

Sedona Anderson

Spatial Analysis of Protected Area Effectiveness in Safeguarding Global Biodiversity

Master's thesis in Industrial Ecology

Supervisor: Francesca Verones

Co-supervisor: Jan Borgelt

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Abstract

International agreements have spurred the rapid expansion of protected areas in an effort to halt and even reverse ongoing biodiversity loss. However, extinctions continue at critical rates, even as goals for global protected area coverage are achieved. With biodiversity declines continuing, protected areas are not effectively safeguarding biodiversity. In this study, I find that today there is a higher rate of vulnerability-weighted species richness *outside* of protected areas in nearly half of 64 biogeographic units. Additionally, well-documented taxa such as birds and mammals are more extensively protected than less-documented taxa including amphibians. Using scientifically-backed indicators such as vulnerability-weighted species richness to select future areas for protection is critical to reverse negative biodiversity trends. I have presented the top 30% of species rich areas within each biome realm that, in combination with future analysis of other indicators, could serve as a basis for prioritization in the movement towards Action Target 3 of the post-2020 framework, which calls for protecting 30% of the planet by 2030.

Sammendrag

Internasjonale avtaler har ansporet til den raske utvidelsen av beskyttede områder i et forsøk på å stoppe og til og med reversere pågående tap av biologisk mangfold. Utryddelser fortsetter imidlertid med kritiske hastigheter, selv når målene for global beskyttet områdedekning er nådd. Når biologisk mangfold fortsetter å synke, ivaretar ikke verneområder det biologiske mangfoldet effektivt. I denne studien finner jeg at det i dag er en høyere grad av sårbarhetsvektet artsrikdom utenfor verneområder i nesten halvparten av 64 biogeografiske enheter. I tillegg er godt dokumenterte taxaer som fugler og pattedyr mer omfattende beskyttet enn mindre dokumenterte taxa inkludert amfibier. Å bruke vitenskapelig støttede indikatorer som sårbarhetsvektet artsrikdom for å velge fremtidige områder for beskyttelse er avgjørende for å snu negative biologiske mangfoldstrender. Jeg har presentert de øverste 30 % av artsrike områdene innenfor hvert biomerik som, i kombinasjon med fremtidig analyse av andre indikatorer, kan tjene som grunnlag for prioritering i bevegelsen mot Action Target 3 i post-2020-rammeverket, som krever beskytte 30 % av planeten innen 2030.

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1. Introduction

Protected areas are considered a critical tool in combatting global biodiversity loss¹⁻⁵. Today, as a result of human actions including habitat fragmentation, climate change, and species overexploitation, we are on the brink of a 6th mass extinction⁶⁻⁸. Extinction rates are currently hundreds to thousands of times higher than background rates⁹. Genetic diversity has been considered the most transgressed planetary boundary^{10,11}, indicating that life on earth is increasingly vulnerable to human pressures. As calls for action accelerate around the globe, governments and private actors have relied on protected areas as a key component of conservation¹². However, the declaration of land or sea areas as protected does not necessarily mean that they are effectively safeguarding biodiversity. Significant gaps remain in the protected area coverage of species-rich areas across the globe, especially for certain taxa such as invertebrates (e.g. mollusks and insects), and some vertebrates like amphibians^{7,13}. Within this study, I evaluate whether protected areas are sufficiently covering vulnerable species, if protected area coverage is biased towards certain taxa, and which areas should be prioritized for future expansion of the global protected area network.

Protected areas (PAs) are defined by the International Union for Conservation of Nature (IUCN) as *“an area of land and/or sea especially dedicated to the protection and maintenance of biological diversity, and of natural and associated cultural resources, and managed through legal or other effective means”*¹⁴. PAs have proven to be useful bulwarks against biodiversity loss^{5,15}. Effectively established and managed PAs can protect against habitat degradation, safeguarding species richness and genetic diversity^{1,2}. High levels of genetic diversity create resilient ecosystems and allow species to withstand pressures like climate change in place^{1,16}. In addition, well-connected PA networks create corridors that allow mobile species to adapt to pressures through migration¹⁶. Though marine protected areas (MPAs) and terrestrial protected areas (PAs) are both important, the scope of this study includes only terrestrial protected areas.

In recent decades there has been a significant push for increases in protected area coverage^{5,17}. Aichi Target 11, a major international goal adopted by the Convention on Biological Diversity in 2011, called for 17% of terrestrial land to be protected by 2020¹⁸. That

target was met when the Living Planet Report announced that in 2020, 16.64% of terrestrial area was protected – though they predicted that the actual number was likely equal to or over 17%¹⁹. However, though Target 11 was only narrowly achieved, it has been criticized for not being ambitious *enough*⁴. Though protected areas have tripled in size in the last 40 years, we are still seeing rapid biodiversity loss¹⁵. Therefore, calls continue for rapid expansion of protected area networks around the world, as well as explicit and scientifically-backed benchmarks to measure progress^{4,5}. 30 by 30 is an initiative that calls for 30% of marine and terrestrial area to be protected by 2030⁴. It has been adopted by the CBD and included in the latest draft of the post-2020 Global Biodiversity Framework as Action Target 3²⁰.

Protected areas *can* be an effective tool in safeguarding species, but there are factors that may keep them from succeeding. One major factor is where the protected area is established. Aichi Target 11 focused most notably on quantifying areal extent. From 2010-2020, areas set aside for protection were commonly unsuitable for agriculture and economically marginal, rather than being key areas of biodiversity²¹⁻²³. Setting aside land of this nature is unlikely to draw contention and also meets areal coverage targets – but it does little to prevent biodiversity losses^{17,24}.

Another factor that can impact overall ecosystem health, and consequently PA effectiveness, is taxonomic bias. There are significant, and sometimes drastic, differences in the amount of data available for different taxa. Charismatic taxa like mammals and birds tend to be well-documented, with low levels of data deficiency^{25,26}. Meanwhile, other vertebrates like amphibians and reptiles, and especially invertebrates, lack the same attention and funding^{25,26}. This is reflected in protected area coverage. Certain taxa may be systemically neglected in the establishment of protected area networks while others are well-represented. However, for healthy and functioning ecosystems with rich genetic diversity, a wide variety of taxa are important^{26,27}.

In my research, I utilized species richness – a foundational indicator of biodiversity – to assess current PA effectiveness through a globally comprehensive spatial analysis of today's protected area coverage compared to vulnerability-weighted species richness levels. Based on species distribution maps, I quantified vulnerability-weighted species richness averages for 64

different biome-realms across the planet, both inside and outside of PAs, to evaluate if they sufficiently cover areas of high biodiversity. I have repeated this process for 4 different vertebrate groups to evaluate potential taxonomic bias in protected area coverage. I have then identified biomes with insufficient PA coverage, and using vulnerability-weighted species richness, recommended future areas of protection to improve the effectiveness of PAs while moving towards 30% terrestrial area protection.

2. Methodology

2.1 Data Collection and Processing

I utilized 324,089 geospatial records in my analysis. These included 52,247 species range maps, 14,458 ecoregion records, and 257,384 protected area records, all in the form of shapefile polygons. Analyses were conducted using the packages `sf`²⁸, `fasterize`²⁹, `raster`³⁰, `dplyr`³¹, and `writexl`³² in R Version R-4.0.5³³ and Rstudio Version 1.4.1106³⁴. I used ArcGIS Pro³⁵ to format final TIFF files into figures. All shapefiles were rasterized to grids using latitude/longitude projection and WGS84 datum at a resolution of 0.1 degrees (approximately 11.1 km at the equator). The same projection, datum, and resolution were used in ArcGIS. Masking was used to limit the scope to only terrestrial species and biomes.

2.1.1 Species Ranges

The species range data was taken from the December 2021 release of the IUCN Red List Assessment (retrieved from <https://www.iucnredlist.org/resources/spatial-data-download>)³⁶ and the 2018 release of BirdLife International species distribution data (<http://www.birdlife.org/datazone/home>)³⁷.

An older (2018) version of BirdLife data has been used due to access limitations, as compared to the other species range data which is immediately accessible from IUCN. IUCN range maps visualize species distributions through the capture of all permanent or periodic occurrences³⁸.

I have chosen to work with terrestrial vertebrate taxa; mammals, reptiles, amphibians, and birds. Terrestrial vertebrates have the most extensive and accurate geospatial data available^{26,39}. I have therefore excluded datasets available for fishes, marine groups, plants, and

freshwater groups. Within my analyses I have also chosen to remove species labelled with the IUCN category of Extinct (EX) or Extinct in the Wild (EW), following the precedent of Venter et al (2014) and Butchart et al. (2015).

