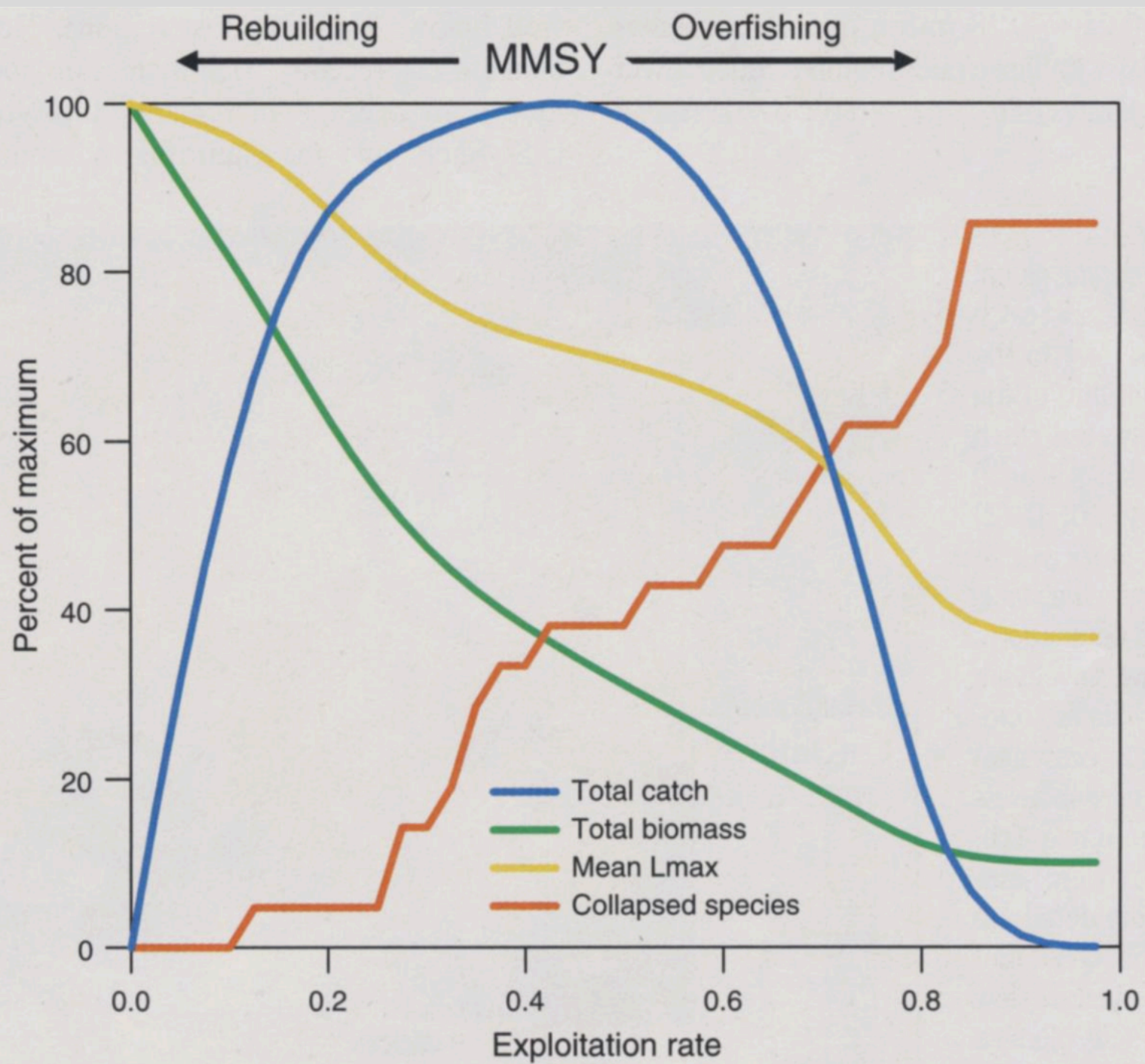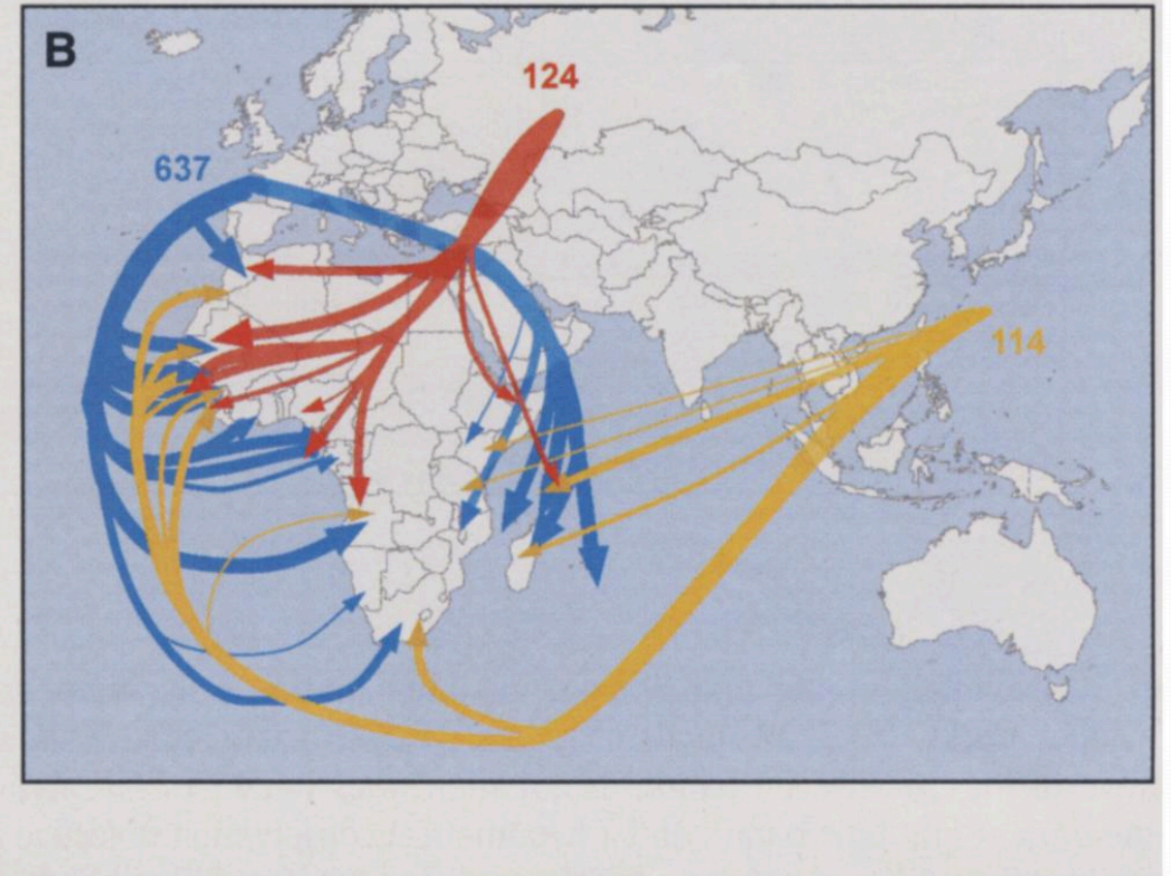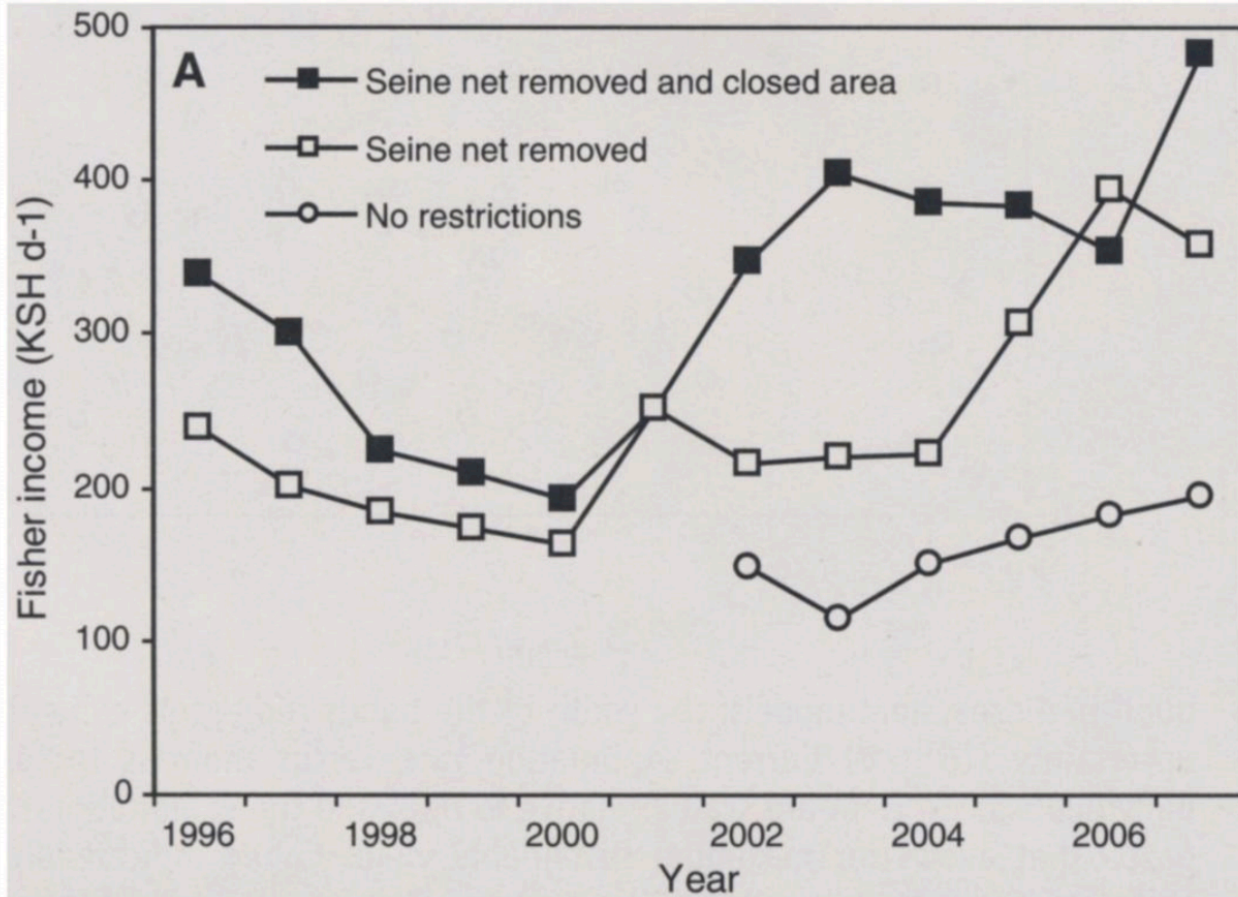
Fig. 5. Problems and solutions for small-scale fisheries. (**A**) Rebuilding of Kenyan small-scale fisheries through gear restrictions and closed area management. Updated, after (*27*). (**B**) Movement of fishing effort from developed nations to Africa in the 1990s. Data indicate total access years in distant-water fishing agreements. Updated, after (*39*).

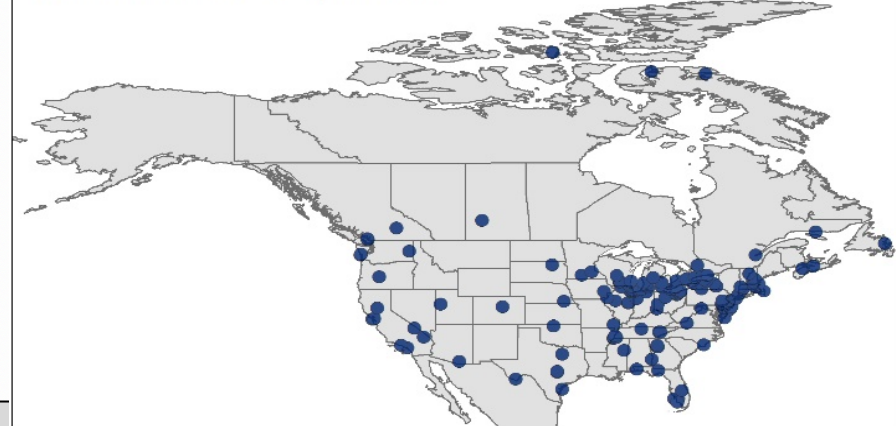# Decadal-scale Avifaunal Change from Museum and Observational Data for Sites across the United States and Canada

Running Title: Avifaunal turnover in the US and Canada

Fernando Machado-Stredel[1], Benedictus Freeman[1], Daniel Jiménez-Garcia[2], Marlon E. Cobos[1], Claudia Nuñez-Penichet[1], Laura Jiménez[1], Ed Komp[3], Utku Perktas[1,4,5], Ali Khalighifar[1], Kate Ingenloff[1], Walter Tapondjou[1], Thilina de Silva[1], Sumudu Fernando[1], Luis Osorio-Olvera[6], Lindsay Campbell[1], and A. Townsend Peterson*[1]

Total number of bird records
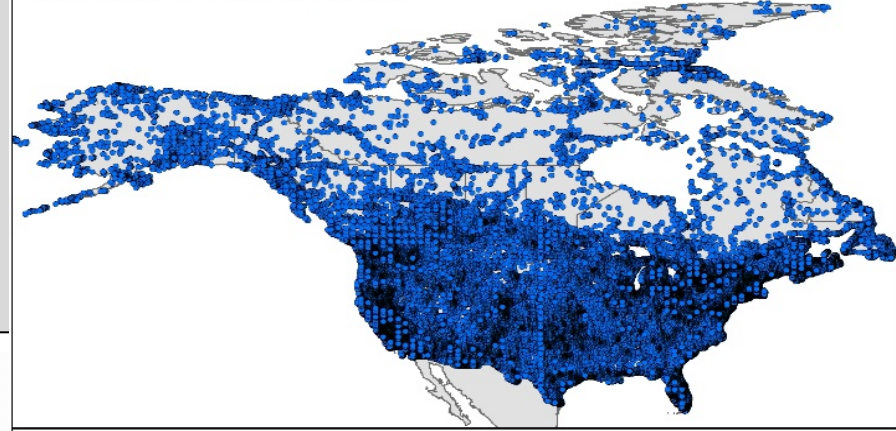
Well-inventoried sites pre-1980

Sites not well-inventoried removed (red X's)

Jaccard index
- 0.01 - 0.12
- 0.12 - 0.27
- 0.27 - 0.49
- 0.49 - 0.59
- 0.59 - 0.66
- 0.66 - 0.71
- 0.71 - 0.75
- 0.75 - 0.78
- 0.78 - 0.81
- 0.81 - 0.85