2.1.2 Biome Realms

I conducted my calculations within 64 unique terrestrial “biome realms” (BRs) created from the World Wildlife Fund’s (WWF) 2012 release of the terrestrial ecoregions of the world (<https://www.worldwildlife.org/publications/terrestrial-ecoregions-of-the-world>)⁴⁰. According to the WWF, ecoregions are biogeographic units described as “*relatively large units of land or water containing a distinct assemblage of natural communities sharing a large majority of species, dynamics, and environmental conditions*”⁴⁰. Each of the 857 ecoregions is assigned both a “biome” and a “realm”. There are 14 biomes and 8 realms (Tables 1-2).

Table 1: Biomes as defined by the WWF 2012 release

Biomes
Tropical/Subtropical Moist Broadleaf Forests
Tropical/Subtropical Dry Broadleaf Forests
Tropical/Subtropical Coniferous Forests
Temperate Broadleaf and Mixed Forests
Boreal Forests/Taiga
Tropical/Subtropical Grasslands, Savannas, Shrublands
Temperate Grasslands, Savannas, Shrublands
Flooded Grasslands, Savannas
Montane Grasslands, Shrublands
Tundra
Mediterranean Forests, Woodlands, Shrublands
Deserts, Xeric Shrublands

Mangroves
Tundra
Temperate Conifer Forests

Note: Information is from Olson (2001)⁴⁰.

Table 2: Realms as defined by the WWF 2012 release

Realms
Australasia
IndoMalay
Pelearctic
Oceania
Neotropic
Antarctic
Afrotropic
Nearctic

Note: Information is from Olson (2001)⁴⁰.

I combined these biogeographic units, creating biome realms (Fig. 1), in order to cohesively interpret and present global data. If I had instead used all 857 ecoregions, analyses would have been too finite and difficult to synthesize. Biomes and realms on their own were too broad to interpret accurate trends. It is important to consider for current and future PAs that they are more or less equally distributed across ecoregions that represent the diversity of natural habitats and conditions on earth. The combination of biomes and realms provides a middle ground that is specific enough to yield pointed take-aways, but still coherently present results on a global scale. A full table of the biome realm names and descriptions can be found in Supplementary Materials (Table S1).

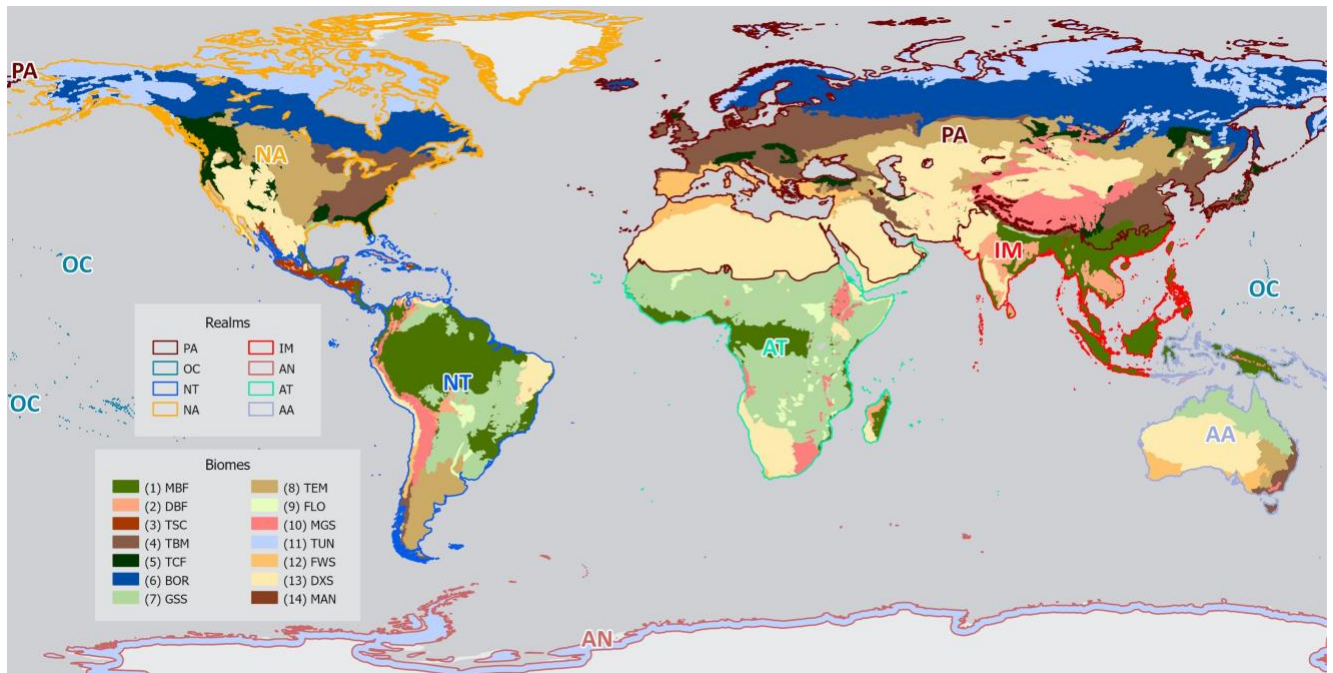


Figure 1. Global biomes and realms as defined by the WWF 2012 release. Biomes and realms are combined to form biome realms. For example, biome 1 in each different realm is a separate biome realm; 1PA, 1IM, 1AA etc. Realms are as follows; (PA) Pelearctic, (OC) Oceania, (NT) Neotropic, (NA) Nearctic, (IM) IndoMalay, (AN) Antarctic, (AT) Afrotropic, (AA) Australasia. Biomes are as follows; (1) MBF: Tropical/Subtropical Moist Broadleaf Forests, (2) DBF: Tropical/Subtropical Dry Broadleaf Forests, (3) TSC: Tropical/Subtropical Coniferous Forests, (4) TBM: Temperate Broadleaf and Mixed Forests, (5) TCF: Temperate Coniferous Forests, (6) BOR: Boreal Forests/Taiga, (7) GSS: Tropical/Subtropical Grasslands, Savannas, Shrublands, (8) TEM: Temperate Grasslands, Savannas, Shrublands, (9) FLO: Flooded Grasslands, Savannas, (10) MGS: Montane Grasslands, Shrublands, (11) TUN: Tundra, (12) FWS: Mediterranean Forests, Woodlands, Shrublands, (13) DXS: Desert and Xeric Shrublands, (14) MAN: Mangroves. Data derived from the WWF 2012 release⁴⁰.

2.1.3 Protected Areas

Protected area shapefiles were retrieved from the March 2022 update from the World Database on Protected Areas (WDPA)

(<https://www.protectedplanet.net/en/resources/january-2022-update-of-the-wdpa-and-wd-oecm>)⁴¹. The March 2022 update contains 269,673 geospatial records of protected areas. I needed spatial records with defined edges in order to make calculations based on intersections with biome realms. To accomplish this, I excluded 12,289 point files without defined edges, and included 257,384 polygon files.

The WDPA is the most comprehensive global database of protected areas¹⁹. They accept protected areas fitting the IUCN or CBD definition;

IUCN definition:

“A protected area is a clearly defined geographical space, recognized, dedicated, and managed, through legal or other effective means, to achieve the long-term conservation of nature with associated ecosystem services and cultural values.” (Dudley 2008)

CBD definition:

“A geographically defined area, which is designated or regulated and managed to achieve specific conservation objectives.” (Article 2 of the Convention on Biological Diversity)

Some protected areas, though included in the WDPA dataset, may not fit the above definitions as countries often have their own national definition of what a protected area is. However, the majority of records should be assumed to align with the above definitions⁴².

I have not made any exclusions from the polygons provided in the WDPA March 2022 release. Protected areas are assigned an IUCN management category that delineates varying degrees of protection, including categories of Not Reported, Not Applicable, and Not Assigned. It could have been an option to exclude protected areas that do not fall under an IUCN management category. However, all categories are included by the CBD when assessing progress towards terrestrial area protection, and my goal is to assess biodiversity protection in line with international goals to protect 30% of terrestrial land.

There are both publicly protected areas (PAs) and privately protected areas (PPAs).

PPAs are established and controlled by individual actors or groups of individuals, NGOs, corporations, for-profit owners, research entities, or religious entities⁴³.

Privately protected areas, though recognized as important for reaching conservation goals, are globally under-reported⁴³. The WDPA currently reports only on publicly protected areas. As such, privately protected areas were excluded from my scope.

Additionally, as mentioned in the introduction I have excluded marine protected areas (MPAs) from my scope. MPAs and terrestrial PAs have significant differences in the way that they are established, managed, and evaluated. There are more publications and greater amounts of data available for analysis for terrestrial PAs, making it a more ideal subject choice for the scope of my research. However, MPAs are also critical for achieving conservation efforts, and Action Target 2 calls for both 30% of land and marine areas to be protected by 2030^{5,20}.

2.2 Analysis

All code is available in supplementary materials (Source Code S1-3).

2.3.1 Creating Vulnerability Weighted Species Richness Maps

The first objective of my study was to assess if the current protected area network is adequately positioned to safeguard areas of high biodiversity, based on the indicator of species richness. Species richness is defined as the quantity of species in a given geographic area and is an important ecological health indicator⁴⁴. Vulnerable species are generally considered a higher conservation priority than species that are not actively at risk for extinction. In order to represent this prioritization, I created vulnerability-weighted species richness maps at a global scale at 0.1 degree resolution. To account for vulnerability, I took the aforementioned species range shapefiles, removed extinct species, and added an attribute for category weight. I used the weighting method by Pouzols et al. (2014)³, assigning varying weights to different vulnerability categories (table 2).

Table 3. IUCN risk category weights used to account for conservation priority of vulnerable species

Category	Weight
Critically Endangered	8
Endangered	6
Vulnerable	4
Near Threatened	2
Data Deficient	2
Least Concern	1

Note: data from Pouzols et al. (2014)³

I then rasterized the species range maps, summing the category weights to be used as raster cell values. For comparison, I calculated both unweighted species richness and vulnerability-weighted species richness maps for each taxa group, which can be found in supplementary materials (Figures S1a-i).

2.2.2 Calculating the Average Vulnerability Weighted Richness

The next step was to calculate the mean vulnerability weighted species richness in each BR, both inside and outside of protected areas. If the mean value of the protected areas is higher than the mean value outside of protected areas, then it can be assumed that the PA network within that biome realm is adequately covering biodiversity-rich areas, based on this indicator.

I created the biome realm polygons using the WWF's ecoregion spatial data, and then masked the vulnerability weighted richness raster by each biome realm, resulting in a richness raster containing only cell values within the respective BR. I used an intersect function to analyze which protected areas fell within the biome realm, rasterized the selected PA polygons, and set all values outside of the biome realm to NA. This left me with a vulnerability-weighted species richness raster of the protected area inside the BR. I duplicated the species richness raster of the entire biome realm, and in instance 1 set all values outside of PAs to NA, and in instance 2 set all values inside of PAs to NA. I then calculated the mean for each of these raster

layers to give me the average vulnerability-weighted richness both inside of PAs and outside of PAs within each biome realm.

2.2.3 Isolating Biodiversity Hotspots Outside of PAs for Future Protection

My last objective was to identify future areas that should be prioritized for protection in order to reach 30% of terrestrial area coverage in line with the 30 by 30 initiative. I wanted to determine how much land *outside* of what is protected today needs to be prioritized up until 30% coverage. To do this I calculated the area of each BR that is currently protected, using `st_intersection` and `st_union` functions to take only the area of PAs that fell inside of each biome realm. Then I calculated the total area of each biome realm and the percentage of each that is currently protected. Using the average cell area, I then calculated how many more cells need to be protected in each individual BR to reach 30% protection.

I wanted the results to be easily comparable within and across each biome realm, so I utilized a ratio to rank each cell from 0 to 1 (0 being least important, 1 being most important) by dividing each raster cell value within a BR by the highest value in that BR. I then sorted the cells by decreasing value and set all cells outside of the top x% (determined in the previous steps to reach 30% land area when combined with current PA coverage) to NA. This gave me a raster of the most important areas in each BR to prioritize, based on vulnerability-weighted species richness, as we designate more area for protection in an effort to reach 30%.

2. Results & Discussion

3.1 Protected Area Richness Coverage

Within the results section, for the sake of displaying figures concisely I'll be focusing on mammals and amphibians as examples of a well-documented and less-documented taxon. Although birds have more extensive data than mammals, I have chosen to use mammals for the case example as the data is more recent.

When looking at all taxa, between 44-53% (Table 4, Table S5, Fig. 2a-b, Fig. S2c-d) of biome realms have a higher average species richness *outside* of protected areas than inside. For mammals, one of the best-documented taxa with one of the lowest rate of data-deficient

species, approximately 45% of biome realms have higher species richness outside of protected areas, meaning that in 45% of the biome realms protection coverage for mammals is insufficient. At the opposite end of the spectrum, amphibians are one of the poorest-documented vertebrates with the highest rate of species categorized as data deficient (of the 4 taxa studied). For amphibians, approximately 53% of biome realms have higher rates of biodiversity outside of protected areas, showing that more than half of all biome realms do not adequately protect vulnerable amphibians.

Table 4. Mean vulnerability-weighted species richness values in protected areas (PA) as well as non-protected areas (NPA) and whether level of protection is higher in PA or NPA, for Amphibians and Mammals across each of 64 biome realms. Where species richness is higher inside PAs, mean species richness (MSP) is labelled “Higher in PA” in green, where it is higher outside of PAs, MSP is labelled “Higher in NPA” in red. Data for birds and reptiles provided in supplementary figures (Table S5).

BR	% of land currently protected	Amphibians			Mammals		
		NPA	PA	MSP	NPA	PA	MSP
10AA	59.29	12.40	10.96	Higher in NPA	34.96	22.78	Higher in NPA
10AT	10.49	17.96	19.41	Higher in PA	105.48	124.71	Higher in PA
10IM	50.47	53.75	65.44	Higher in PA	279.00	283.56	Higher in PA
10NT	18.45	5.58	6.35	Higher in PA	49.21	60.32	Higher in PA
10PA	7.36	1.54	1.80	Higher in PA	52.18	58.81	Higher in PA
11AA	100.00	0.00	0.00	N/A	0.00	18.08	Higher in PA
11AN	1.33	0.00	0.00	N/A	1.03	6.65	Higher in PA
11NA	22.95	0.22	0.31	Higher in PA	21.07	19.97	Higher in NPA
11PA	17.70	0.69	0.54	Higher in NPA	24.13	20.98	Higher in NPA
12AA	22.75	7.05	6.09	Higher in NPA	23.91	22.74	Higher in NPA
12AT	21.27	12.34	13.28	Higher in PA	90.14	94.41	Higher in PA
12NA	13.41	14.36	13.24	Higher in NPA	54.88	53.99	Higher in NPA

12NT	3.13	5.12	5.76	Higher in PA	26.53	28.73	Higher in PA
12PA	17.54	8.10	10.29	Higher in PA	56.70	61.18	Higher in PA
13AA	27.19	4.33	3.60	Higher in NPA	25.63	25.00	Higher in NPA
13AT	16.66	6.18	6.38	Higher in PA	67.19	68.50	Higher in PA
13IM	5.75	9.42	5.30	Higher in NPA	63.18	42.58	Higher in NPA
13NA	13.64	9.11	6.84	Higher in NPA	69.40	60.50	Higher in NPA
13NT	9.70	23.77	23.51	Higher in NPA	115.75	138.69	Higher in PA
13PA	7.14	0.69	0.92	Higher in PA	34.18	39.97	Higher in PA
14AA	21.79	8.22	6.84	Higher in NPA	44.95	38.32	Higher in NPA
14AT	26.41	33.14	33.56	Higher in NPA	125.34	117.58	Higher in NPA
14IM	12.80	13.20	10.86	Higher in NPA	122.43	95.68	Higher in NPA
14NT	54.55	27.26	23.83	Higher in NPA	118.29	118.10	Higher in NPA
1AA	10.90	14.11	16.29	Higher in PA	69.06	68.94	Higher in NPA
1AT	19.21	33.93	38.10	Higher in PA	153.61	167.78	Higher in PA
1IM	8.06	23.92	32.19	Higher in PA	150.79	200.73	Higher in PA
1NT	36.01	58.26	67.49	Higher in PA	180.75	197.40	Higher in PA
1OC	8.37	1.88	1.55	Higher in NPA	12.05	12.64	Higher in PA
1PA	0.70	33.45	33.47	Higher in PA	137.85	150.65	Higher in PA
2AA	10.31	7.12	6.53	Higher in NPA	51.04	45.33	Higher in NPA
2AT	13.26	11.59	19.30	Higher in PA	53.22	88.12	Higher in PA
2IM	7.03	17.63	31.79	Higher in PA	105.33	169.43	Higher in PA
2NA	5.41	11.24	12.14	Higher in PA	68.06	67.61	Higher in NPA
2NT	14.48	23.97	29.05	Higher in PA	123.83	144.09	Higher in PA
2OC	8.01	2.74	3.00	Higher in PA	13.09	8.56	Higher in NPA
3IM	4.35	12.36	15.63	Higher in PA	107.17	132.33	Higher in PA
3NA	17.82	11.61	12.94	Higher in PA	78.45	84.47	Higher in PA
3NT	14.21	16.85	21.79	Higher in PA	117.26	104.98	Higher in NPA
4AA	22.53	23.27	19.71	Higher in NPA	48.61	42.71	Higher in NPA
4IM	8.51	14.92	10.93	Higher in NPA	113.15	143.85	Higher in PA
4NA	6.70	21.25	18.97	Higher in NPA	60.87	59.49	Higher in NPA
4NT	49.11	6.75	4.81	Higher in NPA	27.06	23.79	Higher in NPA