Species lost
- 0 - 3
- 4 - 7
- 8 - 11
- 12 - 16
- 17 - 27
- 28 - 41

Lanius ludovicianus

Poecile hudsonicus

Loss
Gain
Neutral

Tympanuchus cupido

Thryomanes bewickii
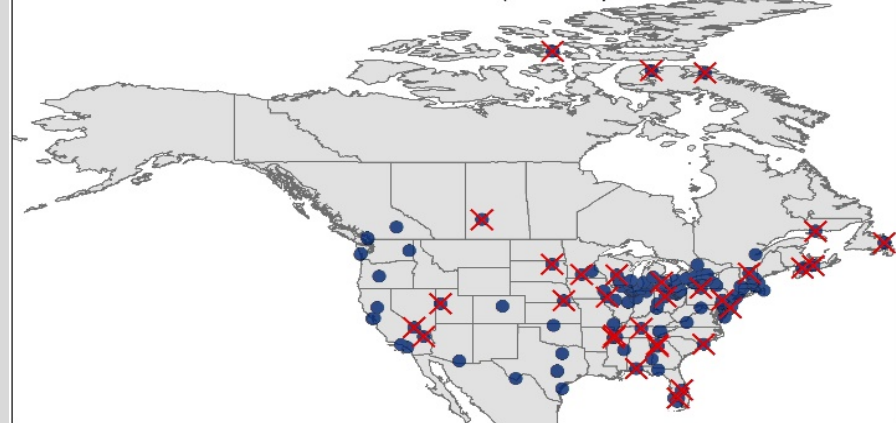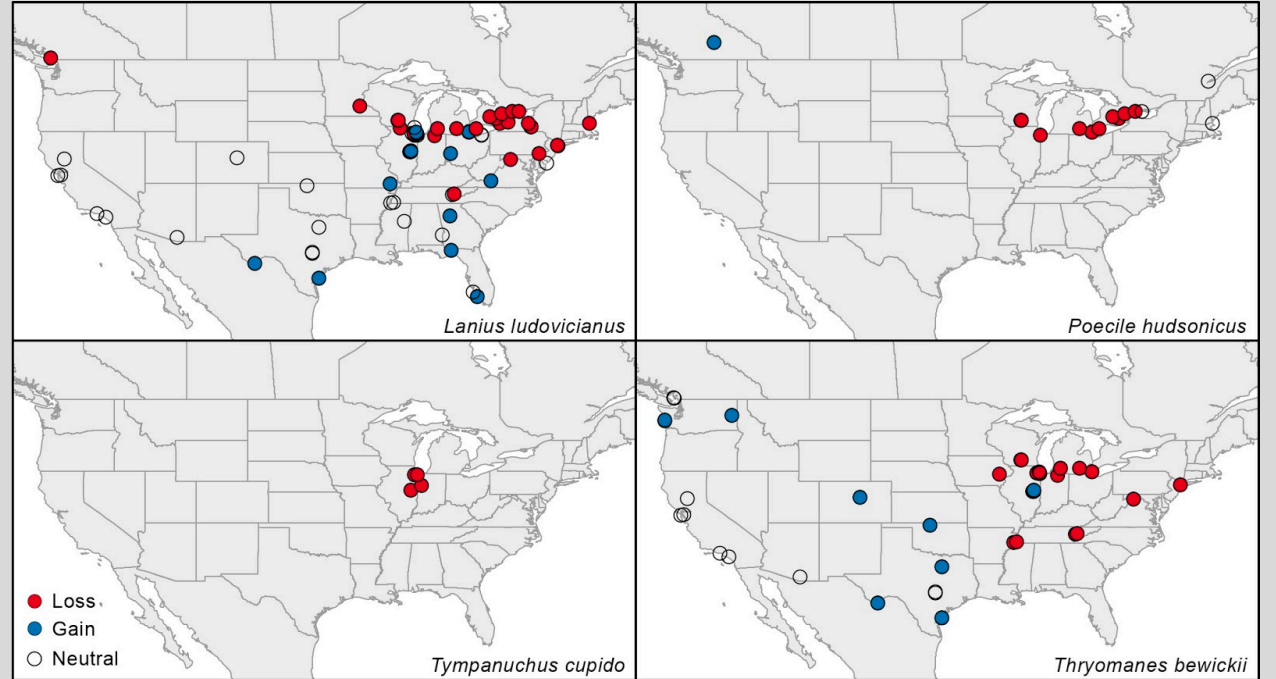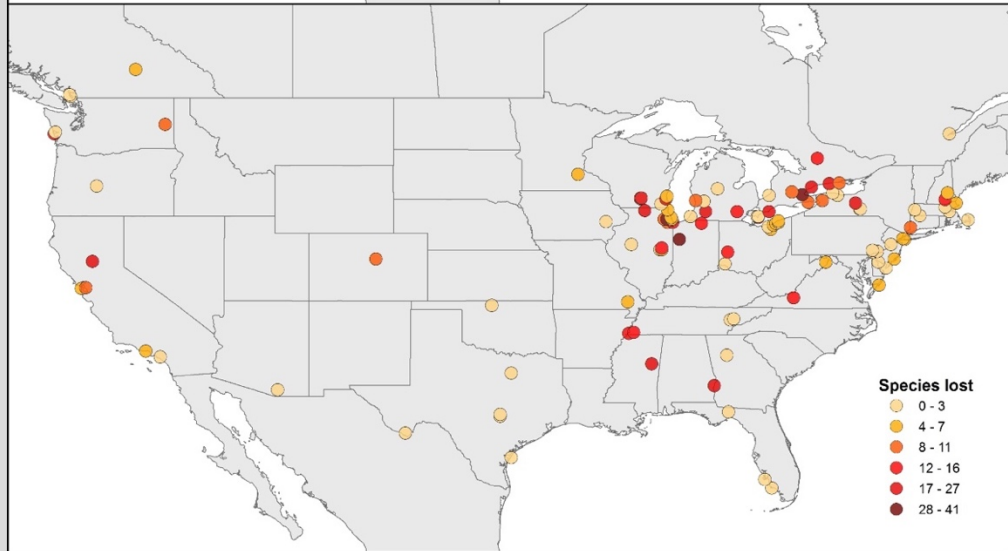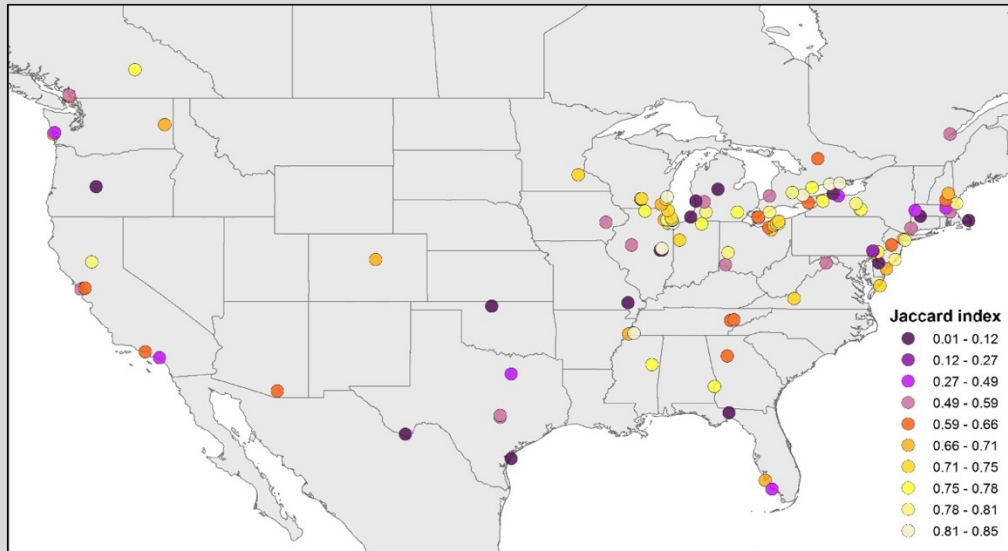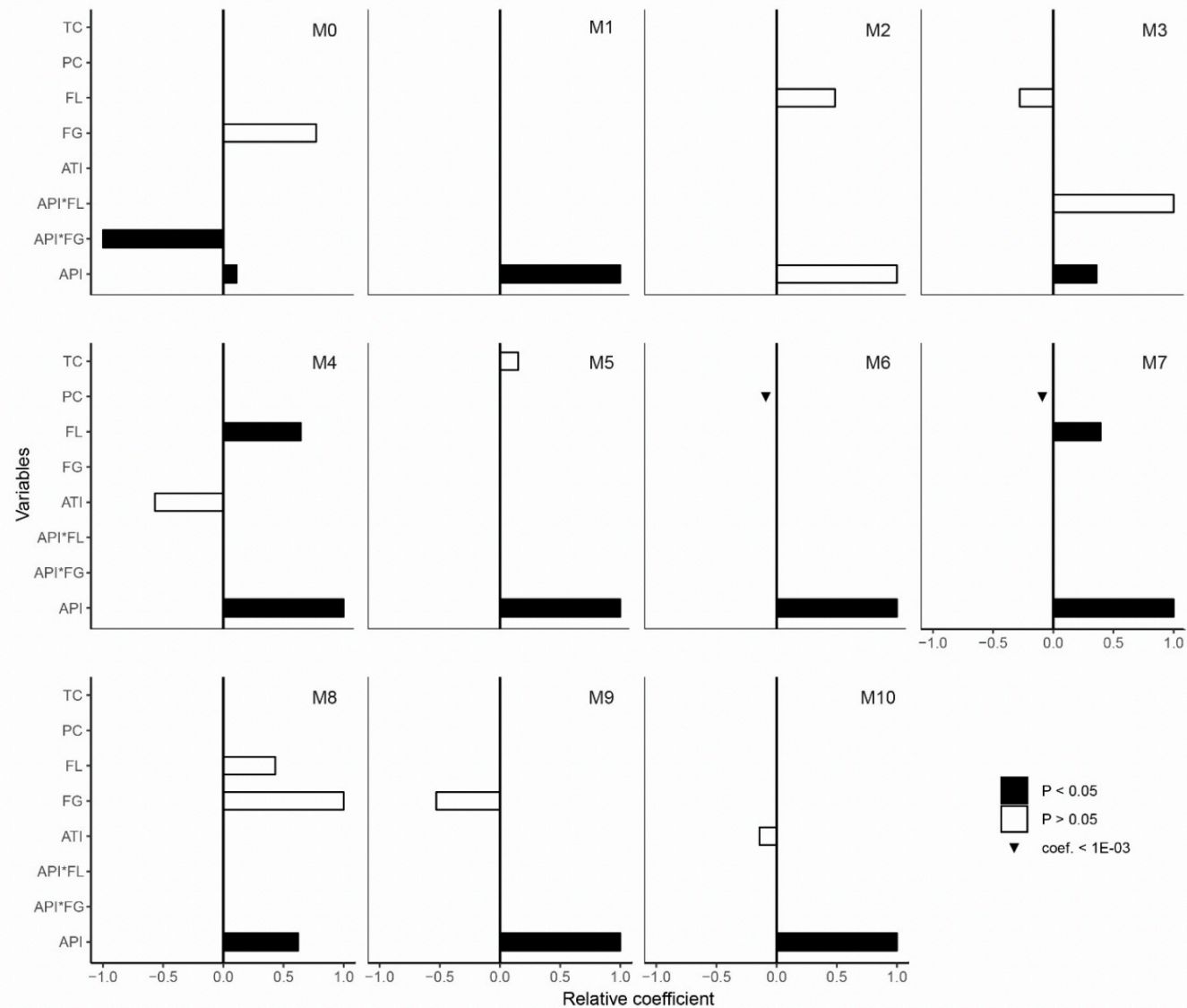
Figure 4. Coefficient relative contribution of the best models for incidence loss, from a set of 252 candidate models, where top-right labels refer to models for the dataset with (this model termed M0) and without the outlier (termed M1-M10). Variables are abbreviated as explained in the text, and two interactions are shown (API*FL and API*FG). The direction of the horizontal bars represents the sign of the coefficient, and significant effects (P <0.05) for each variable are indicated by filled bars. Inverted black triangles show small coefficients. The eigenvector coefficients are not shown (see Appendix S3).

Contributed Paper

Range Size and Extinction Risk in Forest Birds

GRANT HARRIS*† AND STUART L. PIMM*
*Nicholas School of the Environment and Earth Sciences, Duke University, NC 27708, U.S.A.

Abstract: *Small geographical range size is the single best predictor of threat of extinction in terrestrial species. Knowing how small a species' range has to be before authorities consider it threatened with extinction would allow prediction of a species' risk from continued deforestation and warming climates and provide a baseline for conservation and management strategies aspiring to mitigate these threats. To determine the threshold at which forest-dependent bird species become threatened with extinction, we compared the range sizes of threatened and nonthreatened species. In doing so, we present a simple, repeatable, and practical protocol to quantify range size. We started with species' ranges published in field guides or comparable sources. We then trimmed these ranges, that is, we included only those parts of the ranges that met the species' requirements of elevation and types of forest preferred. Finally, we further trimmed the ranges to the amount of forest cover that remains. This protocol generated an estimate of the remaining suitable range for each species. We compared these range estimates with those from the World Conservation Union Red List. We used the smaller of the two estimates to determine the threshold, 11,000 km², below which birds should be considered threatened. Species considered threatened that have larger ranges than this qualified under other (nonspatial) red list criteria. We identified a suite of species (18) that have not yet qualified as threatened but that have perilously small ranges—about 11% of the nonthreatened birds we analyzed. These birds are likely at risk of extinction and reevaluation of their status is urgently needed.*

Essay

Assumption-versus data-based approaches to summarizing species' ranges

A. Townsend Peterson,* ¶ Adolfo G. Navarro-Sigüenza,† and Alejandro Gordillo†
*Biodiversity Institute, University of Kansas, Lawrence, KS 66045, U.S.A.
†Facultad de Ciencias, Universidad Nacional Autónoma de México, Mexico, D.F., 04510, Mexico

Abstract: *For conservation decision making, species' geographic distributions are mapped using various approaches. Some such efforts have downscaled versions of coarse-resolution extent-of-occurrence maps to fine resolutions for conservation planning. We examined the quality of the extent-of-occurrence maps as range summaries and the utility of refining those maps into fine-resolution distributional hypotheses. Extent-of-occurrence maps tend to be overly simple, omit many known and well-documented populations, and likely frequently include many areas not holding populations. Refinement steps involve typological assumptions about habitat preferences and elevational ranges of species, which can introduce substantial error in estimates of species' true areas of distribution. However, no model-evaluation steps are taken to assess the predictive ability of these models, so model inaccuracies are not noticed. Whereas range summaries derived by these methods may be useful in coarse-grained, global-extent studies, their continued use in on-the-ground conservation applications at fine spatial resolutions is not advisable in light of reliance on assumptions, lack of real spatial resolution, and lack of testing. In contrast, data-driven techniques that integrate primary data on biodiversity occurrence with remotely sensed data that summarize environmental dimensions (i.e., ecological niche modeling or species distribution modeling) offer data-driven solutions based on a minimum of assumptions that can be evaluated and validated quantitatively to offer a well-founded, widely accepted method for summarizing species' distributional patterns for conservation applications.*
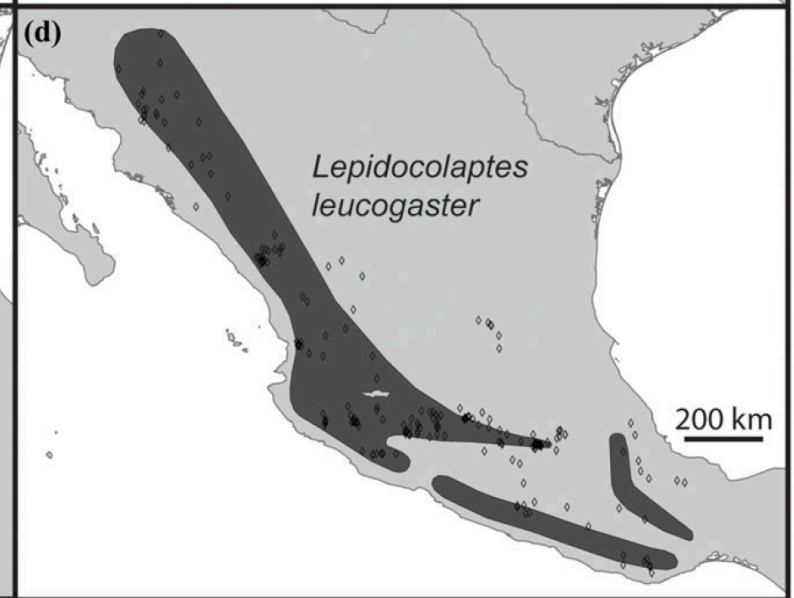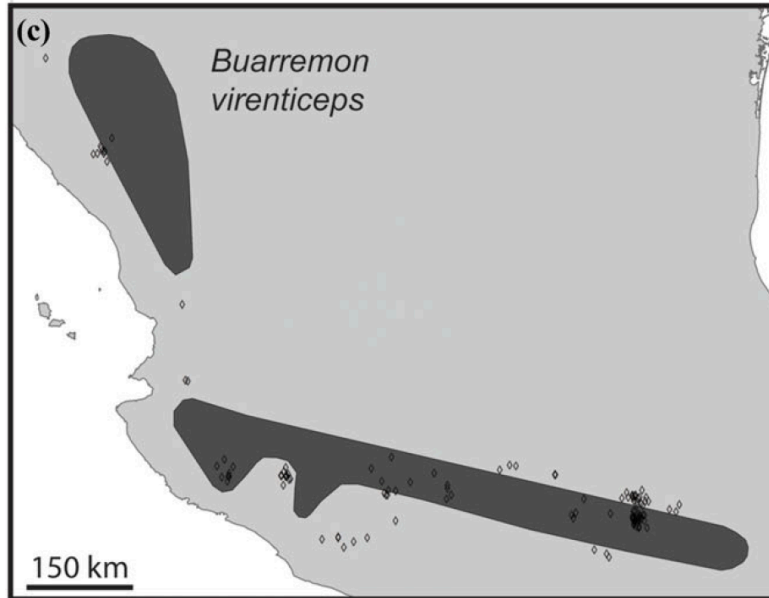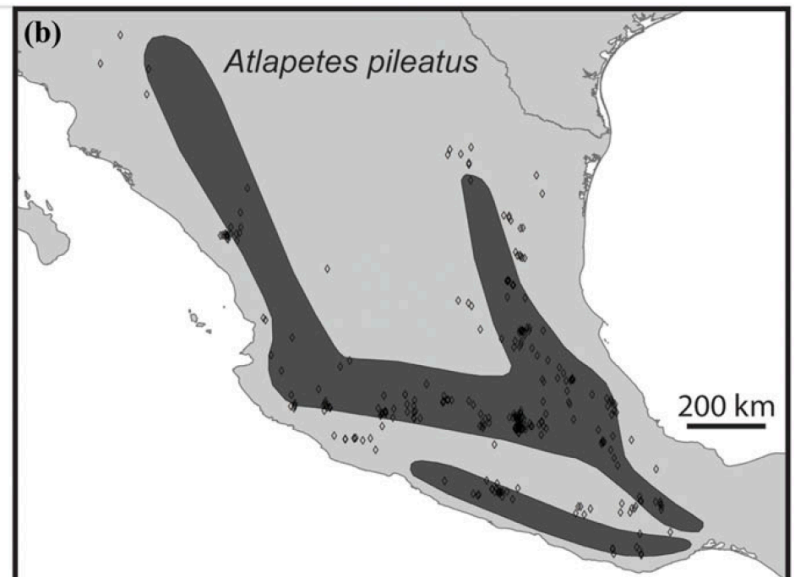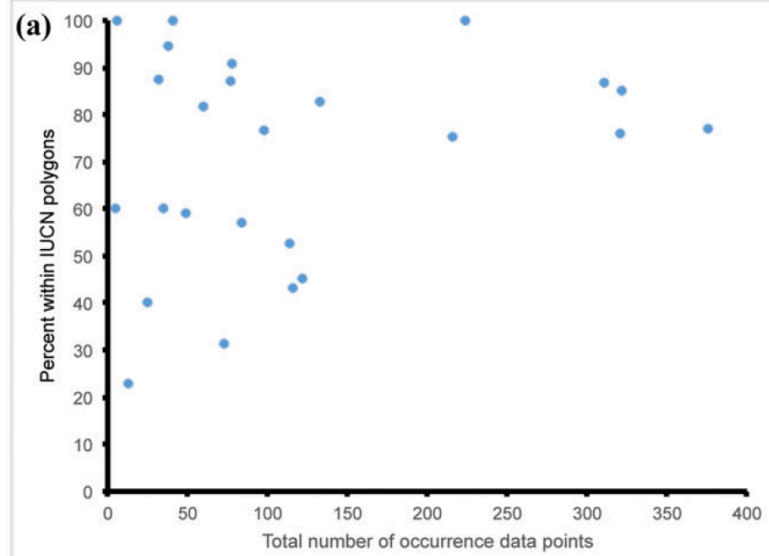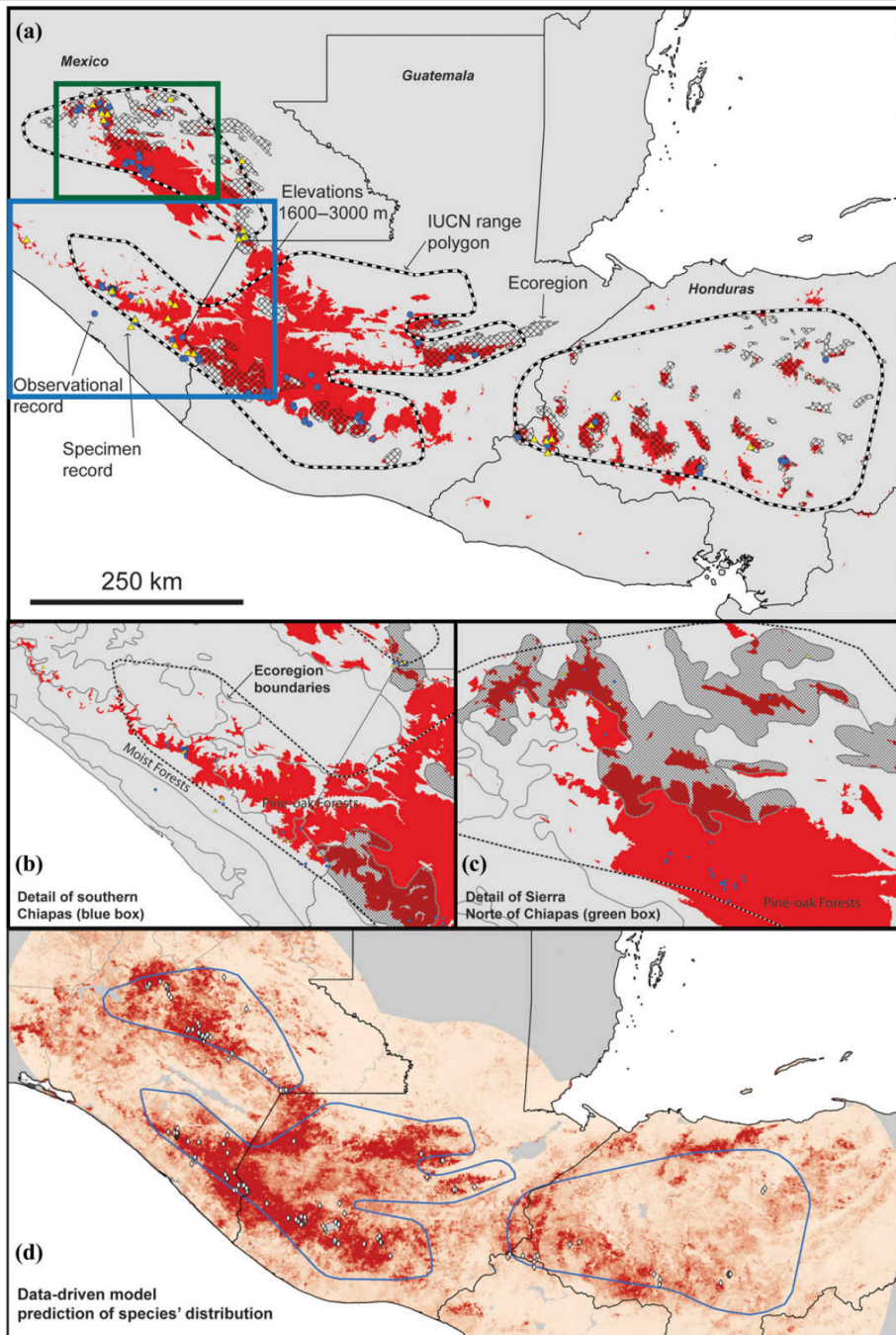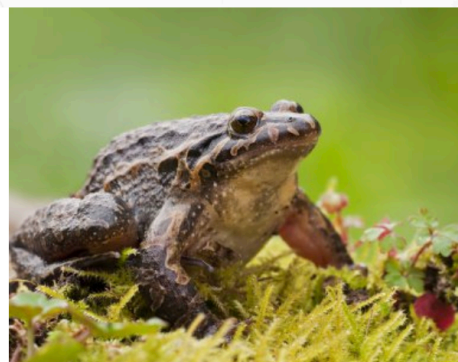
Figure 2. (a) Percent of known occurrences falling within International Union for Conservation of Nature (IUCN) range polygons relative to numbers of actual occurrence points for 25 endemic Mexican bird species. (b–d) Occurrences of 3 species endemic to Mexico (points) and species' distributions based on IUCN distributional polygons.

MOL
MAP OF LIFE
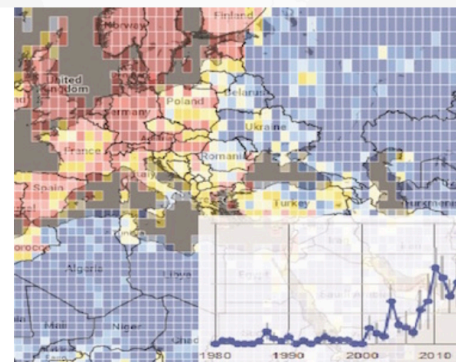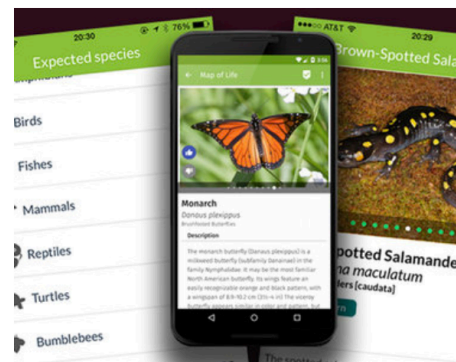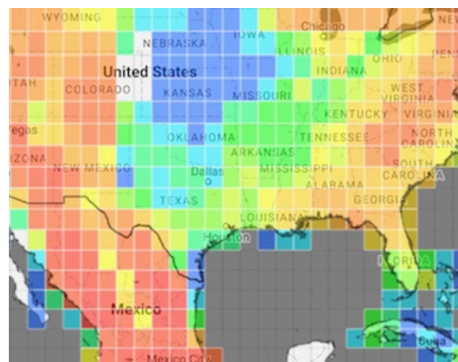
login / register   en de es fr zh

Species   **Locations**   **Indicators**   **Patterns**

Species Home   Summary Map   Detailed Map   Projection   Search for a species

Von Der Decken's Hornbill

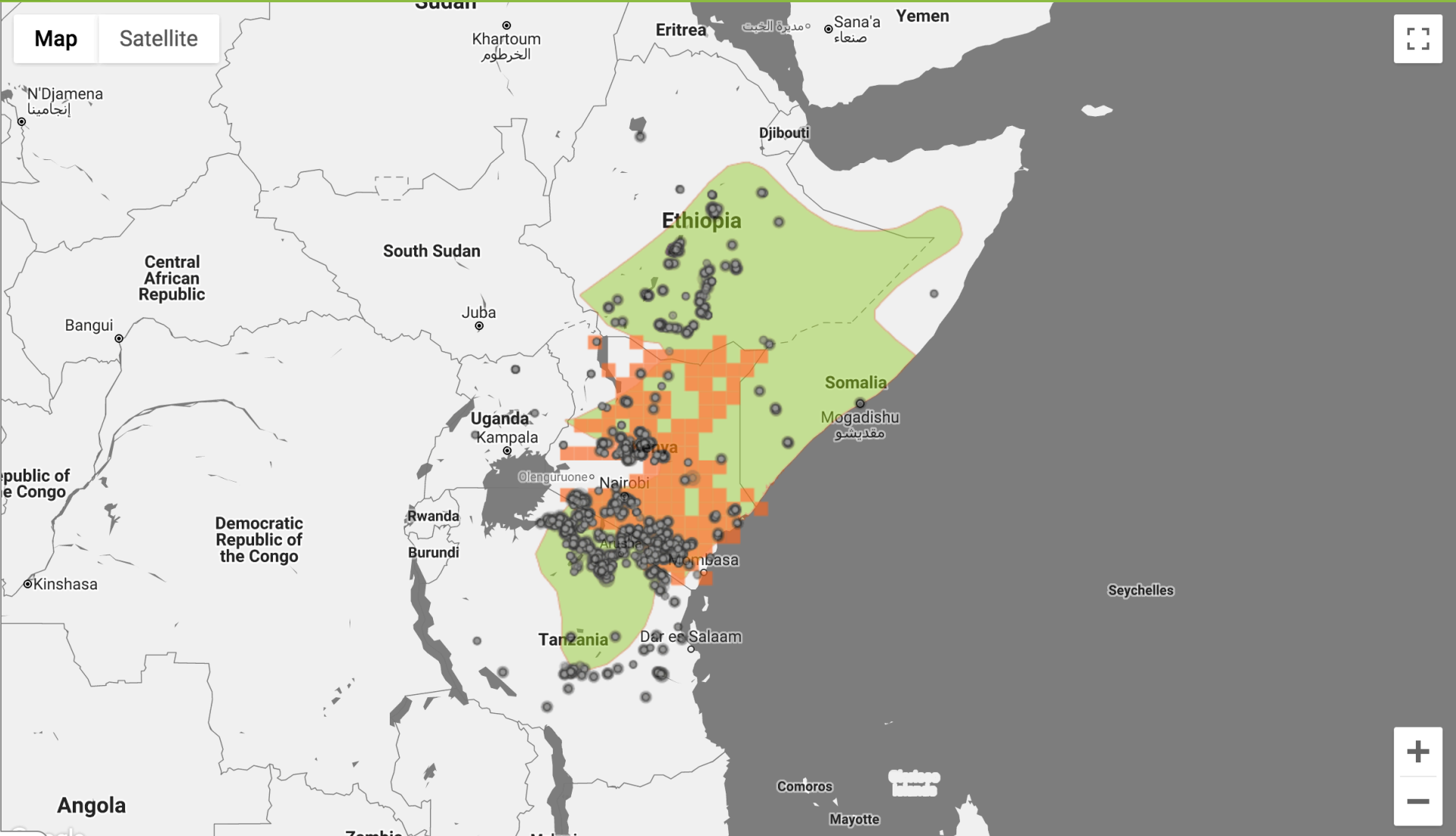*Tockus deckeni*

Least Concern (IUCN 2016)

Sources

Local inventories		2	
Expert range maps		2	
MOL grid of BirdLife			
Jetz et al. (2012)			
Point observations		2,689	
Gridded surveys		130	
Regional checklists		178	

Map   Satellite

Sudan   Eritrea   Yemen   Sana'a   Khartoum   N'Djamena   Djibouti   Ethiopia   Central African Republic   South Sudan   Bangui   Juba   Somalia   Uganda   Kampala   Mogadishu   Kenya   Republic of the Congo   Olenguruone   Nairobi   Rwanda   Democratic Republic of the Congo   Burundi   Arusha   Mombasa   Kinshasa   Seychelles   Tanzania   Dar es Salaam   Angola   Comoros   Mayotte   Zambia

DOI 10.15468/dl.apavea
Format: Simple

Occurrences: 203,088

| Scientific name | Musophagiformes |

RERUN QUERY

DOI 10.15468/dl.eorsr2
Date: 18 September 2019
Format: Simple

Occurrences: 183,830
Involved datasets: 143

And
- Country or area — Mexico
- Scientific name — Corvidae

RERUN QUERY

Warren. A. Williams

Species Populations

Ideally …

- Comprehensive population data for species worldwide
- Populations of native / rare / endemic species
  - Increasing → good
  - Decreasing → bad
- Populations of invasive / pest / disturbed-habitat species
  - Increasing → bad
  - Decreasing → good

The **Red List Index** (RLI), based on the IUCN Red List of Threatened Species, is an indicator of the changing state of global biodiversity. It defines the conservation status of major species groups, and measures trends in extinction risk over time. By conducting conservation assessments at regular intervals, **changes in the threat status of species** in a taxonomic group can be used to monitor trends in extinction risk. RLIs have been calculated for **birds and amphibians**, using changes in threat status for species in each of the groups.

Biodiversity Indicators Based on Trends in Conservation Status: Strengths of the IUCN Red List Index

STUART H. M. BUTCHART,* H. RESIT AKCAKAYA,‡ ELIZABETH KENNEDY,§ AND CRAIG HILTON-TAYLOR**

*BirdLife International, Wellbrook Co
‡Applied Biomathematics, 100 North
§Conservation International, 1919 M
**IUCN Species Programme Office, 2

Measuring Global Trends in the Status of Biodiversity: Red List Indices for Birds

Stuart H. M. Butchart[1]*, Alison J. Stattersfield[1], Leon A. Bennun[1], Sue M. Shutes[1], H. Resit Akçakaya[2], Jonathan E. M. Baillie[3], Simon N. Stuart[4], Craig Hilton-Taylor[5], Georgina M. Mace[3]

ematics, Setauket, New York, United States of America, 3 Institute of Zoology, Zoological Society of
ssessment Unit, Center for Applied Biodiversity Science, Conservation International, Washington,
me, IUCN/SSC United Kingdom Office, Cambridge, United Kingdom

Improvements to the Red List Index

Stuart H. M. Butchart[1]*, H. Resit Akçakaya[2], Janice Chanson[3], Jonathan E. M. Baillie[4], Ben Collen[4], Suhel Quader[5,8], Will R. Turner[6], Rajan Amin[4], Simon N. Stuart[3], Craig Hilton-Taylor[7]

1 BirdLife International, Cambridge, United Kingdom, 2 Applied Biomathematics, Setauket, New York, United States of America, 3 Conservation International/Center for Applied Biodiversity Science-World Conservation Union (IUCN)/Species Survival Commission Biodiversity Assessment Unit, IUCN Species Programme, Center for Applied Biodiversity Science, Conservation International, Washington, D. C., United States of America, 4 Institute of Zoology, Zoological Society of London, London, United Kingdom, 5 Department of Zoology, University of Cambridge, Cambridge, United Kingdom, 6 Center for Applied Biodiversity Science, Conservation International, Washington, D. C., United States of America, 7 World Conservation Union (IUCN) Species Programme, Cambridge, United Kingdom, 8 Royal Society for the Protection of Birds, Sandy, United Kingdom

The Red List Index uses information from the IUCN Red List to track trends in the projected overall extinction risk of sets of species. It has been widely recognised as an important component of the suite of indicators needed to measure progress towards the international target of significantly reducing the rate of biodiversity loss by 2010. However, further application of the RLI (to non-avian taxa in particular) has revealed some shortcomings in the original formula and approach: It performs inappropriately when a value of zero is reached; RLI values are affected by the frequency of assessments; and newly evaluated species may introduce bias. Here we propose a revision to the formula, and recommend how it should be applied in order to overcome these shortcomings. Two additional advantages of the revisions are that assessment errors are not propagated through time, and the overall level extinction risk can be determined as well as trends in this over time.
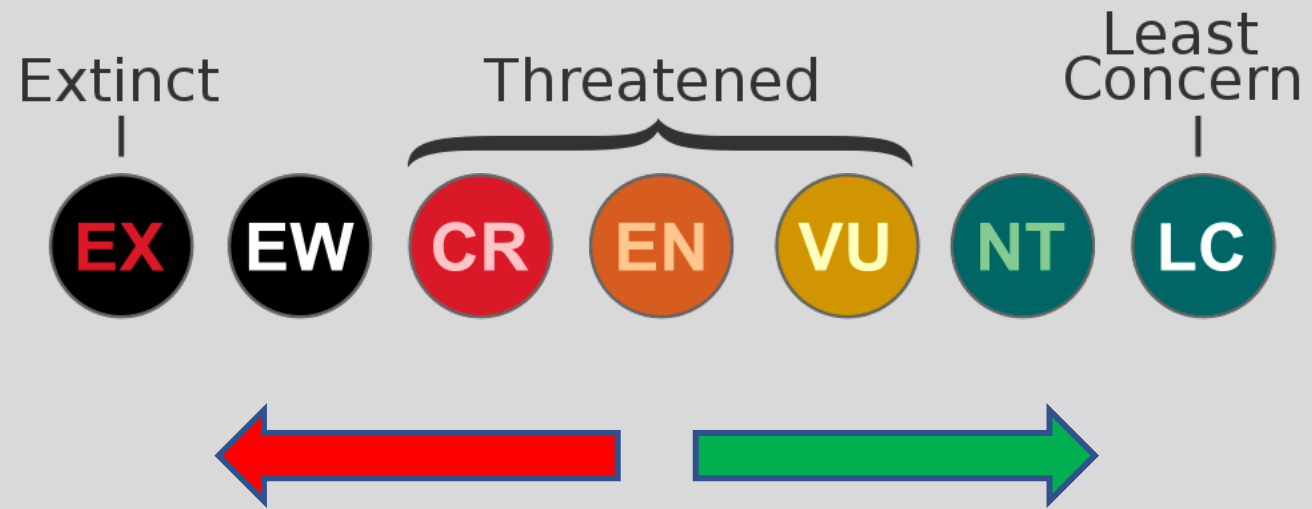
Table 1. Simplified Overview of Thresholds for the IUCN Red List Criteria

| Criterion	Critically Endangered	Endangered	Vulnerable	Qualifiers and Notes
A1: Reduction in population size	≥90%	≥70%	≥50%	Over 10y/3 generations in the past, where causes are reversible, understood and have ceased
A2–A4: Reduction in population size	≥80%	≥50%	≥30%	Over 10y/3 generations in past, future or combination
B1: Small range (extent of occurrence)	<100 km^2	<5,000 km^2	<20,000 km^2	Plus two of (a) severe fragmentation/few localities (1, ≤5, ≤10), (b) continuing decline, (c) extreme fluctuation
B2: Small range (area of occupancy)	<10 km^2	<500 km^2	<2,000 km^2	Plus two of (a) severe fragmentation/few localities (1, ≤5, ≤10), (b) continuing decline, (c) extreme fluctuation
C: Small and declining population	<250	<2,500	<10,000	Mature individuals. Continuing decline either (1) over specific rates and time periods or (2) with (a) specified population structure or (b) extreme fluctuation.
D1: Very small population	<50	<250	<1,000	Mature individuals
D2: Very small range	NA	NA	<20 km^2 or ≤5 locations	Capable of becoming CR or EX within a very short time
E: Quantitative analysis	≥10% in 100 y/3 generations	≥20% in 20 y/5 generations	≥50% in 100 y	Estimated extinction risk using quantitative models, e.g., population viability analyses

Table 2. Number of Species in Each IUCN Red List Category as Published in Collar and Andrew (1988), Collar et al. (1994), BirdLife International. (2000, 2004c), and the Number of Species Undergoing Genuine Status Changes in Each Period

|		1988	1994	2000	2004
Number of species in each category	EX	115	130	128	129
	EW		4	3	4
	PE				18
	CR	1,030	168	182	161
	EN		235	320	345
	VU		704	681	689
	NT (including CD)	634	886	727	773
	Total (EW to NT)	1,664	1,997	1,913	1,990
	LC	7,987	7,537	7,755	7,720
	DD		66	79	78
	NE	1	4	3	0
	NR	678	711	564	528
	Total	10,445	10,445	10,445	10,445
Number of species undergoing status changes for given reason	Recent genuine status change		25	128	42
	Genuine status change since first assessment		0	30	19
	Knowledge		957	912	139
	Taxonomy		349	396	104
	Criteria revision		0	1	2
	Other		5	6	0
	Total		1,336	1,473	306
Other statistics	Number of species undergoing genuine status changes[a] (percent of previous total excluding EX, DD, LC, NE, NR)		60 (3.6)	145 (7.3)	45 (2.4)
	Percent change in RLI		−2.14	−3.83	−0.93
	Percent change/year in RLI		−0.36	−0.64	−0.23
	Cumulative percent change in RLI		−2.14	−5.97	−6.90
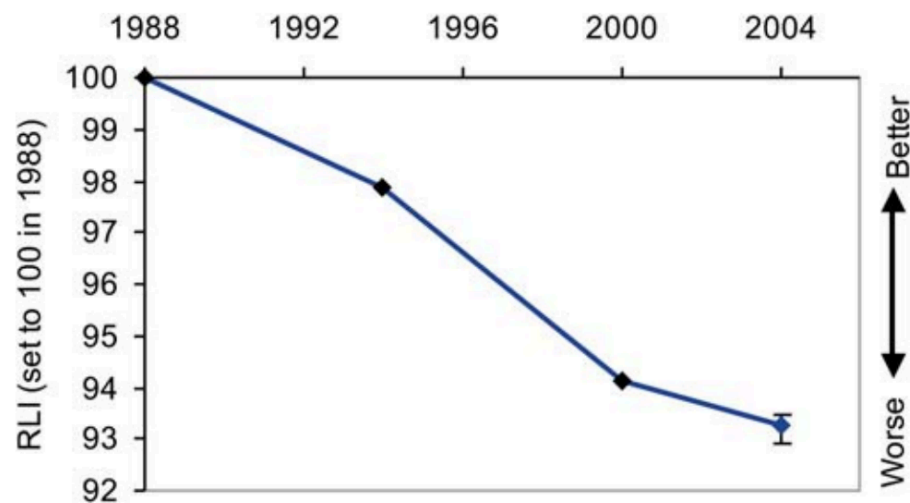
Figure 1. The RLI for All Bird Species

Sample size: 250 genuine status changes/2,469 species in categories Extinct in the Wild to Near Threatened in at least one assessment. Error bars for 2004 RLI value based on estimated number of genuine status changes for 2000–2004 not yet detected owing to information time lags (see Materials and Methods for further details).
DOI: 10.1371/journal.pbio.0020383.g001
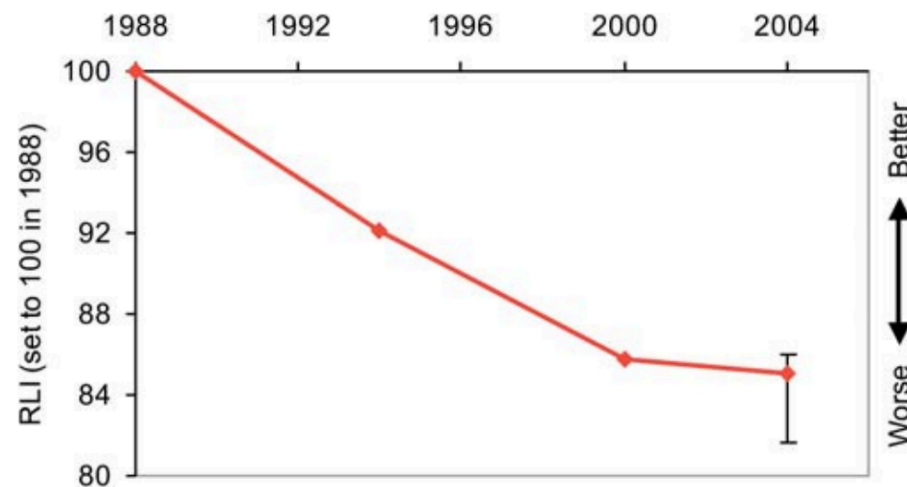
Figure 3. The RLI for All Bird Species with Categories Weighted by Relative Extinction Risk