4PA	12.30	10.40	10.52	Higher in PA	65.95	67.65	Higher in PA
5IM	16.63	10.09	9.27	Higher in NPA	92.87	112.15	Higher in PA
5NA	15.18	12.84	8.74	Higher in NPA	58.58	58.64	Higher in PA
5PA	16.49	5.72	5.89	Higher in PA	70.63	75.38	Higher in PA
6NA	14.40	2.51	2.16	Higher in NPA	40.49	40.51	Higher in PA
6PA	10.86	2.73	2.29	Higher in NPA	41.14	37.08	Higher in NPA
7AA	15.40	14.31	17.89	Higher in PA	40.23	49.44	Higher in PA
7AT	16.76	18.90	23.92	Higher in PA	103.58	130.64	Higher in PA
7IM	10.13	15.25	16.78	Higher in PA	125.13	138.43	Higher in PA
7NA	8.93	24.11	20.21	Higher in NPA	47.52	43.78	Higher in NPA
7NT	13.29	35.91	40.21	Higher in PA	132.30	151.07	Higher in PA
7OC	15.88	2.82	2.80	Higher in NPA	5.50	3.60	Higher in NPA
8AA	4.74	12.38	12.05	Higher in NPA	31.28	29.69	Higher in NPA
8AT	3.63	1.95	1.60	Higher in NPA	40.60	40.50	Higher in NPA
8NA	2.53	9.82	8.23	Higher in NPA	59.81	57.55	Higher in NPA
8NT	5.87	5.94	4.18	Higher in NPA	36.23	32.70	Higher in NPA
8PA	6.15	3.32	3.11	Higher in NPA	56.77	59.06	Higher in PA
9AT	44.72	20.16	23.49	Higher in PA	111.25	123.43	Higher in PA
9IM	3.30	5.46	3.78	Higher in NPA	50.61	53.67	Higher in PA
9NT	19.73	39.56	35.00	Higher in NPA	127.59	107.96	Higher in NPA
9PA	13.31	5.88	3.56	Higher in NPA	53.75	49.71	Higher in NPA

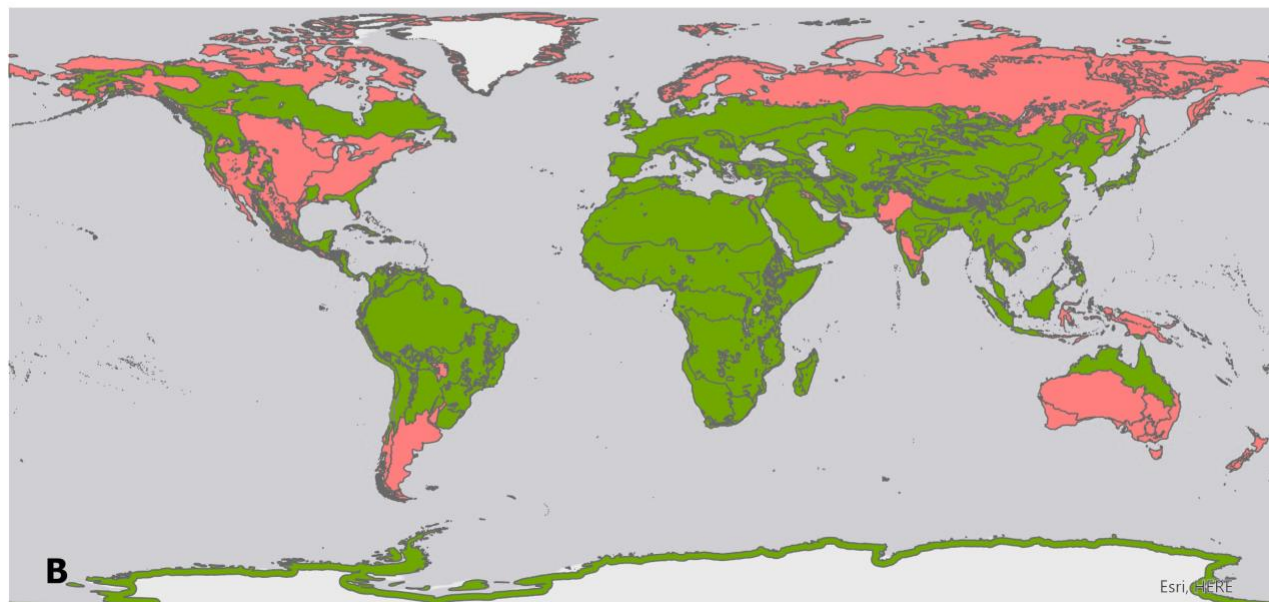
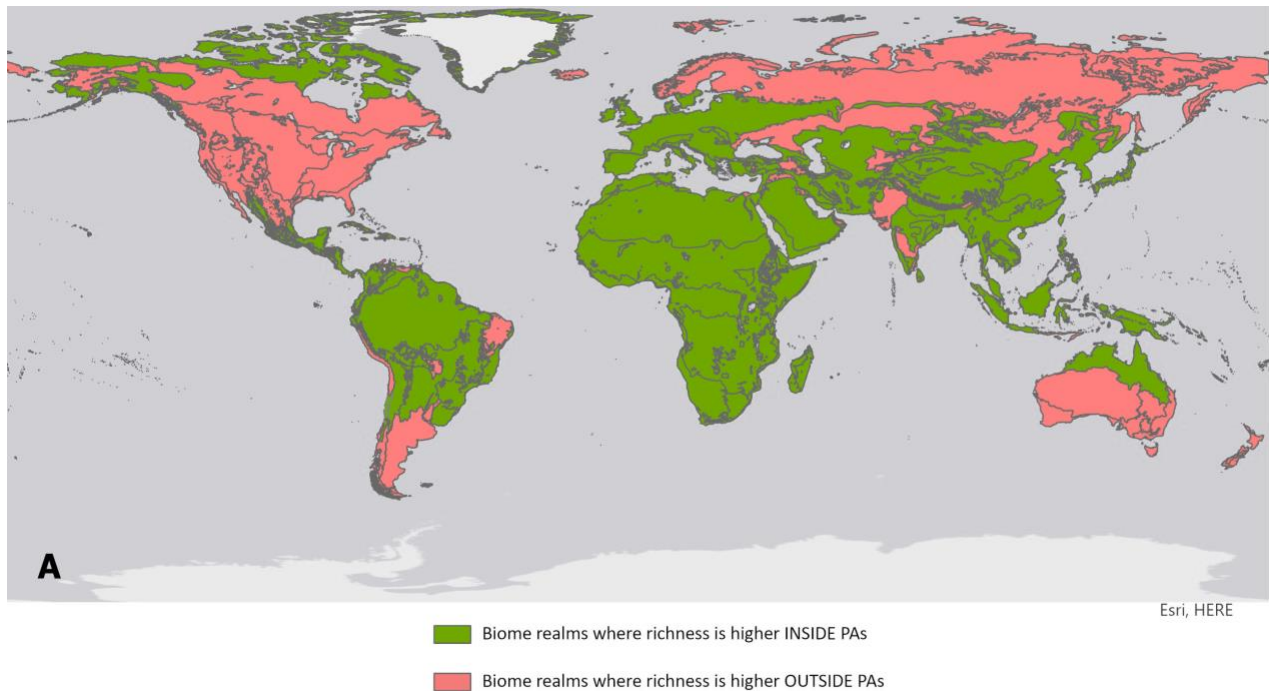


Figure 2a-b. Mammals (A) and Amphibians (B). Biome realms represented in red have higher vulnerability-weighted richness averages outside of protected areas. Biome realms symbolized in green have higher richness values inside of PAs, meaning protected areas are adequately covering richness hotspots within the biome realm. Data utilized to create biome realms from Olson (2001)⁴⁰.

While the IUCN provides the most taxonomically and geographically extensive data on global species distributions³⁸, there are limitations that should be acknowledged when considering the results of this study. Species range maps are overestimates and most appropriate at coarser scales⁴⁵. This can lead to identifying biodiversity hotspots incorrectly, underestimating species' risk of extinction, or overestimating protected area coverage⁴⁶. Still, species range data is critical for a variety of conservation functions and is used extensively⁴⁵. The risk of commission errors can be mitigated by using coarser resolutions of 20-30 km (.2-.3 degrees), or including other factors in the analysis such as habitat suitability models⁴⁷. The 0.1 degree resolution used in my analysis (approximately 11.1 km at the equator) is close to the recommendation of 20-30 km, but also allows me to account for necessary fine-scale spatial data such as small PAs.

Covering areas with high rates of vulnerable species richness is an important factor for PA success⁴⁸, yet nearly half of global biome realms have a higher mean vulnerability-weighted species richness *outside* of protected areas. Geographic bias, varying degrees of PA protection, and different indicator prioritization are all possible explanations for this contradiction.

For decades, geographic or location bias has been identified as an issue with PA establishment and success^{21,49,50}. Historically and today, protected areas have been said to be “rock and ice” – the land that is set aside tends to be that which is economically unviable, sparsely populated, and has low opportunity costs for protection^{10,21}. This trend is particularly acute since more aggressive international areal targets were introduced by the CBD²¹. Land that is species poor, located in desert or dry ecoregions, and already well-represented by PA systems has made up nearly a third of newly protected land since 2010²³. Choosing land that is unlikely to compete with other uses enables governments to meet land area targets while avoiding economic costs or political and public contention^{17,21}. This trend has far-reaching negative consequences. Establishing protected areas based on marginality rather than threatened species presence is costly and ineffective. Venter et al. (2018)²¹ concluded that if protected areas established between 2004-2014 had strategically targeted threatened

vertebrates, over 30 times more species could have been protected with the same amount of land.

Another explanation for lower rates of species richness in some protected areas could be the degree of protection allocated to that PA. The IUCN defines 6 different protection categories, ranging from strict protection with little human interference, to allowing commercial use of natural resources (activities like logging, extraction, etc.)⁵¹. Studies have found that IUCN protection categories are also impacted by location bias, with more strictly protected areas in more remote locations where threats tend to be lower, and lower protection levels for PAs nearer to urban centers⁵⁰. The same authors found that species richness and biodiversity tended not to be an influencing factor for protection categorization. However, resource use and land transformation within protected areas does influence species richness levels¹⁵. Identifying protected areas that cover species richness hotspots and allocating higher levels of protection based on scientific evidence could prevent declining species richness in PAs, or even increase richness.

Lastly, prioritization of varying indicators could lead to lower averages of species richness. Species richness is a consistently relied on indicator of biodiversity health, but there are a myriad of other measures as well. Experts differ in opinion on what is most important for ensuring stable and functional ecosystems. These factors include metrics such as land connectivity¹, functional diversity⁵², phylogenetic diversity⁵³, endemism⁵⁴, indicator species⁵⁵, and more. Protected areas may be established focusing on one indicator (such as a specific species or taxa) while disregarding others, such as overall species richness. Ideally, a multitude of indicators should be used to provide a comprehensive picture of ecosystem health and PA effectiveness. Focusing exclusively on a single species or taxa, for example, can result in taxa bias and declining rates of biodiversity.

3.2 Taxa Bias

We can see a marked difference when comparing results between taxa (Fig. 2a-b). In total, for amphibians 34 out of 64 biome realms had higher species richness outside of PAs (Table 4). For mammals, 29 out of 64 biome realms had higher species richness outside of PAs

(Table 4). While it is evident that amphibians have less adequate PA coverage overall, there are also certain areas that perform poorly across all taxa. The majority of the United States, as well as Australia consistently have higher biodiversity outside of protected areas. Additionally, mangroves are a small biome and difficult to see on a global map, but mangrove biomes (Biome 14) in every realm are not adequately protected (except for a select few for birds). This type of information is valuable to visualize in order to see where certain taxa should be prioritized, as well as where all taxonomic groups need more effective protection.

When making decisions about areas for prioritization, data availability can greatly affect conservation efforts²⁶. Between mammals and amphibians, there is a large difference in amount of data available. For mammals, there are 12,871 species range records. Of that number, 7.93% of records are marked as data deficient. Amphibians have significantly fewer species range records, with 8,773 available for analysis. Of those, 13.93% of all records are marked as data deficient. Amphibians have nearly double the data deficiency of mammals, with only about 3/5 of the species range records. These numbers represent species range records, not unique species. It is valuable to look at how much data is gathered overall, as it speaks to funding and active research.

These are examples of taxonomic bias in data and, consequently, in protection. Taxonomic bias is most thoroughly recorded in the collection of inventory measure data like species occurrence records²⁶. Overwhelmingly, vertebrates are overrepresented and invertebrates are underrepresented. Even within vertebrates, there are significant variations. Troudet et al. (2017)²⁶ found that though birds represented only 1% of species recorded, they represented over half of occurrence records. Amphibians and reptiles are among the least recorded vertebrates²⁶.

Fewer records mean a less accurate analysis of species condition and welfare. This can, consequently, affect the placement of protected areas. As an example, the N2000 network of protected areas in Europe is considered one of the most extensive conservation networks to date and is widely considered successful in its protection of key species⁵⁶. However, nearly all studies of the N2000 network focus on birds. A study of butterflies – a non-target group – in the N2000 network found them to be insufficiently protected⁵⁶. Butterfly populations declined

both inside and outside of protected areas over the 10 years studied ⁵⁶. Another study of areas within the N2000 network showed that Germany had experienced a 75% decline in flying insect biomass ⁵⁷. Insects and butterflies require different ecosystems and buffer zones to thrive than birds do, and these ecosystems held a less favorable conservation status within the N2000 network ⁵⁶.

Taxonomic bias can impact decision-makers' ability to make science-based decisions ⁵⁸. It can also inhibit accurate evaluations of how effective PAs and other intervention measures are at safeguarding threatened biodiversity ⁵⁸. As we continue to expand protected areas to meet the 30 by 30 target ²⁰, both of these things will be crucial to slowing biodiversity decline. When we are selecting future areas to protect, we should take special care to consider a more representative group of taxa is considered.

3.3 Future PAs

The CBD is currently working to finalize a post-2020 framework²⁰. Action Target 3 of the drafted post-2020 Global Biodiversity Framework, commonly called the 30x30 initiative, calls for 30% of the planet (terrestrial and marine) to be protected by 2030:

“Action Target 3. Ensure that at least 30 per cent globally of land areas and of sea areas, especially areas of particular importance for biodiversity and its contributions to people, are conserved through effectively and equitably managed, ecologically representative and well-connected systems of protected areas and other effective area-based conservation measures, and integrated into the wider landscapes and seascapes.” ²⁰

The previous international goal, Aichi Target 11, failed to halt or reverse biodiversity loss even though it was achieved. It lacked quantitative benchmarks for ecological integrity and was criticized for vague and ambiguous language beyond the single quantified areal goal. As of the most recently published draft, Action Target 3 lacks quantifiable thresholds for ecological integrity or PA effectiveness in the same way that the previous target 11 did. This begs the question; which 30% should be prioritized? Selecting which land to protect needs to be based

on proven methods of measuring biodiversity. In Figure 3a-b, I have selected the cells with the highest vulnerability-weighted species richness, until in combination with current PAs, 30% of land area is reached. In figures 4a-b and 5a-b I have include closer looks at specific regions that had little protected area coverage, as well as generally poor protection of species richness across multiple taxa. For birds and reptiles, figures S3-S5 can be found in supplementary materials.