Sample size: 250 genuine status changes/2,469 species in categories Extinct in the Wild to Near Threatened in at least one assessment. Error bars for 2004 RLI value based on estimated number of genuine status changes for 2000–2004 not yet detected owing to information time lags (see Materials and Methods for further details).
DOI: 10.1371/journal.pbio.0020383.g003
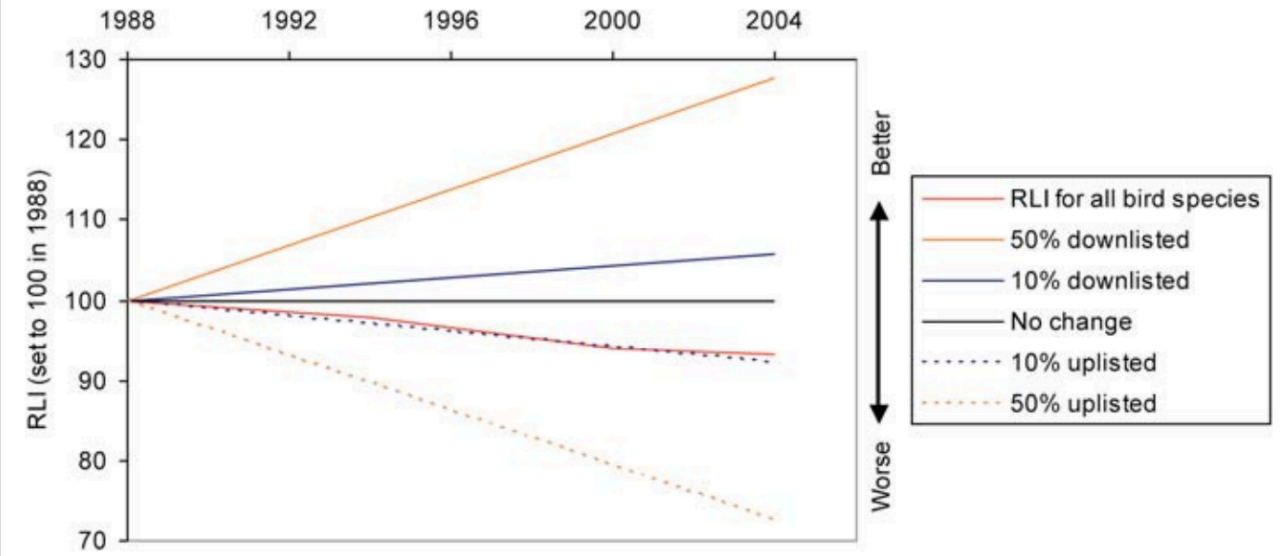
Figure 2. The RLI for All Bird Species in 1988–2004 Compared to Hypothetical Indices

Hypothetical indices show trends if no species had changed category, and if 10% or 50% of species in the categories from Near Threatened to Critically Endangered had been uplisted to a higher category of threat or downlisted to a lower category of threat over the period.
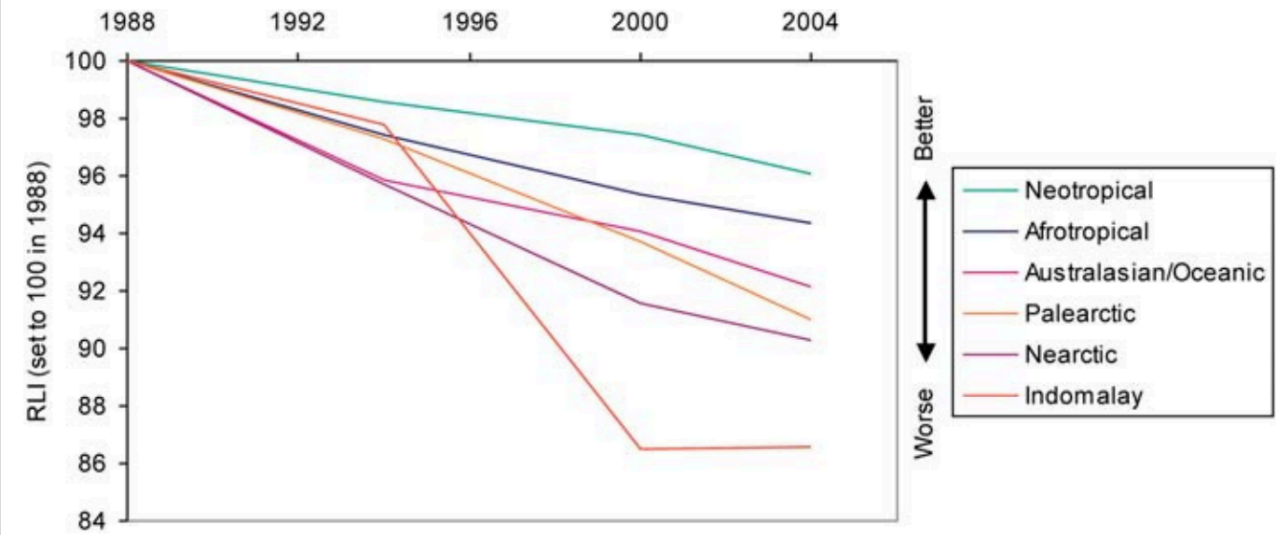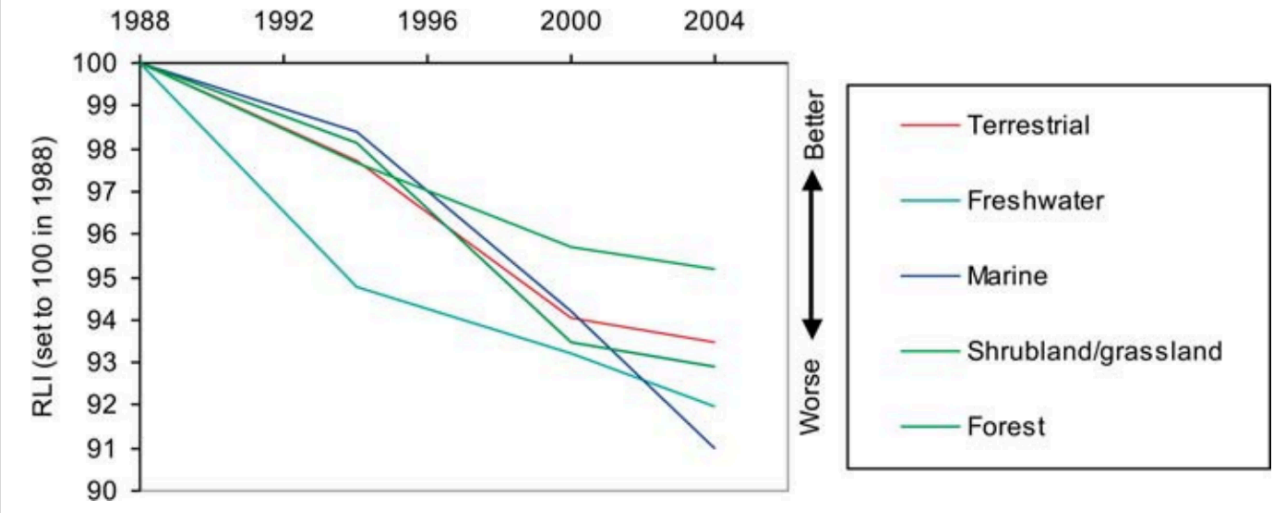
Figure 4. RLIs for Birds in Different Biogeographic Realms

Sample sizes: Neotropical, 49 genuine status changes/834 species in categories Extinct in the Wild to Near Threatened in at least one assessment; Afrotropical, 41/394; Australasian/Oceanic, 53/614; Palearctic, 34/238; Nearctic, 9/92; Indo-Malayan, 100/585.
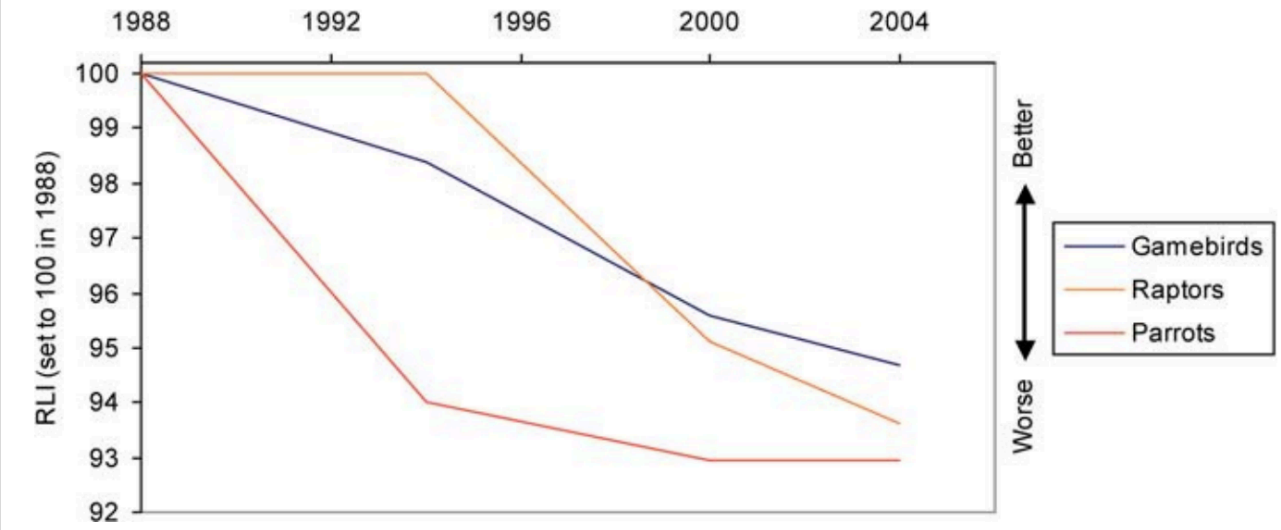
DOI: 10.1371/journal.pbio.0020383.g004

Figure 5. RLIs for Birds in Different Habitats

Figure 6. RLIs for Three Bird Families with High Conservation Profiles

Sample sizes: game birds, 15 genuine status changes/123 species in categories Extinct in the Wild to Near Threatened in at least one assessment; raptors, 10/93; parrots, 19/148.

HOWEVER, Red List Indices …

- Depend on the accuracy of threat assessments
- Depend on the frequency of threat assessments
- Are by nature restricted to relatively well-known taxonomic groups

(and the groups that develop them are not always well-composed of scientists from the regions where the species of concern are located…)

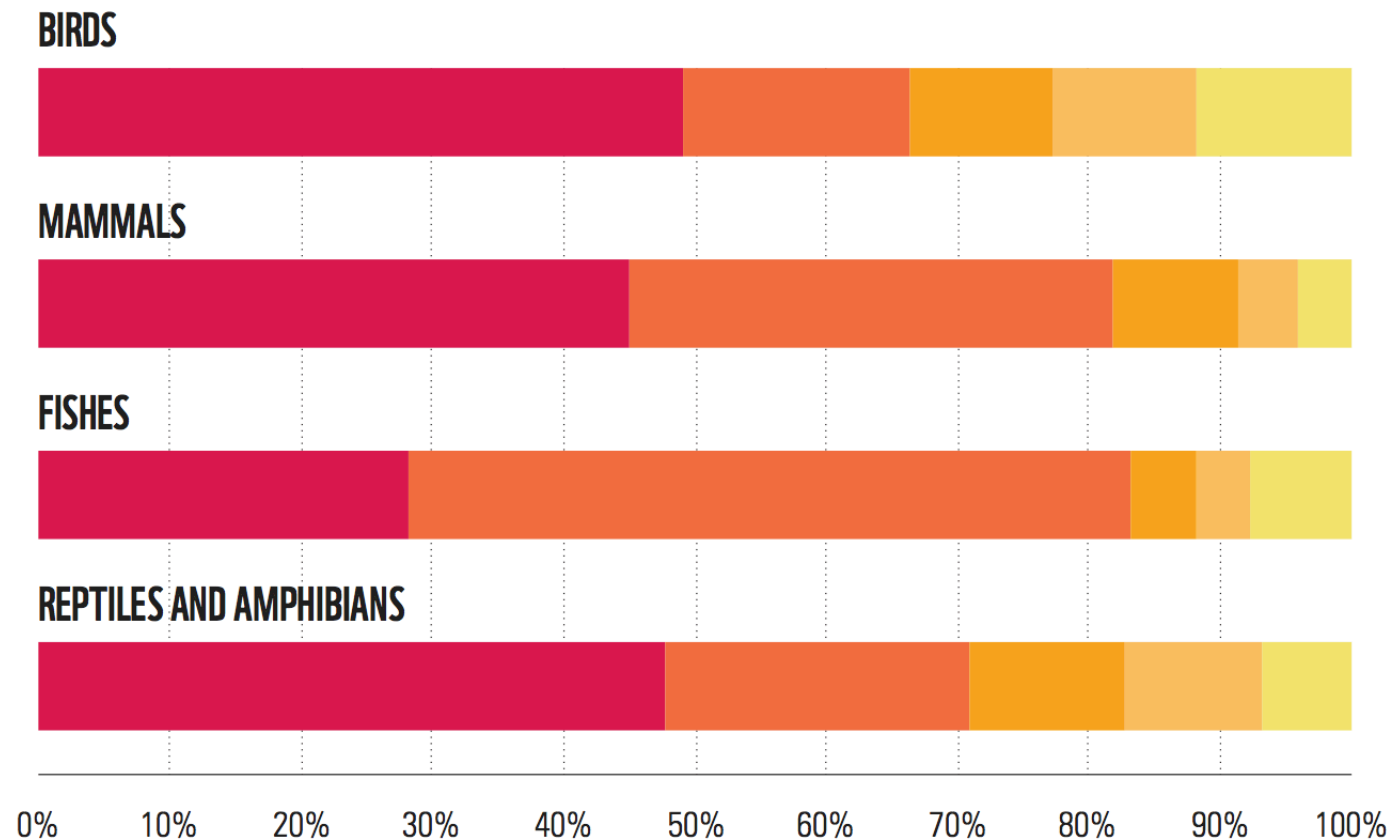# Living Planet Report

2018: Aiming higher

The Living Planet Index also tracks the state of global biodiversity by measuring the population abundance of thousands of vertebrate species around the world. The latest index shows an overall decline of 60% in population sizes between 1970 and 2014. Species population declines are especially pronounced in the tropics, with South and Central America suffering the most dramatic decline, an 89% loss compared to 1970. Freshwater species numbers have also declined dramatically, with the Freshwater Index showing an 83% decline since 1970. But measuring biodiversity – all the varieties of life that can be found on Earth and their relationships to each other – is complex, so this report also explores three other indicators measuring changes in species distribution, extinction risk and changes in community composition. All these paint the same picture – showing severe declines or changes.

Figure 15: Relative frequency of major threats by taxonomic group

Threat data is available for 3,789 populations in the global LPI database. Each of these populations could be associated with up to three different threats. There were 6,053 threats recorded in all [98].

Key

- ■ Habitat degradation/loss
- ■ Exploitation
- ■ Invasive species and disease
- ■ Pollution
- ■ Climate change

BIRDS

MAMMALS

FISHES

REPTILES AND AMPHIBIANS

0% 10% 20% 30% 40% 50% 60% 70% 80% 90% 100%
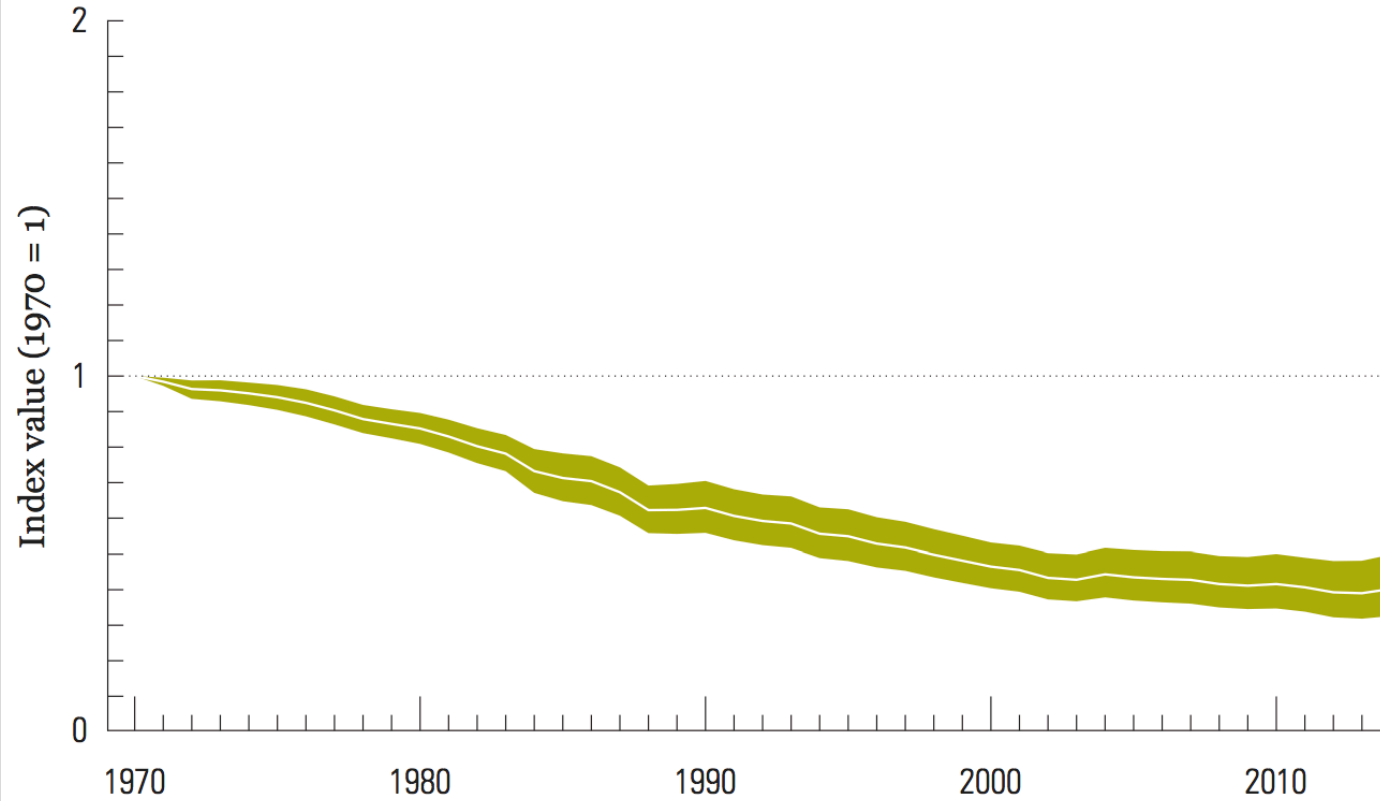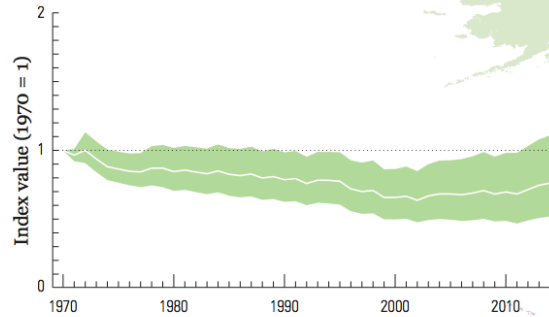
Figure 20: The Global Living Planet Index: 1970 to 2014
Average abundance of 16,704 populations representing 4,005 species monitored across the globe declined by 60%. The white line shows the index values and the shaded areas represent the statistical certainty surrounding the trend (range: -50% to -67%)[1].

Key

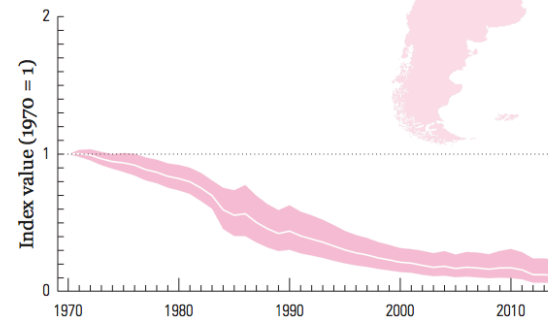Global Living Planet Index

Confidence limits

The Nearctic Living Planet Index
The average abundance for 2,417 terrestrial and freshwater populations (representing 875 species). These populations declined by 23% (+11% to -47%) between 1970 and 2014[1].

NEARCTIC

NEOTROPICAL

Figure 22: The Living Planet Index for each realm
The white line in the LPI graph shows the index values and the shaded areas represent the statistical certainty surrounding the trend (95%). Threat data is available for 3,789 – just under a quarter – of the populations in the global LPI[1]. This is explored in chapter 2.

The Neotropical Living Planet Index
The average abundance for 1,040 populations (representing 689 species) in the Neotropical biogeographic realm. Vertebrate populations declined by an average of 4.8% annually between 1970 and 2014, translating to an overall decline of 89%. This represents the most dramatic change in any biogeographic realm[1].

The Palearctic Living Planet Index
The average abundance for 2,866 terrestrial and freshwater populations (representing 576 species). These populations declined by 31% (-6% to -50%) between 1970 and 2014 [1].
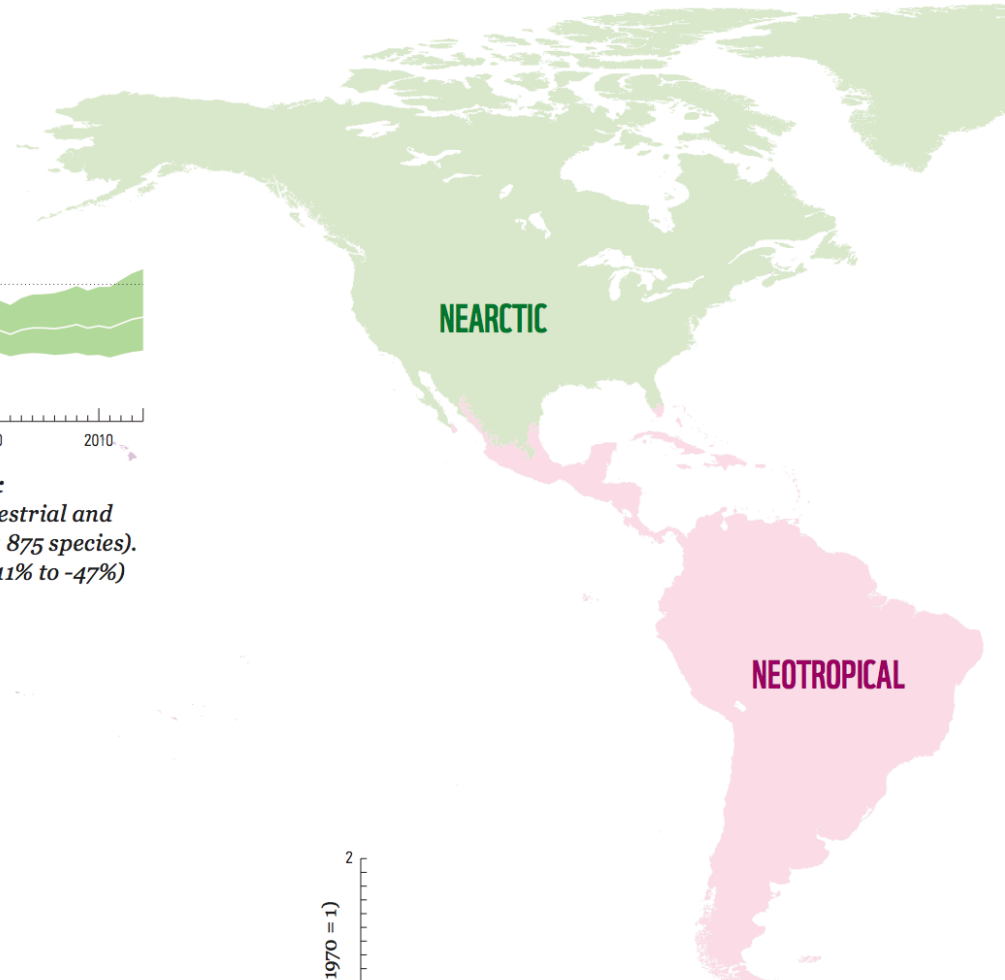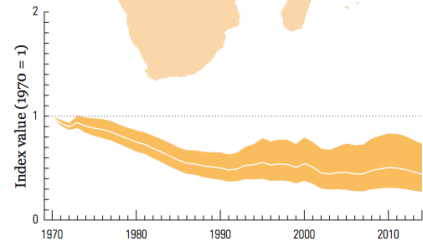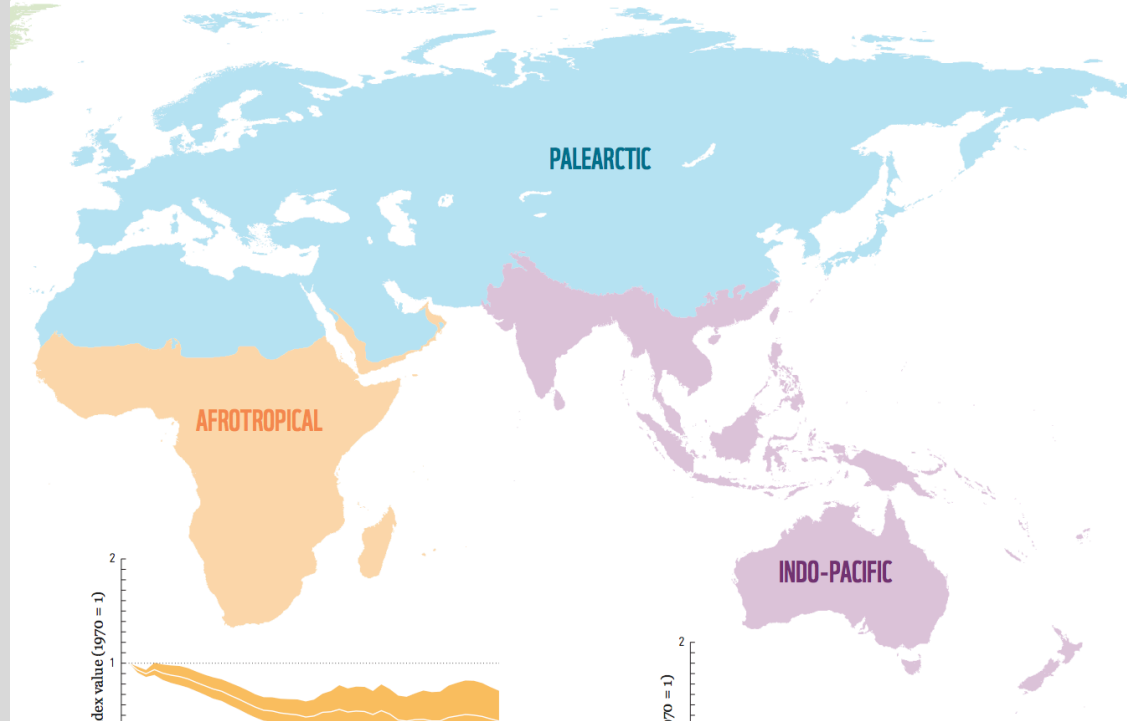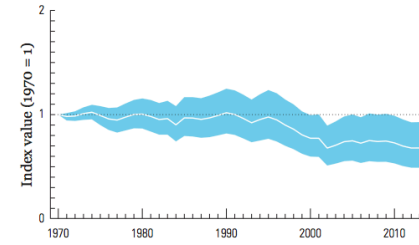

PALEARCTIC

AFROTROPICAL

INDO-PACIFIC

The Afrotropical Living Planet Index
The average abundance for 1,115 terrestrial and freshwater Afrotropical populations (representing 320 species). These populations declined by 56% between 1970 and 2014. The decrease was particularly steep in the 1980s [1].
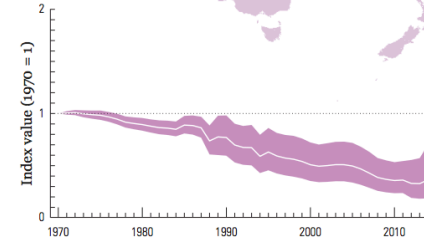
The Indo-Pacific Living Planet Index
The average abundance for 1,083 terrestrial and freshwater populations (representing 488 species) in the Indo-Pacific biogeographic realm. The Indo-Pacific Index experienced the second most pronounced decline, after the Neotropical index: 64% overall between 1970 and 2014 [1].

Figure 23: Locations of Living Planet Index species populations
Map showing the locations of the monitored populations in the LPI. Newly added populations since the last report are highlighted in orange, or in red for species new to the LPI[1].
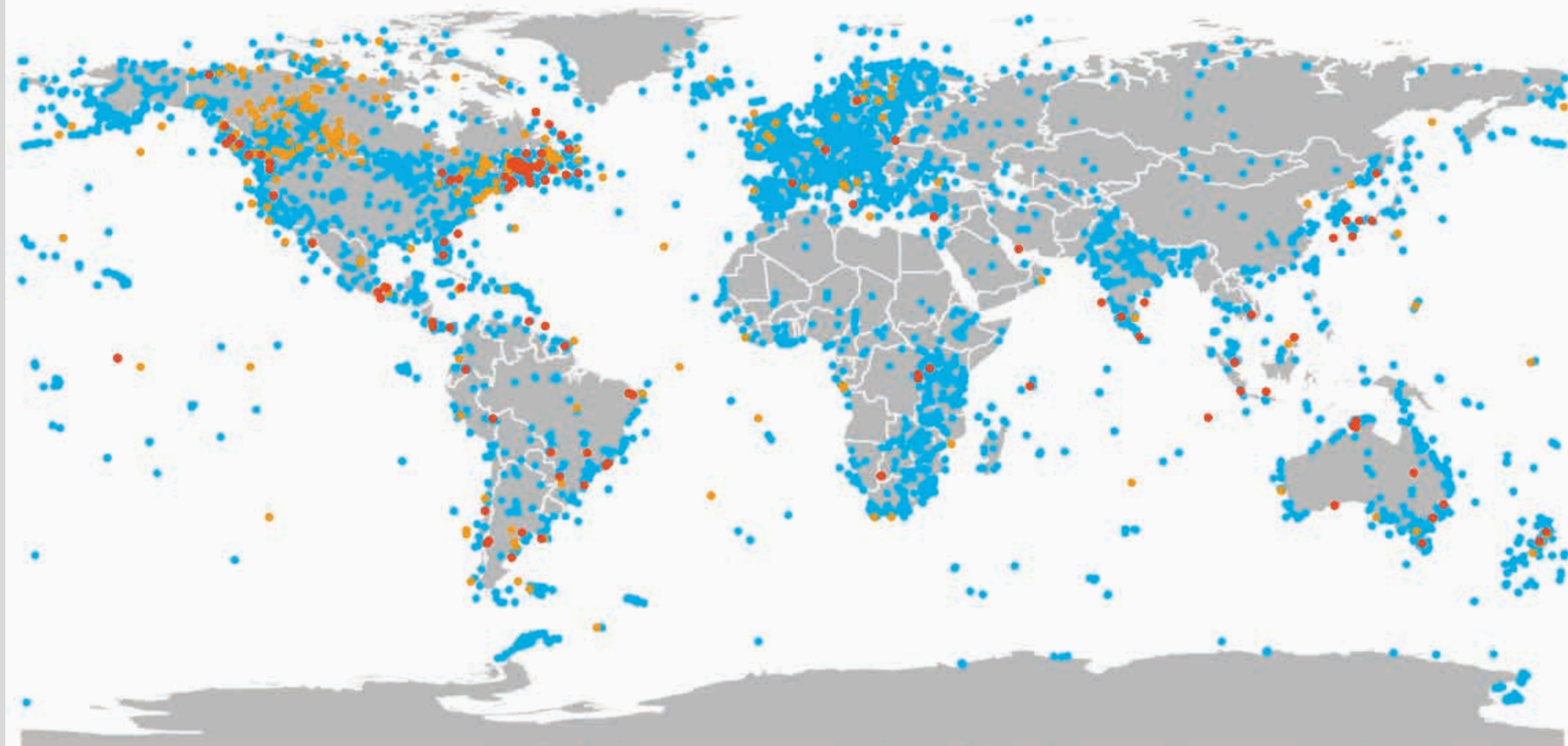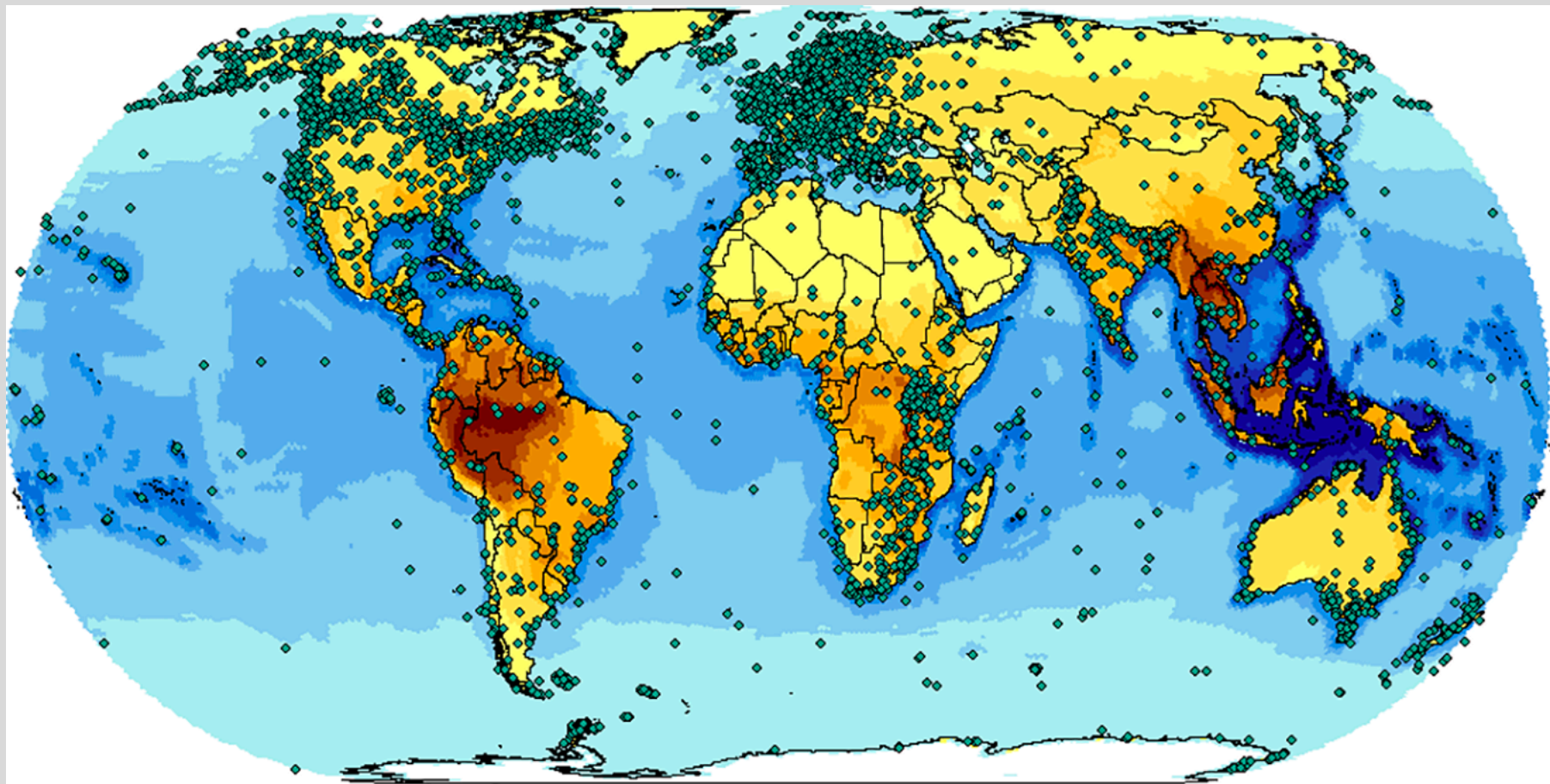
Terr/fw vertebrate species richness
Estimated no. of species

- 1 - 200
- 201 - 400
- 401 - 600
- 601 - 800
- 801 - 1000
- 1001 - 1200
- 1201 - 1400
- >1400

Marine vertebrate species richness
Estimated no. of species

- 1 - 250
- 251 - 500
- 501 - 750
- 751 - 1000
- 1001 - 1500
- 1501 - 2000
- 2001 - 2500
- >2500
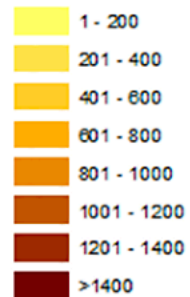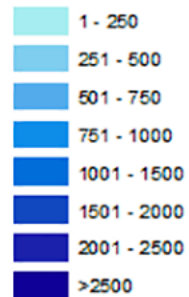
Contributed Paper