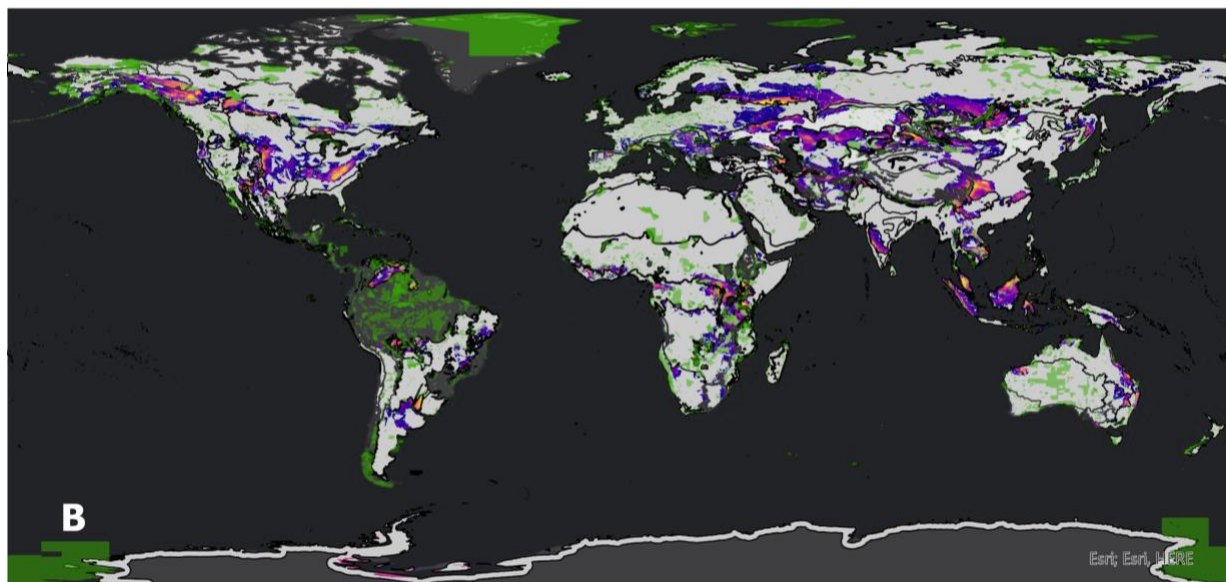
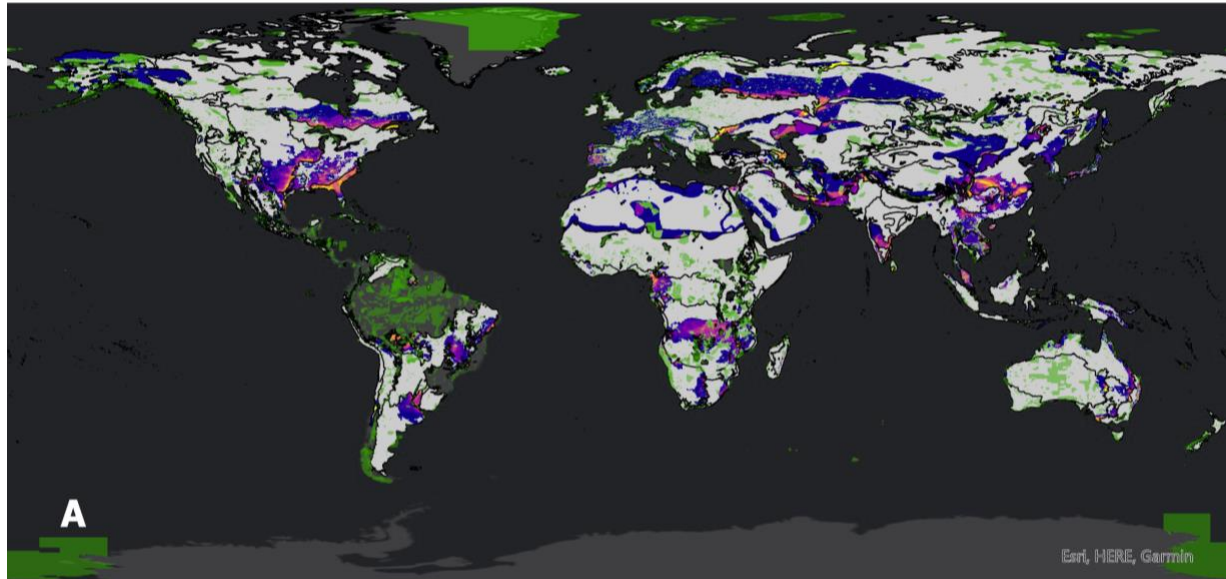


Figure 3a-b. Areas to prioritize for future PAs based on vulnerability-weighted species richness for amphibians (A) and mammals (B). Richness values have been ranked from 0-1 (0 being lowest richness, 1 being highest) for ease of comparison within and between biome realms. The areas highlighted, in combination with current protected area, equal roughly 30% of terrestrial area within each biome realm. Areas in dark grey are biome realms that already exceed 30% of land area protection, so no suggestions for future protection have been made. Biome realm data is sourced from Olson (2001)⁴⁰, vulnerability-weighted richness data is derived from the IUCN (2021)³⁶, and protected area data is derived from the WDPA (2022)⁴¹.

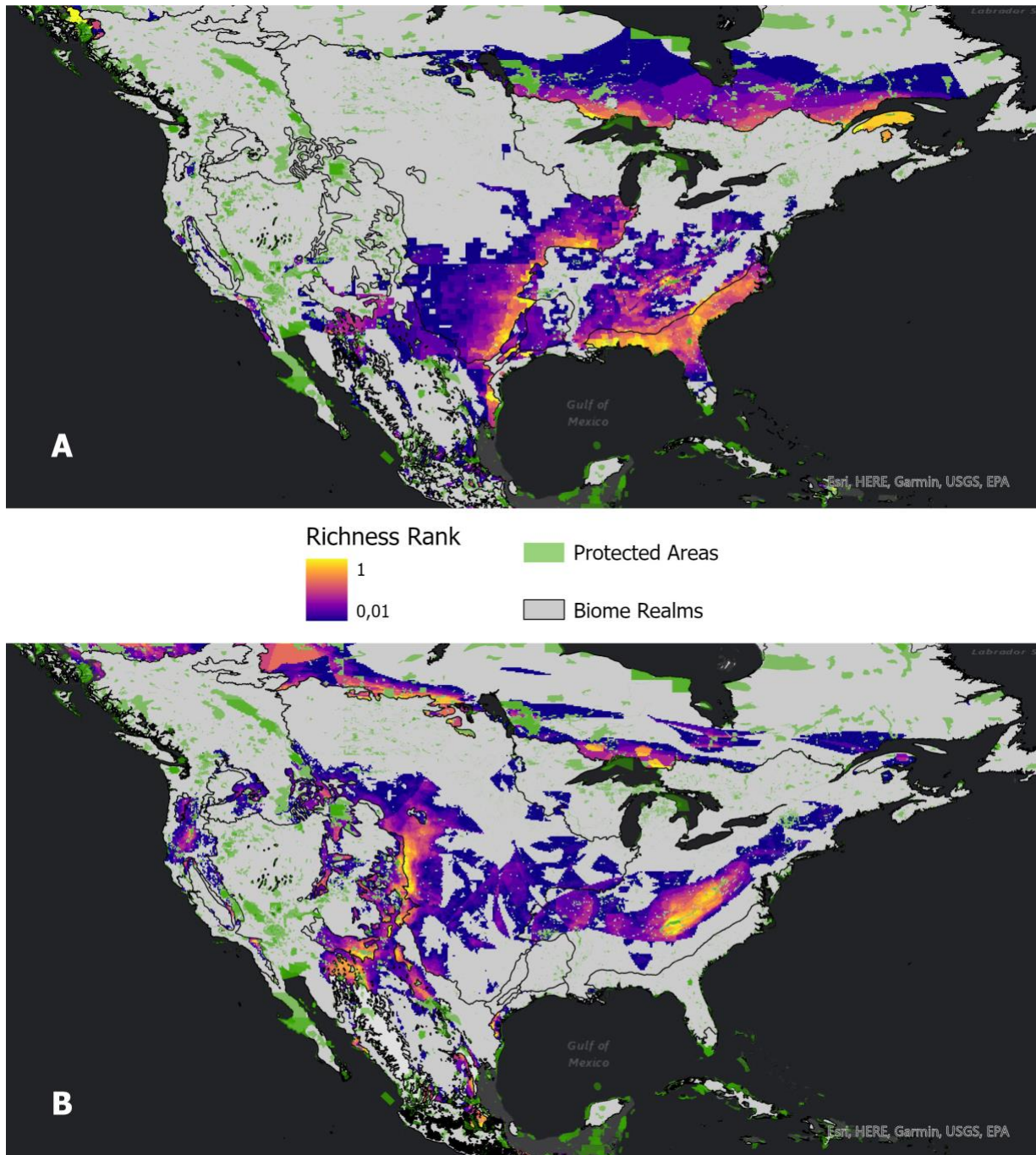


Figure 4a-b. A closer view of areas to prioritize for future protection for amphibians (A) and mammals (B) in the United States and parts of Mexico and Canada. Biome realm data is sourced from Olson (2001)⁴⁰, vulnerability-weighted richness data is derived from the IUCN (2021)³⁶, and protected area data is derived from the WDPA (2022)⁴¹.