Monitoring Change in Vertebrate Abundance: the Living Planet Index

BEN COLLEN,*§ JONATHAN LOH,*† SARAH WHITMEE,* LOUISE McRAE,* RAJAN AMIN,‡
AND JONATHAN E. M. BAILLIE*‡

*Institute of Zoology, Zoological Society of London, Regent's Park, London NW1 4RY, United Kingdom
†WWF International, Avenue du Mont-Blanc CH-1196, Gland, Switzerland
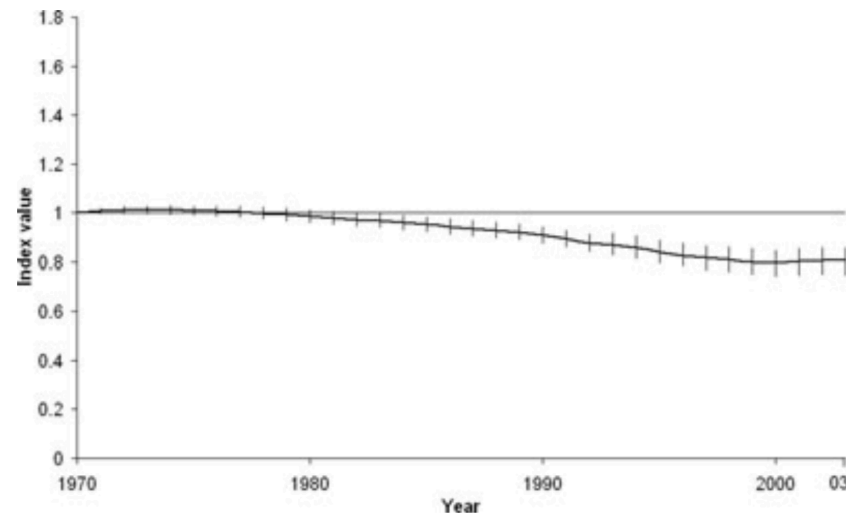
Figure 1. Average global Living Planet Index values for the 3 component indices (terrestrial, freshwater, and marine; 1411 species; 4218 populations). Confidence intervals (vertical lines) for the index are 95% values around the mean, generated with 10,000 bootstrap replicates (see Methods).
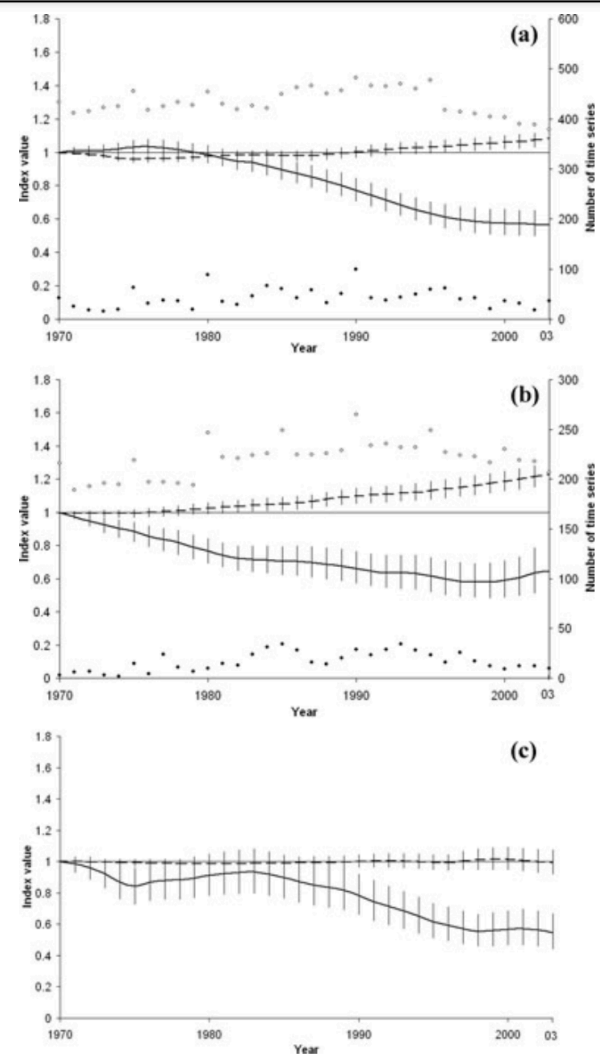
Figure 3. Living Planet indices for (a) Nearctic terrestrial (dashed) and Afrotropical terrestrial (solid) realms, (b) temperate forest (dashed) and tropical forest (solid) biomes, and (c) grassland birds (dashed) and grassland mammals (solid). Scatter plots ([a] and [b]) are the number of species contributing to the index in each year (right-hand axis) (filled circles go with the solid line and open circles with the dotted line). Confidence intervals (vertical lines) are 95% values around the mean, generated with 10,000 bootstrap replicates (see Methods).

The Living Planet Index: using species population time series to track trends in biodiversity

Jonathan Loh[1,*], Rhys E. Green[2], Taylor Ricketts[3], John Lamoreux[3], Martin Jenkins[4], Valerie Kapos[4] and Jorgen Randers[5]

[1]*WWF International, Avenue du Mont-Blanc CH-1196, Gland, Switzerland*
[2]*RSPB and Conservation Biology Group, Department of Zoology, University of Cambridge, Downing Street, Cambridge CB2 3EJ, UK*
[3]*Conservation Science Program, WWF-US, 1250 Twenty-fourth Street, NW, Washington DC 20037, USA*
[4]*UNEP-WCMC, Huntingdon Road, Cambridge CB3 0DL, UK*
[5]*Norwegian School of Management, Elias Smiths vei 15, Box 580 N-1302, Sandvika, Norway*

The Living Planet Index was developed to measure the changing state of the world's biodiversity over time. It uses time-series data to calculate average rates of change in a large number of populations of terrestrial, freshwater and marine vertebrate species. The dataset contains about 3000 population time series for over 1100 species. Two methods of calculating the index are outlined: the chain method and a method based on linear modelling of log-transformed data. The dataset is analysed to compare the relative representation of biogeographic realms, ecoregional biomes, threat status and taxonomic groups among species contributing to the index.

The two methods show very similar results: terrestrial species declined on average by 25% from 1970 to 2000. Birds and mammals are over-represented in comparison with other vertebrate classes, and temperate species are over-represented compared with tropical species, but there is little difference in representation between threatened and non-threatened species. Some of the problems arising from over-representation are reduced by the way in which the index is calculated. It may be possible to reduce this further by post-stratification and weighting, but new information would first need to be collected for data-poor classes, realms and biomes.

Modest recovery of biodiversity in a western European country: The Living Planet Index for the Netherlands

Arco J. van Strien [a,*], Adriaan W. Gmelig Meyling [a,b], Jelger E. Herder [c], Hans Hollander [d], Vincent J. Kalkman [e], Martin J.M. Poot [a], Sander Turnhout [f], Berry van der Hoorn [g], Willy T.F.H. van Strien-van Liempt [h], Chris A.M. van Swaay [i], Chris A.M. van Turnhout [j,k], Richard J.T. Verweij [a], Natasja J. Oerlemans [l]

[a] Statistics Netherlands, P.O. Box 24500, 2490 HA The Hague, The Netherlands
[b] Anemoon Foundation, P.O. Box 29, 2120 AA Bennebroek, The Netherlands
[c] Reptile, Amphibian and Fish Conservation The Netherlands (RAVON), P.O. Box 1413, 6501 BK Nijmegen, The Netherlands
[d] Dutch Mammal Society, P.O. Box 6531, 6503 GA Nijmegen, The Netherlands
[e] EIS Kenniscentrum Insecten/Naturalis Biodiversity Center, P.O. Box 9517, 2300 RA Leiden, The Netherlands
[f] SoortenNL, Toernooiveld 1, 6500 GL Nijmegen, The Netherlands
[g] Naturalis Biodiversity Center, P.O. Box 9517, 2300 RA Leiden, The Netherlands
[h] Brederostraat 10, 2332 BB Leiden, The Netherlands
[i] Dutch Butterfly Conservation, P.O. Box 506, 6700 AM Wageningen, The Netherlands
[j] Sovon Dutch Centre for Field Ornithology, P.O. Box 6521, 6503 GA Nijmegen, The Netherlands
[k] Institute for Water and Wetland Research, Radboud University, P.O. Box 9010, 6500 GL Nijmegen, The Netherlands
[l] WWF NL, Driebergseweg 10, 3798 JB Zeist, The Netherlands

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Nearly 30% of birds in U.S., Canada have vanished since 1970

However, LPI…

- Highly biased spatially
- Takes into account only 1970-present
- Is based on far more data in North than in South
- Regionwide assessment only

Terr/fw vertebrate species richness
Estimated no. of species
- 1 - 200
- 201 - 400
- 401 - 600
- 601 - 800
- 801 - 1000
- 1001 - 1200
- 1201 - 1400
- >1400

Marine vertebrate species richness
Estimated no. of species
- 1 - 250
- 251 - 500
- 501 - 750
- 751 - 1000
- 1001 - 1500
- 1501 - 2000
- 2001 - 2500
- >2500

PALEARCTIC

AFROTROPICAL

INDO-PACIFIC

The Afrotropical Living Planet Index
The average abundance for 1,115 terrestrial and freshwater Afrotropical populations (representing 320 species). These populations declined by 56% between 1970 and 2014. The decrease was particularly steep in the 1980s [1].

The Indo-Pacific Living Planet Index
The average abundance for 1,083 terrestrial and freshwater populations (representing 488 species) in the Indo-Pacific biogeographic realm. The Indo-Pacific Index experienced the second most pronounced decline, after the Neotropical index: 64% overall between 1970 and 2014 [1].

Jorge Soberón and A. Townsend Peterson

Monitoring Biodiversity Loss with Primary Species-occurrence Data: Toward National-level Indicators for the 2010 Target of the Convention on Biological Diversity

Development of effective indicators is indispensable for countries and societies to monitor effects of their actions on biodiversity, as is recognized in decision VI/26 of the Convention on Biological Diversity. Good indicators would ideally be scalable, at least for the different scales that characterize biodiversity patterns and process. Existing indicators are mostly global in scope, and often based on secondary information, such as classifications of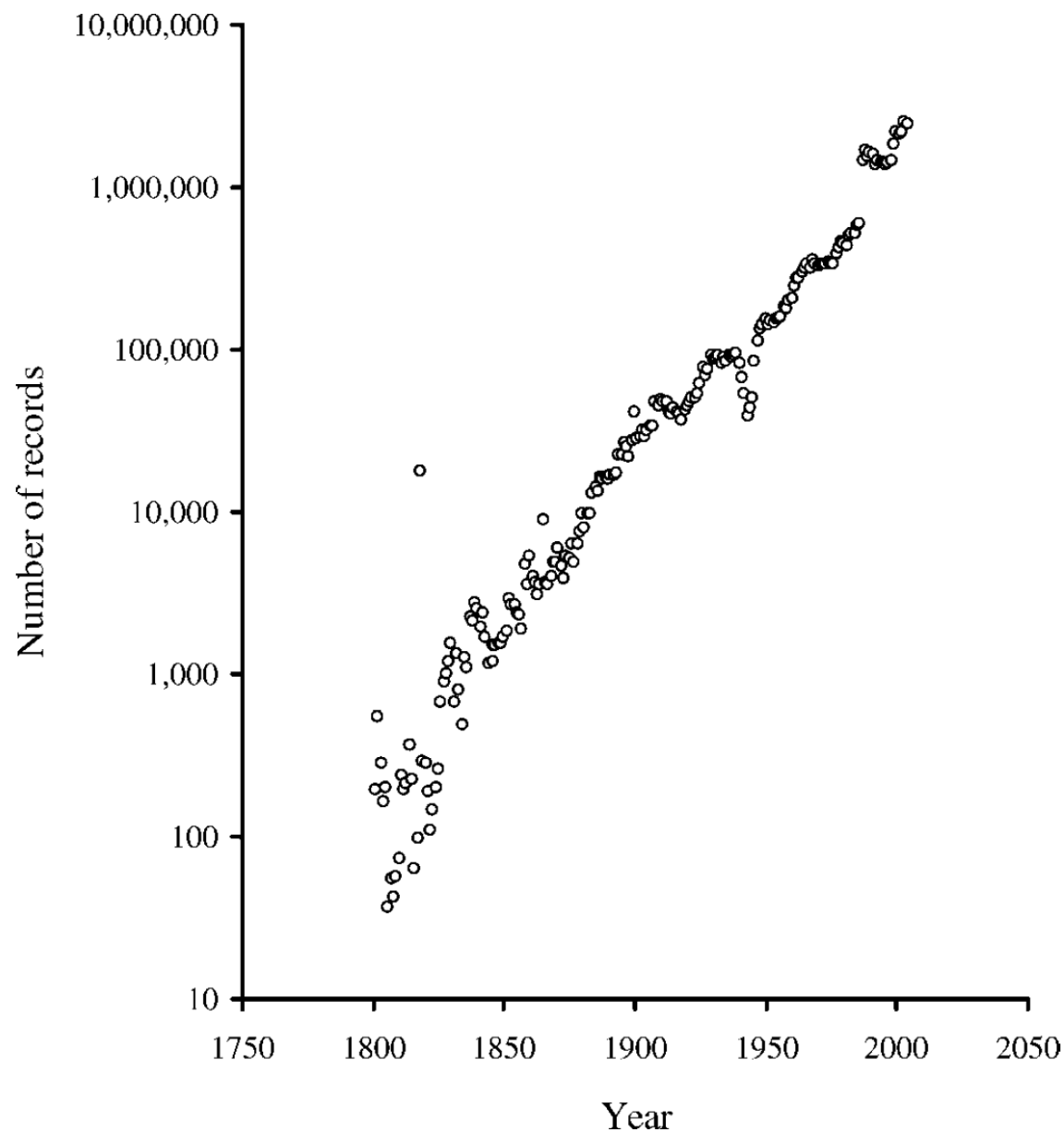 endangered species, rather than on primary data. We propose a complementary approach, based on the increased availability of raw data about occurrences of species, cutting-edge modeling techniques for estimating distributional areas, and land-use information based on remotely sensed data to allow estimation of rates of range loss for species affected by land-use conversion. This method can be implemented by developing countries, given increasing availability of data and the open and well-documented nature of the techniques required.

makers at a national scale because of the low density of the information on which they are based. For example, one of the two major databases on which the LPI is based (9) contains only a single time series for Mexico and five for all of Brazil. What is more, because they are based on secondary information (the RLI is calculated on the basis of changes in expert-assessed status of threat [4]; LPI is calculated as the average of time series of population counts, stock estimates, or proxies of population sizes [6]), and on composite databases (including information that, in practice, is inaccessible to most interested parties), their development, updating, and use tend to remain restricted to experts based in the developed world. Unfortunately, ample experience shows that biodiversity management and governance is a multiscalar challenge and that, without direct involvement of stakeholders at local scales, biodiversity knowledge is seldom converted into effective decision-making (10–14). Hence, the applicability and utility of global indicators of biodiversity loss are mostly limited to global, and perhaps regional, questions. In this contribution, we present and illustrate a complementary

Figure 1. Summary of accumulation of biodiversity information through time (i.e., date of record of the species) on a semilogarithmic scale. Data served via the Global Biodiversity Information Facility (http://www.gbif.org) data portal.

- Numbers of primary biodiversity data records PER YEAR are increasing 10x every 42 years
- Stark contrast with RLI and LPI as far as availability of information
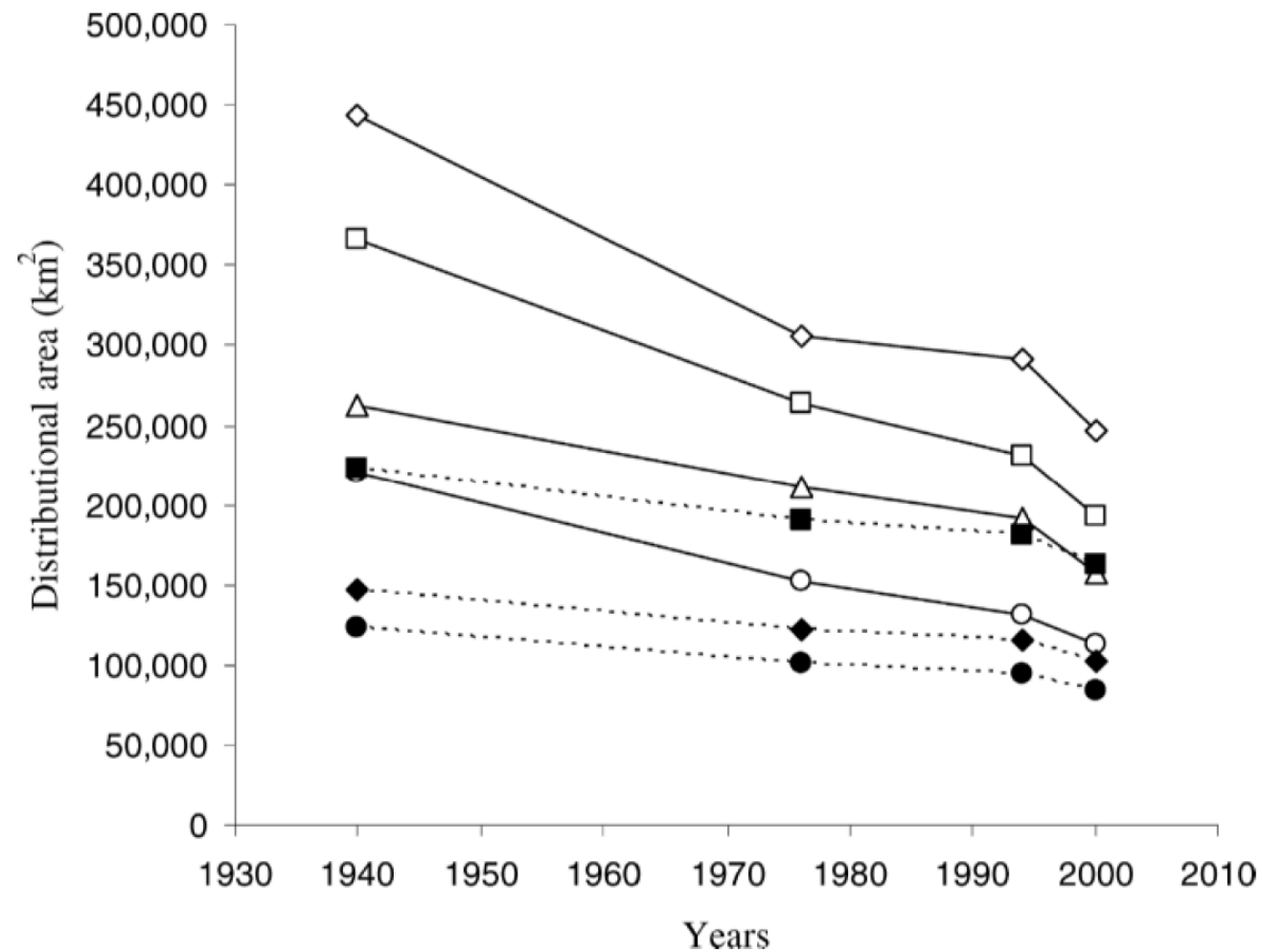
Figure 3. Changes in distributional areas of seven species of special interest in Mexico, reconstructed over the latter half of the twentieth century via ecological niche modeling and satellite estimations of land-use change. Open symbols, species of tropical rain forest; closed symbols, species of pine-oak forest; open diamond, *Tamandua mexicana*; open square, *Ateles geoffroyi*; open circle, *Alouatta palliata*; open triangle, *Guaiacum sanctum*; closed square, *Sciurus aberti*; closed diamond, *S. nayaritensis*; closed circle, *Peromyscus spicilegus*.

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Species Populations

The dynamics of species populations, i.e. the variation of species geographic distributions and abundances in space and time, represent one of the most fundamental aspects of biodiversity and its change.

Species Populations

EBVs

What are EBVs?