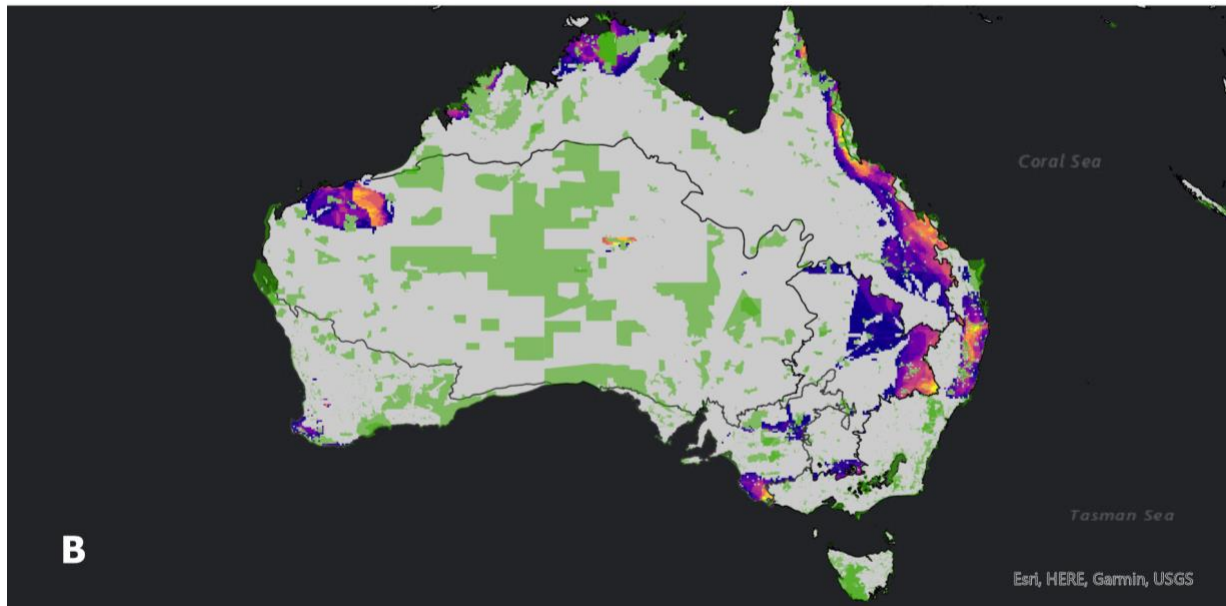
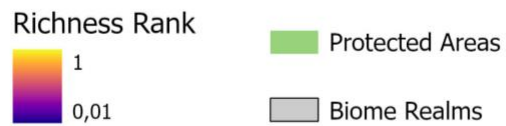
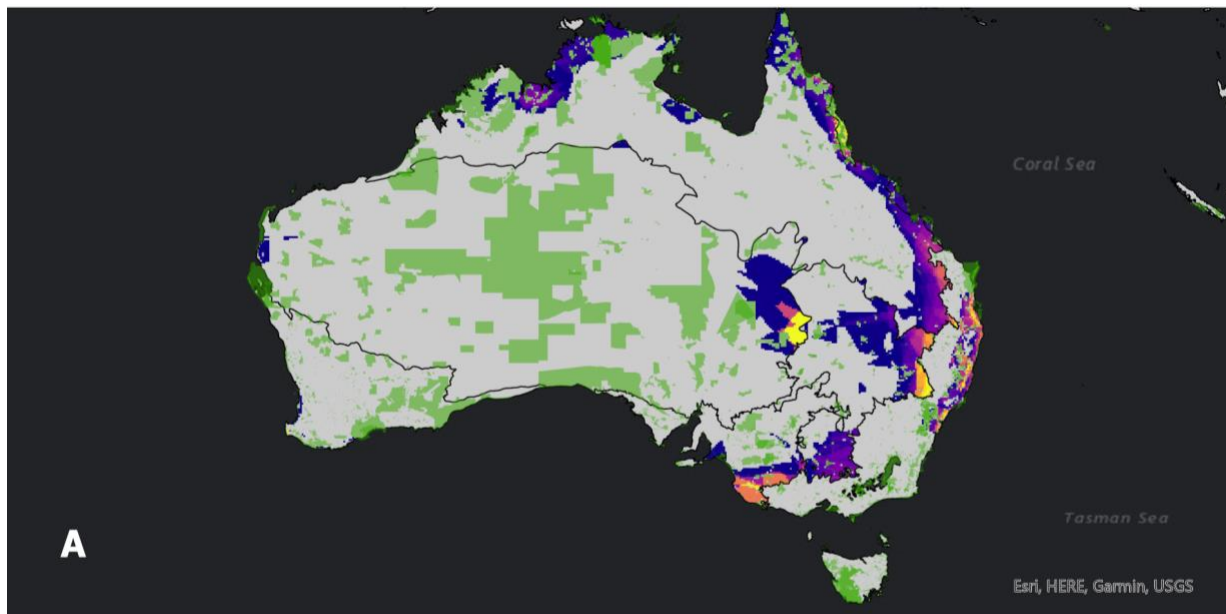


Figure 5a-b. A closer view of areas to prioritize for future protection for amphibians (A) and mammals (B) in Australia. Biome realm data is sourced from Olson (2001)⁴⁰, vulnerability-weighted richness data is derived from the IUCN (2021)³⁶, and protected area data is derived from the WDPA (2022)⁴¹.

Globally, results vary quite markedly between taxa. However, certain biome realms have very little existing protected area coverage and so expansion in Russia, central USA, central and Eastern Asia appears consistently important. In Figure 4a, areas important to protect for amphibians appear clustered along the Southeastern part of the United States, while in 4b mammal richness is concentrated around the Appalachian and Rocky mountain ranges. Some prominent protected areas exist near these mountain ranges and can be seen in figure 4b. For amphibians, very few significant protected areas can be seen already established in the most species-rich areas. These results are fitting with the data from Table 4 signifying that amphibians fare worse than mammals in terms of average species richness inside current protected areas. Agriculturally valuable land like the American Midwest is less likely to be protected²¹ and that is represented in the results – almost no currently protected area is represented in the middle of the country.

I have also included a more detailed view of Australia. Although Australia has a relatively high rate of protected area coverage compared to areas like the Midwestern US, the majority of the continent has higher rates of biodiversity *outside* of PAs. In Figure 5 it is visible that the majority of protected area is located in the interior of the country, an area heavy in deserts and semiarid plateaus (Fig. 1), and very low in biodiversity for every taxa except reptiles (Fig. S1a-i). This finding supports other studies on location bias and the selection of land that does not hold traditional economic value.

While the results are generally as expected, vulnerability-weighted species richness is only a single indicator. For a holistic understanding of which areas should be prioritized to best benefit all taxonomic groups and biodiversity as a whole, other factors should be considered for future research. A protected area's IUCN management category has been shown to be correlated to location and possibly location bias⁵⁰, however no study has yet confirmed significant differences in biodiversity indicators between management categories⁵⁹. Corridors and connectedness of protected area networks have been shown to play a crucial role⁶⁰. Though beyond the scope of this study, hybrid methodologies work well for combining multiple forms of data, for example the species threat abatement and restoration (STAR) metric that combines information on species ranges, threats, and extinction level⁶¹. The results presented

here provide a solid base to build upon with other important indicators and methodologies such as the aforementioned.

3. Conclusion

Protected areas are an incredibly valuable tool in the effort to halt or reverse current biodiversity declines¹⁻⁵. However, to date, areal goals like Aichi Target 11 have failed to do just that. Although the target was met and approximately 17% of terrestrial area was successfully protected by 2020, we continue to see alarming negative trends^{8,15}. Indeed, this study found that for all taxonomic groups evaluated, nearly half of protected areas had lower rates of vulnerability-weighted species richness than the unprotected area *outside* their borders. Certain biomes, such as mangroves, as well as some agriculturally important areas like the American Midwest performed poorly across taxa. Location bias is well documented in protected area delineation, where remote and economically marginal areas have been prioritized over biologically significant areas that may cause more contention (such as agriculturally lucrative land)^{21,24,50}. When evaluating protected areas across all biome realms, there was evident taxonomic bias in global protected area coverage. Thoroughly documented taxonomic groups like mammals and birds had higher coverage, while over half of biome realms had inadequate protection for vulnerable amphibians.