Working Groups

Genetic Composition

Species Populations

EBV for Invasion Monitoring

Species Traits

The dynamics of species populations, i.e. the variation of species geographic distributions and abundances in space and time, represent one of the most fundamental aspects of biodiversity and its change. Decreases in the sizes of populations and contractions in the distribution of species result in the loss of potentially significant functions from communities and ecosystems, and in extreme cases may cause their global extinction. Conversely, expanding or shifting populations translate in the perturbation of existing or invasion of new communities, both with multifold consequences for ecosystems. Changes in the occurrence or abundance of species are thus key drivers of changes in ecosystem function and services. When related to information on patterns of environmental change, spatiotemporal data on species populations can inform about the putative causes of biodiversity and ecosystem change. In the context of resource management and conservation, species population data supports spatially explicit planning, risk and threat analysis, and the assessment of management outcomes.

Definitions of Species Population EBVs
Species Distributions: The essential biodiversity variable for species distributions (SD EBV) is: "the probability of occurrence over contiguous spatial and temporal units addressing the global extent of a species group consisting of one to many members." (Jetz, McGeoch, Guralnick et al. 2019).
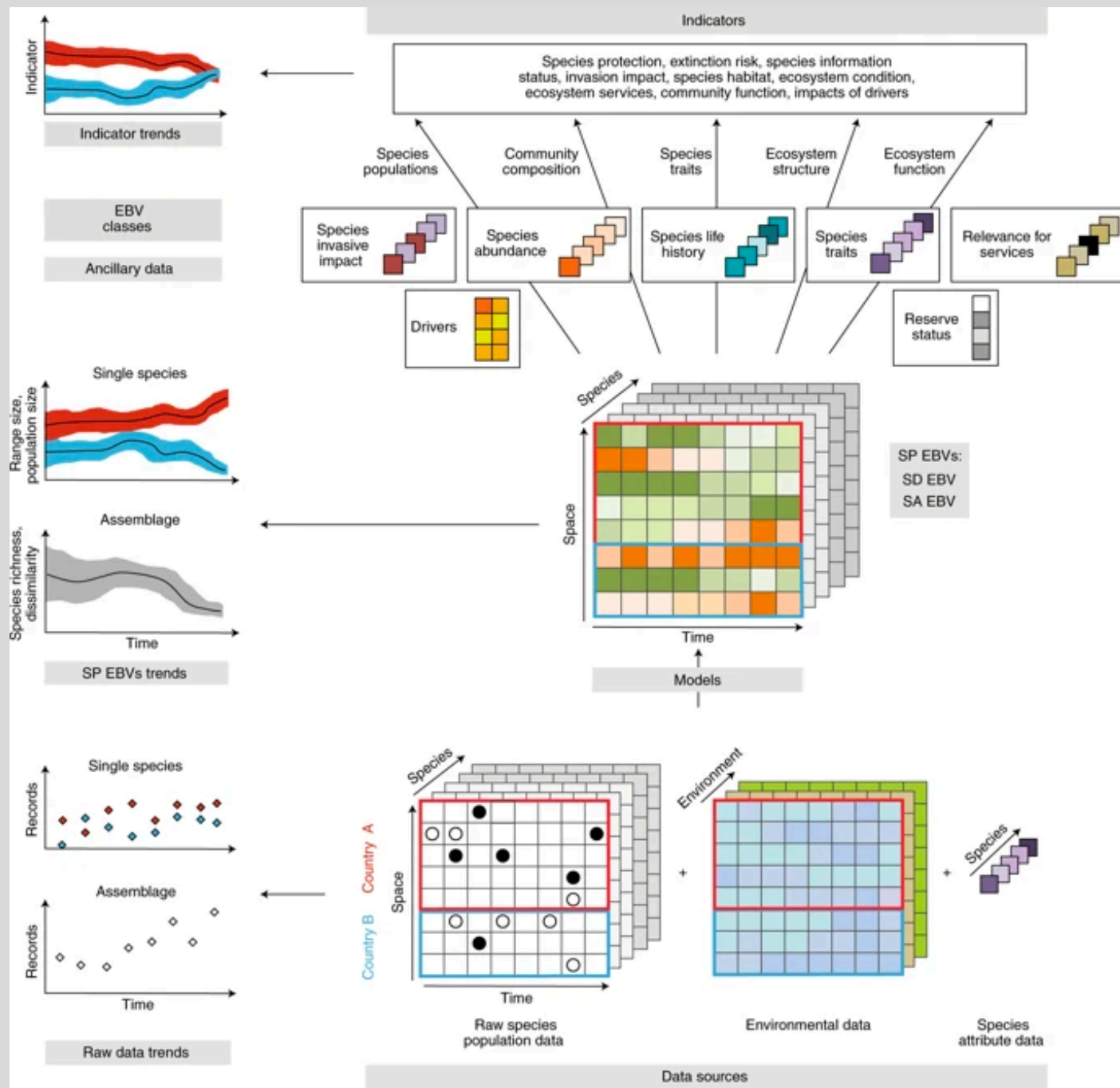
Definitions of Species Population EBVs

Species Distributions: The essential biodiversity variable for species distributions (SD EBV) is: "the probability of occurrence over contiguous spatial and temporal units addressing the global extent of a species group consisting of one to many members." (Jetz, McGeoch, Guralnick et al. 2019).

Species Abundance: The essential biodiversity variable for species abundances (SA EBV) is: "the predicted count of individuals over contiguous spatial and temporal units". (Jetz, McGeoch, Guralnick et al. 2019).

Indicators

Species protection, extinction risk, species information status, invasion impact, species habitat, ecosystem condition, ecosystem services, community function, impacts of drivers

Indicator trends

Indicator

EBV classes

Ancillary data

Species populations

Community composition

Species traits

Ecosystem structure

Ecosystem function

Species invasive impact

Species abundance

Species life history

Species traits

Relevance for services

Drivers

Reserve status

Single species

Range size, population size

Assemblage

Species richness, dissimilarity

Time

SP EBVs trends

Species

Space

Time

SP EBVs:
SD EBV
SA EBV

Models

Single species

Records

Assemblage

Records

Time

Raw data trends

Species

Country A

Country B

Space

Time

Raw species population data

Environment

Environmental data

Species

Species attribute data

Data sources

THE GLOBAL POPULATION DYNAMICS DATABASE

Centre for Population Biology

IMPERIAL COLLEGE LONDON AND
NATURAL ENVIRONMENT RESEARCH COUNCIL

NCEAS

Server Error in '/CPB/gpdd2' Application.

Cannot open database "cpb_gpdd2" requested by the login. The login failed.
Login failed for user 'IC\icwww-gpdd'.

Description: An unhandled exception occurred during the execution of the current web request. Please review the stack trace for more information about the error and where it originated in the code.

Exception Details: System.Data.SqlClient.SqlException: Cannot open database "cpb_gpdd2" requested by the login. The login failed.
Login failed for user 'IC\icwww-gpdd'.
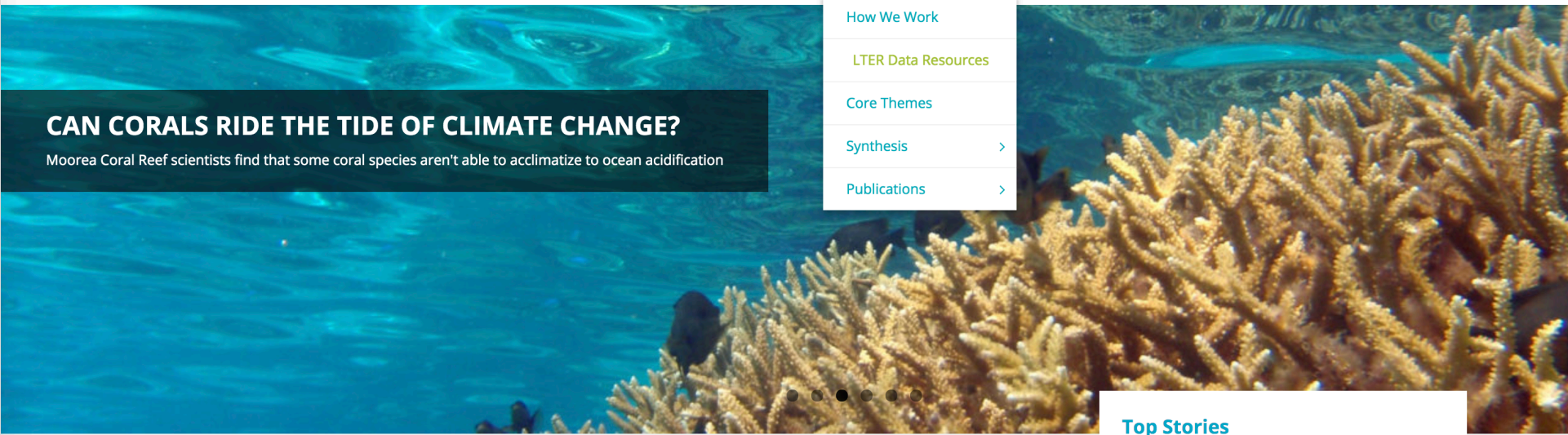
Source Error:

An unhandled exception was generated during the execution of the current web request. Information regarding the origin and location of the exception can be identified using the exception stack trace below.

Stack Trace:

```
[SqlException (0x80131904): Cannot open database "cpb_gpdd2" requested by the login. The login failed.
Login failed for user 'IC\icwww-gpdd'.]
   System.Data.SqlClient.SqlInternalConnection.OnError(SqlException exception, Boolean breakConnection) +6299689
   System.Data.SqlClient.TdsParser.ThrowExceptionAndWarning(TdsParserStateObject stateObj) +245
   System.Data.SqlClient.TdsParser.Run(RunBehavior runBehavior, SqlCommand cmdHandler, SqlDataReader dataStream, BulkCopySimpleResultSet bulkCopyHandler, TdsParserStateObject stateObj) +2843
   System.Data.SqlClient.SqlInternalConnectionTds.CompleteLogin(Boolean enlistOK) +53
   System.Data.SqlClient.SqlInternalConnectionTds.AttemptOneLogin(ServerInfo serverInfo, String newPassword, Boolean ignoreSniOpenTimeout, Int64 timerExpire, SqlConnection owningObject, Boolean withFailover) +353
   System.Data.SqlClient.SqlInternalConnectionTds.LoginNoFailover(String host, String newPassword, Boolean redirectedUserInstance, SqlConnection owningObject, SqlConnectionString connectionOptions, Int64 timerStart) +6319663
   System.Data.SqlClient.SqlInternalConnectionTds.OpenLoginEnlist(SqlConnection owningObject, SqlConnectionString connectionOptions, String newPassword, Boolean redirectedUserInstance) +6319784
   System.Data.SqlClient.SqlInternalConnectionTds..ctor(DbConnectionPoolIdentity identity, SqlConnectionString connectionOptions, Object providerInfo, String newPassword, SqlConnection owningObject, Boolean redirectedUserInstance) +354
   System.Data.SqlClient.SqlConnectionFactory.CreateConnection(DbConnectionOptions options, Object poolGroupProviderInfo, DbConnectionPool pool, DbConnection owningConnection) +703
   System.Data.ProviderBase.DbConnectionFactory.CreatePooledConnection(DbConnection owningConnection, DbConnectionPool pool, DbConnectionOptions options) +54
   System.Data.ProviderBase.DbConnectionPool.CreateObject(DbConnection owningObject) +6321048
   System.Data.ProviderBase.DbConnectionPool.UserCreateRequest(DbConnection owningObject) +81
   System.Data.ProviderBase.DbConnectionPool.GetConnection(DbConnection owningObject) +1657
   System.Data.ProviderBase.DbConnectionFactory.GetConnection(DbConnection owningConnection) +88
   System.Data.ProviderBase.DbConnectionClosed.OpenConnection(DbConnection outerConnection, DbConnectionFactory connectionFactory) +6324471
   System.Data.SqlClient.SqlConnection.Open() +258
   System.Web.DataAccess.SqlConnectionHolder.Open(HttpContext context, Boolean revertImpersonate) +82
   System.Web.DataAccess.SqlConnectionHelper.GetConnection(String connectionString, Boolean revertImpersonation) +4054010
   System.Web.Security.SqlMembershipProvider.CreateUser(String username, String password, String email, String passwordQuestion, String passwordAnswer, Boolean isApproved, Object providerUserKey, MembershipCreateStatus& status) +2733
   System.Web.UI.WebControls.CreateUserWizard.AttemptCreateUser() +357
   System.Web.UI.WebControls.CreateUserWizard.OnNextButtonClick(WizardNavigationEventArgs e) +208
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   System.Web.UI.Control.RaiseBubbleEvent(Object source, EventArgs args) +70
   System.Web.UI.Page.RaisePostBackEvent(IPostBackEventHandler sourceControl, String eventArgument) +29
   System.Web.UI.Page.ProcessRequestMain(Boolean includeStagesBeforeAsyncPoint, Boolean includeStagesAfterAsyncPoint) +2981
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Version Information: Microsoft .NET Framework Version:2.0.50727.8810; ASP.NET Version:2.0.50727.8762

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Mark-Recapture of Rodent and Shrew Populations in a Declining Hemlock Stand at Harvard Forest 2012	Degrassi, Allyson Ellison, Aaron	2013	knb-lter-hfr.208.5
Impact of urbanization on small rodent abundance and community composition	Arizona State University, West campus Ball, Becky	2018	knb-lter-cap.654.1
Survey of small mammals using trapping data on all Virginia Coast Reserve barrier islands south of Paramore Island (inclusive) 1975-1978	Dueser, Raymond McCuskey, Susan Hogue, Gregory Porter, John	1991	knb-lter-vcr.1.21
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Title:	Mark-Recapture of Rodent and Shrew Populations in a Declining Hemlock Stand at Harvard Forest 2012
Creators:	Degrassi, Allyson Ellison, Aaron
Publication Date:	2013
Citation:	Degrassi A., A. Ellison. 2013. Mark-Recapture of Rodent and Shrew Populations in a Declining Hemlock Stand at Harvard Forest 2012. Environmental Data Initiative. https://doi.org/10.6073/pasta/2fa61f203218fbeeef396067dda710fe. Dataset accessed 9/16/2019.
Abstract:	Eastern Hemlocks (Tsuga canadensis) are foundation species, which are known to have a large influence on the species composition and ecosystem dynamics. The purpose of this study was to understand how rodent species rich... Show more >

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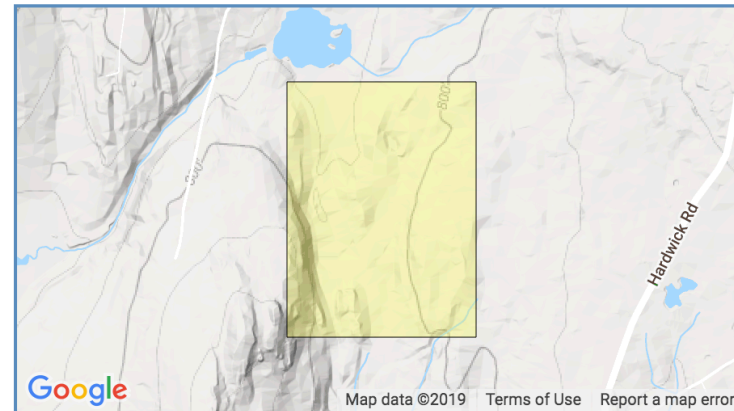
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Package ID:	knb-lter-hfr.208.5 (*Uploaded 2018-01-30*) previous revision all revisions

Resources:	View Full Metadata
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| Dryad Data Packages (11405) | KNB (1250) | TreeBASE (30) | Dryad Data Files (0) |

Mazzoni A, Lindén HA, Cuntz H, Lansner A, Panzeri S, Einevoll GT (2015) Data from: Computing the local field potential (LFP) from integrate-and-fire network models. *PLOS Computational Biology* https://doi.org/10.5061/dryad.j5r51

Yu H, Siewny MGW, Edwards DT, Sanders AW, Perkins TT (2017) Data from: Hidden dynamics in the unfolding of individual bacteriorhodopsin proteins. *Science* https://doi.org/10.5061/dryad.g0n2d

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Janko K, Pačes J, Wilkinson-Herbots H, Costa RJ, Roslein J, Drozd P, Iakovenko N, Rídl J, Hroudová M, Kočí J, Reifová R, Šlechtová V, Choleva L (2017) Data from: Hybrid asexuality as a primary postzygotic barrier between nascent species: on the interconnection between asexuality, hybridization and speciation. *Molecular Ecology* https://doi.org/10.5061/dryad.7nt8f

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Haenel Q, Laurentino TG, Roesti M, Berner D (2018) Data from: Meta-analysis of chromosome-scale crossover rate variation in eukaryotes and its significance to evolutionary genomics. *Molecular Ecology* https://doi.org/10.5061/dryad.p1j7n43

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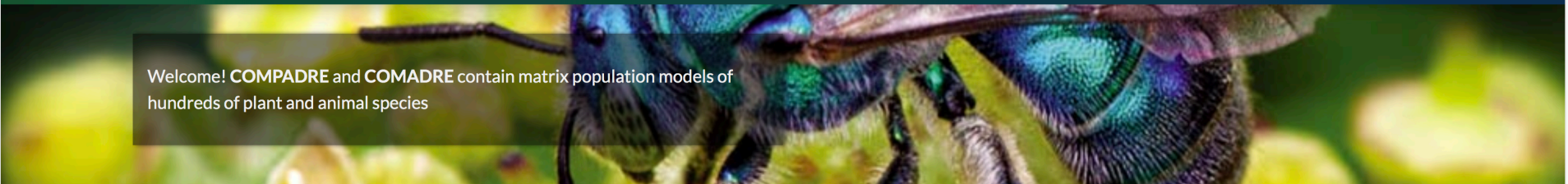Adaptation (659)
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Publication Name
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Evolution (774)
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COMPADRE and COMPADRE contain thousands of plant and animal species with tens of thousands of matrix population models and ancillary information. These databases are under continuous development, and more data are released periodically. We maintain a list of species/studies "in store" that we have not yet released for COMPADRE and COMADRE. If you know of some species/study not included herein, please contact us with the source here.

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By clicking on "OK", you agree to the user agreement of COMPADRE & COMADRE. This will download an R data object containing:

1. Version 3.0.0
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3. 640 studies
4. 2280 matrix population models

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Top statistics across regions, surveys, species, sites and surveyors

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COMMENTARY

Essential biodiversity variables are not global

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Abstract Recent initiatives have focused on biological diversity and the ecosystem services that it provides, and have proposed a series of "essential biodiversity variables," as a means of describing and characterizing that diversity. Although such variables would shed considerable and interesting light on distribution of biodiversity-related dimensions, here, we examine the feasibility of assembling such data resources for terrestrial systems on worldwide extents, to evaluate whether they can be feasibly characterized globally. We found large-scale, consistent information gaps across five EBV-related dimensions (genetic composition, species populations, species traits, community composition, and primary biodiversity data), most markedly across Africa, the Middle East, Central Asia, and Eastern Europe; lesser gaps cover much of Asia and South America. Our results raise concerns that

Table 1 Essential biodiversity variables (EBVs), with metrics explored and sources of information

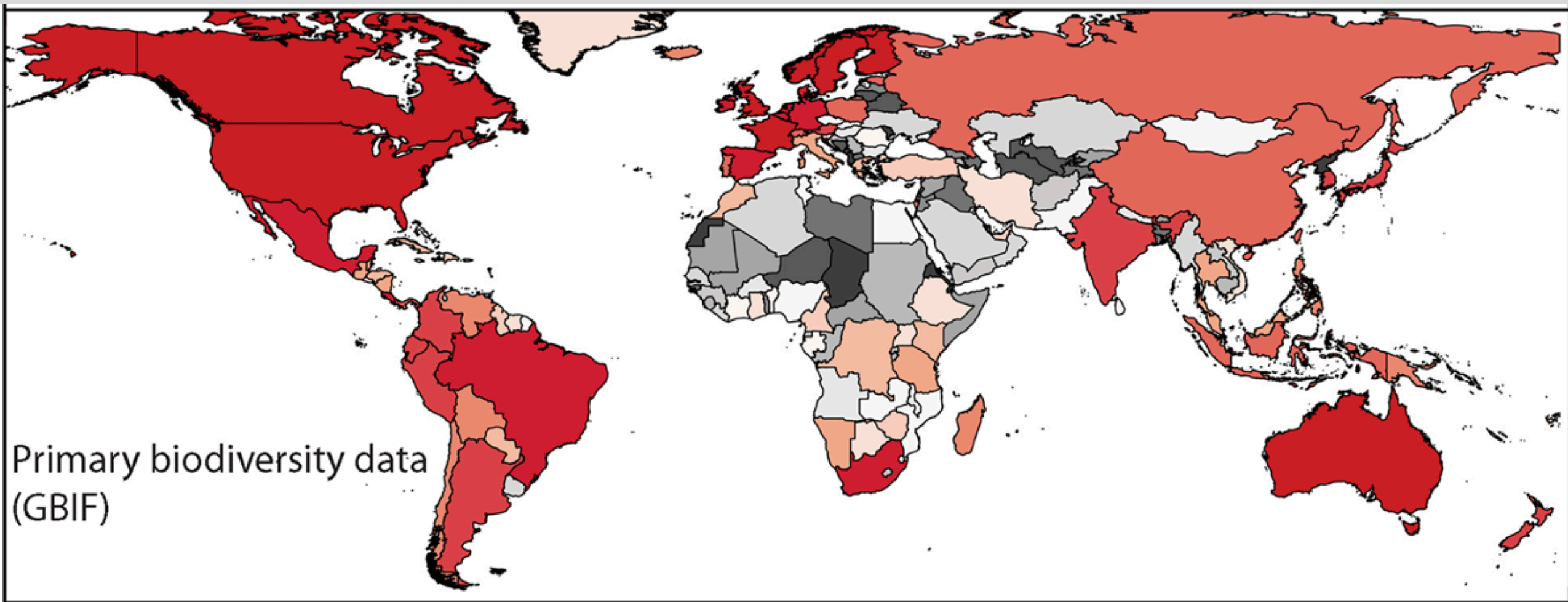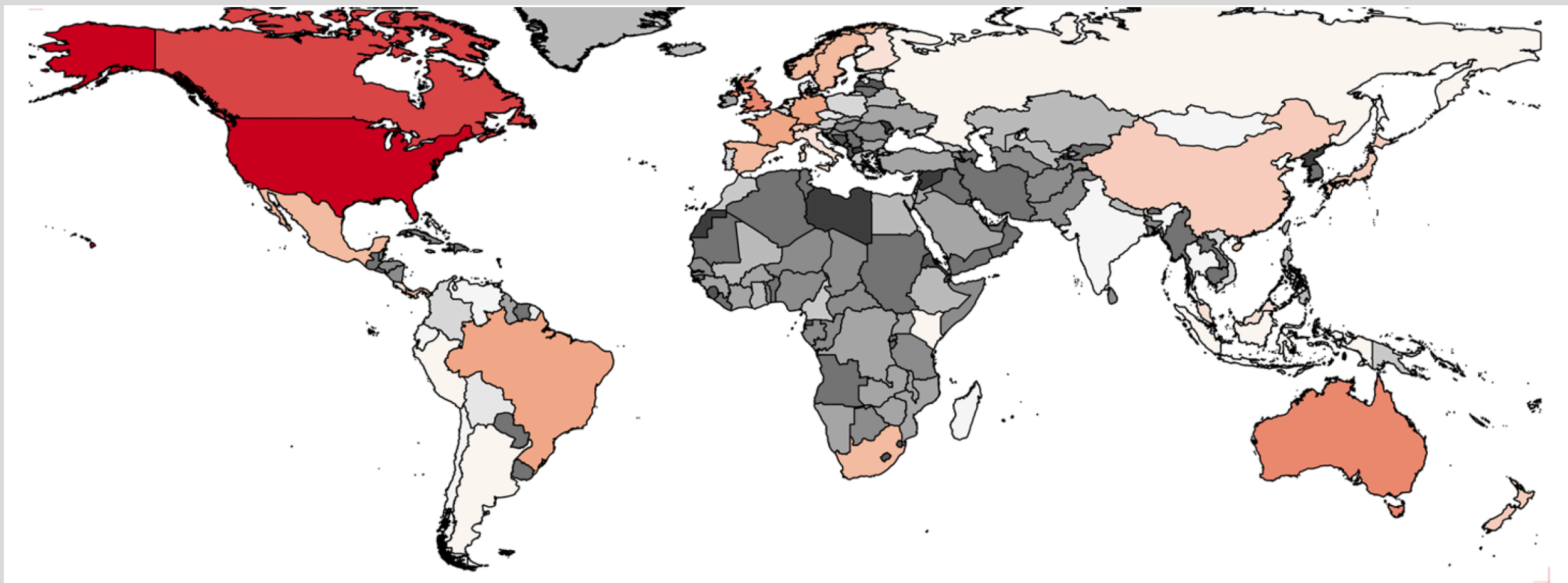| EBV	Metrics explored	Source and details
Genetic composition	Nucleotide sequence data	Genbank, https://www.ncbi.nlm.nih.gov/genbank/; searched "/Country is not null," which yielded ~ 49 × 10⁶ records
Species populations	Population data	Global population dynamics database, http://www.imperial.ac.uk/cpb/gpdd2/search3.aspx; searched on all latitude–longitude combinations, which yielded 5105 records; when a continent was mentioned, all component countries got the credit
Species traits	Plant trait data	Plant trait database (TRY v3), https://www.try-db.org/; went to trait-research-list-of-datasets, plotted latitude–longitude combinations, and counted by country
Community composition	Community composition data	GloBI (Martin et al. 2012; Poelen et al. 2014)
	Shared occurrence of species at sites	Global biodiversity information facility (GBIF), http://www.gbif.org; country totals derived, and plotted directly
Ecosystem structure	Vegetation structure, forest extent and change	Global information available (Simard et al. 2011); also Global Forest Watch, http://www.globalforestwatch.org/
Ecosystem function	Ecosystem process measurements using remote sensing	Numerous mapping efforts and remote-sensing products (e.g., Field et al. 1995; Cramer et al. 1999)

Genetic composition
(GenBank)

Species populations
(NCS, Compadre,
Commadre)
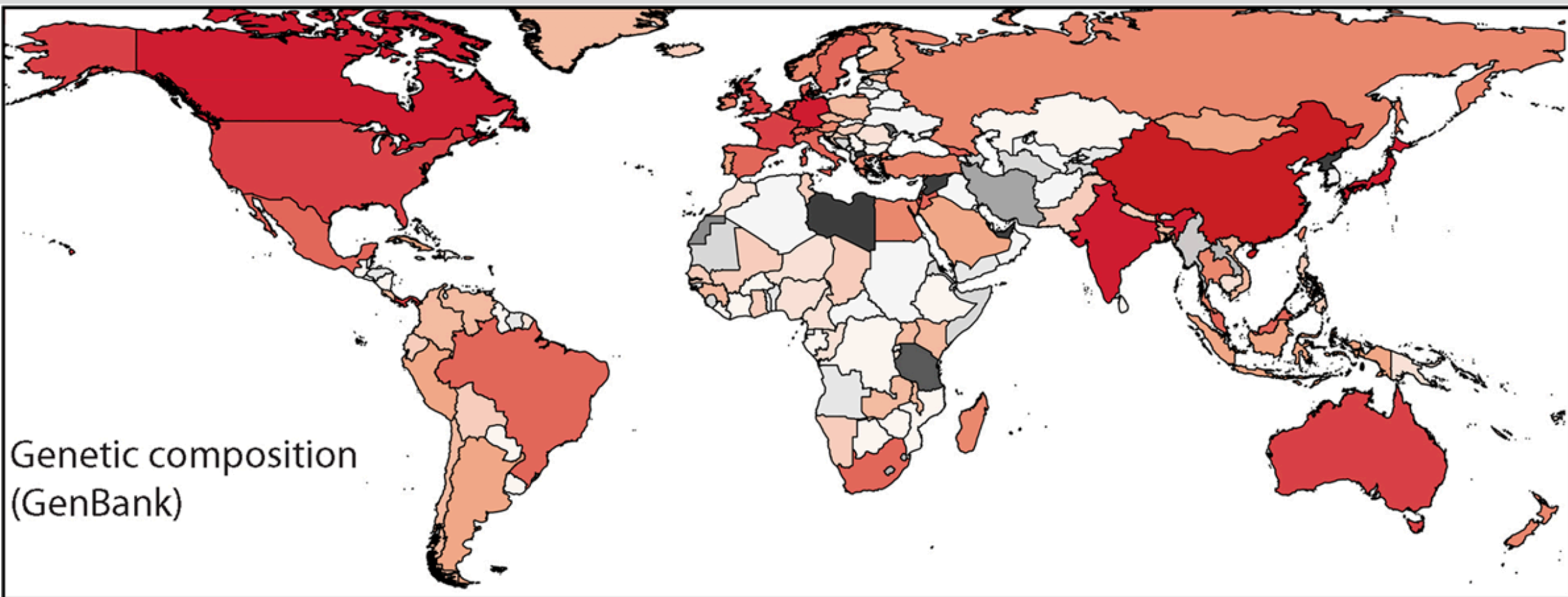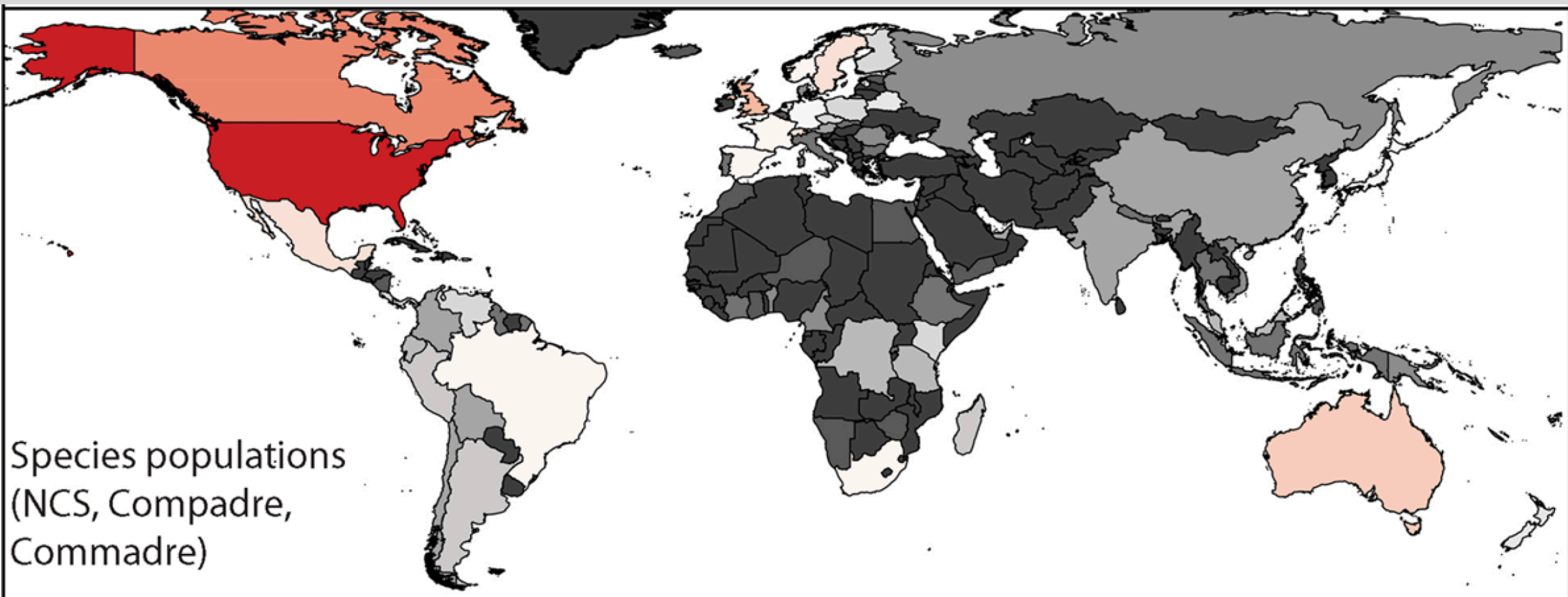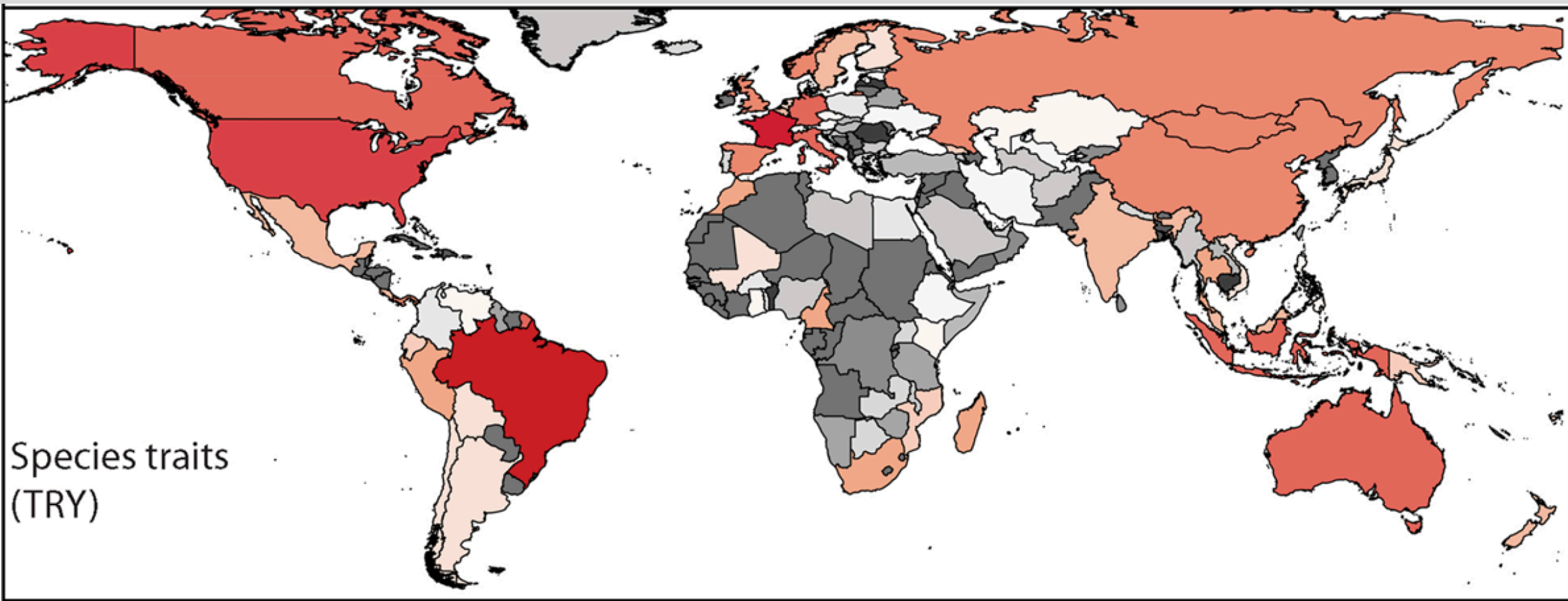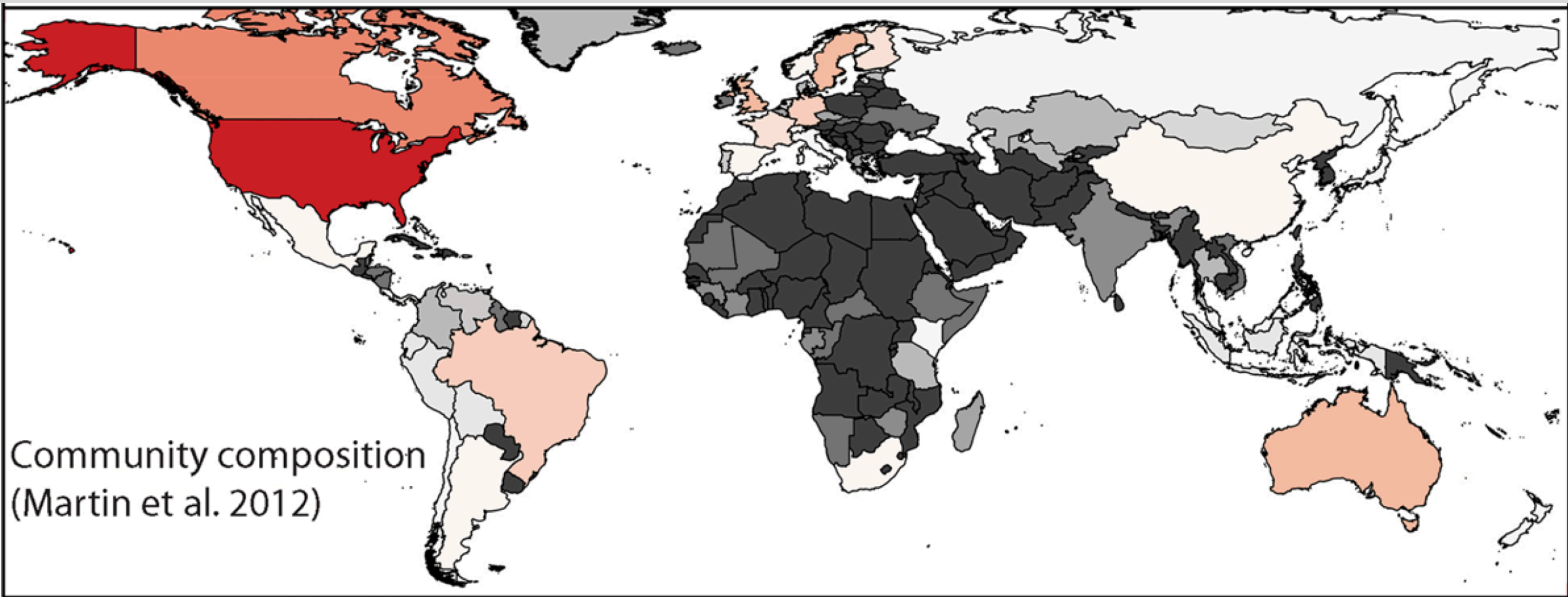
Species traits
(TRY)

Community composition
(Martin et al. 2012)

Primary biodiversity data
(GBIF)

Fig. 2 Overall patterns of richness of information regarding four essential biodiversity variables (genetic composition, species populations, species traits, community composition; see Table 1). Richness of information across EBV dimensions was summarized as values of the first principal component of variation among countries. The color ramp ranges from black (minimal information) to red (large-scale information)

EBVs

- Two can be summarized (at least partially) worldwide quickly and fairly easily
- The rest take enormous amounts of work and investment of resources and time
- The rest of the EBVs are massively biased towards the Global North, leaving major gaps, particularly across Africa
- EBVs will forever be biased both spatially, towards variables that are able to be characterized via remote sensing, and away from variables that require detailed on-ground biodiversity studies
- EBV-based policy and discussions must be taken with a "grain of salt"

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