The Aichi Biodiversity targets encouraged rapid expansion of protected area networks around the world, but ambiguous language and unquantified benchmarks allowed nations to meet international goals without necessarily safeguarding biodiversity²⁴. Target 3 of the post-2020 framework calls – more ambitiously – to protect 30% of terrestrial land by 2030²⁰, but currently it lacks quantifiable ecological integrity thresholds in the same way that Target 11 did. In order to ensure that protected areas are effective, scientifically-backed methods for selecting which land to prioritize need to be utilized. Within this study, I have used a widely accepted indicator of biodiversity – vulnerability-weighted species richness – to suggest land for protection to meet the 30 by 30 target. My results show that for each taxa group, different areas are likely to be most critical for protection. Vulnerability-weighted species richness is a sound base indicator⁴⁴, but it is crucial to consider more than one indicator for a holistic view of

which areas should be prioritized for the benefit of all biodiversity. Continued research is necessary to consider how other factors like connectedness and or phylogenetic diversity impact PA success as we seek to improve global biodiversity protection. In order to halt or reverse the critical levels of species loss we are seeing today, we not only need to protect 30% of land by 2030, but we need to correctly assess and prioritize the *right* 30% of land.

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Problem Formulation

From the master agreement:

Protected areas (PAs) are an essential conservation tool and they can be very effective at safeguarding biodiversity. However, they are often established on economically marginal land that is biologically less significant. Using data from the WDPA and IUCN, I will analyze on a global scale if protected areas successfully safeguard land that is high in species richness and threatened species. I will also assess what, if any, correlation exists between PA management category and effectiveness, and the prioritization of various taxon. Ultimately, I will create vulnerability weighted species richness maps to compare with current PA coverage to determine if there are unprotected biodiversity hotspots that should be prioritized for future protection.

The tasks as listed in the thesis description are:

- 1) Identify and discuss effectiveness of current protected areas
- 2) Suggest and discuss which additional areas should be protected

Supplementary Materials

Table S1. Full list of biome realm abbreviations and biome/realm descriptions

Biome Realm Abbreviation	Biome	Realm
10AA	Montane Grasslands & Shrublands	Australasia
10AT	Montane Grasslands & Shrublands	Afrotropics
10IM	Montane Grasslands & Shrublands	IndoMalay
10NT	Montane Grasslands & Shrublands	Neotropics
10PA	Montane Grasslands & Shrublands	Pelearctic
11AA	Tundra	Australasia
11AN	Tundra	Antarctic
11NA	Tundra	Nearctic
11PA	Tundra	Pelearctic
12AA	Mediterranean Forests, Woodlands & Scrub	Australasia
12AT	Mediterranean Forests, Woodlands & Scrub	Afrotropics
12NA	Mediterranean Forests, Woodlands & Scrub	Nearctic
12NT	Mediterranean Forests, Woodlands & Scrub	Neotropics
12PA	Mediterranean Forests, Woodlands & Scrub	Pelearctic
13AA	Deserts & Xeric Shrublands	Australasia
13AT	Deserts & Xeric Shrublands	Afrotropics
13IM	Deserts & Xeric Shrublands	IndoMalay
13NA	Deserts & Xeric Shrublands	Nearctic
13NT	Deserts & Xeric Shrublands	Neotropics
13PA	Deserts & Xeric Shrublands	Pelearctic
14AA	Mangroves	Australasia
14AT	Mangroves	Afrotropics
14IM	Mangroves	IndoMalay
14NT	Mangroves	Neotropics
1AA	Tropical & Subtropical Moist Broadleaf Forests	Australasia
1AT	Tropical & Subtropical Moist Broadleaf Forests	Afrotropics
1IM	Tropical & Subtropical Moist Broadleaf Forests	IndoMalay
1NT	Tropical & Subtropical Moist Broadleaf Forests	Neotropics
1OC	Tropical & Subtropical Moist Broadleaf Forests	Oceania
1PA	Tropical & Subtropical Moist Broadleaf Forests	Pelearctic
2AA	Tropical & Subtropical Dry Broadleaf Forests	Australasia
2AT	Tropical & Subtropical Dry Broadleaf Forests	Afrotropics
2IM	Tropical & Subtropical Dry Broadleaf Forests	IndoMalay
2NA	Tropical & Subtropical Dry Broadleaf Forests	Nearctic
2NT	Tropical & Subtropical Dry Broadleaf Forests	Neotropics
2OC	Tropical & Subtropical Dry Broadleaf Forests	Oceania

3IM	Tropical & Subtropical Coniferous Forests	IndoMalay
3NA	Tropical & Subtropical Coniferous Forests	Nearctic
3NT	Tropical & Subtropical Coniferous Forests	Neotropics
4AA	Temperate Broadleaf & Mixed Forests	Australasia
4IM	Temperate Broadleaf & Mixed Forests	IndoMalay
4NA	Temperate Broadleaf & Mixed Forests	Nearctic
4NT	Temperate Broadleaf & Mixed Forests	Neotropics
4PA	Temperate Broadleaf & Mixed Forests	Pelearctic
5IM	Temperate Conifer Forests	IndoMalay
5NA	Temperate Conifer Forests	Nearctic
5PA	Temperate Conifer Forests	Pelearctic
6NA	Boreal Forests/Taiga	Nearctic
6PA	Boreal Forests/Taiga	Pelearctic
7AA	Tropical & Subtropical Grasslands, Savannas & Shrublands	Australasia
7AT	Tropical & Subtropical Grasslands, Savannas & Shrublands	Afrotropics
7IM	Tropical & Subtropical Grasslands, Savannas & Shrublands	IndoMalay
7NA	Tropical & Subtropical Grasslands, Savannas & Shrublands	Nearctic
7NT	Tropical & Subtropical Grasslands, Savannas & Shrublands	Neotropics
7OC	Tropical & Subtropical Grasslands, Savannas & Shrublands	Oceania
8AA	Temperate Grasslands, Savannas & Shrublands	Australasia
8AT	Temperate Grasslands, Savannas & Shrublands	Afrotropics
8NA	Temperate Grasslands, Savannas & Shrublands	Nearctic
8NT	Temperate Grasslands, Savannas & Shrublands	Neotropics
8PA	Temperate Grasslands, Savannas & Shrublands	Pelearctic
9AT	Flooded Grasslands & Savannas	Afrotropics
9IM	Flooded Grasslands & Savannas	IndoMalay
9NT	Flooded Grasslands & Savannas	Neotropics
9PA	Flooded Grasslands & Savannas	Pelearctic

Note: Biome and realm names from Olson (2001)⁴⁰.

Table S2. Mean vulnerability-weighted species richness values in protected areas (PA) as well as non-protected areas (NPA) and whether level of protection is higher in PA or NPA, for Birds and Reptiles across each of 64 biome realms. Where species richness is higher inside PAs, mean species richness (MSP) is labelled “Higher in PA” in green, where it is higher outside of PAs, MSP is labelled “Higher in NPA” in red.

BR	% of land currently protected	Reptiles			Birds		
		NPA	PA	MSP	NPA	PA	MSP
10AA	59.29	18.01	15.66	Higher in NPA	135.36	135.50	Higher in PA
10AT	10.49	48.58	52.93	Higher in PA	397.11	437.28	Higher in PA

10IM	50.47	172.00	176.39	Higher in PA	385.44	380.50	Higher in NPA
10NT	18.45	10.12	11.60	Higher in PA	127.28	147.92	Higher in PA
10PA	7.36	8.12	8.84	Higher in PA	158.47	204.59	Higher in PA
11AA	100.00	0.00	0.58	Higher in PA	N/A	85.75	Higher in PA
11AN	1.33	0.00	0.04	Higher in PA	1.60	9.12	Higher in PA
11NA	22.95	0.00	0.01	Higher in PA	54.63	47.77	Higher in NPA
11PA	17.70	0.17	0.22	Higher in PA	89.20	72.23	Higher in NPA
12AA	22.75	58.18	57.06	Higher in NPA	209.33	190.77	Higher in NPA
12AT	21.27	52.93	57.28	Higher in PA	298.40	303.92	Higher in PA
12NA	13.41	24.28	25.06	Higher in PA	229.22	221.65	Higher in NPA
12NT	3.13	11.89	13.29	Higher in PA	107.82	117.31	Higher in PA
12PA	17.54	23.65	21.38	Higher in NPA	181.58	174.19	Higher in NPA
13AA	27.19	77.19	76.95	Higher in NPA	141.37	128.07	Higher in NPA
13AT	16.66	43.53	47.19	Higher in PA	223.01	226.54	Higher in PA
13IM	5.75	69.17	67.08	Higher in NPA	323.01	275.10	Higher in NPA
13NA	13.64	27.27	29.59	Higher in PA	226.16	212.16	Higher in NPA
13NT	9.70	65.73	69.81	Higher in PA	264.60	314.15	Higher in PA
13PA	7.14	19.78	21.57	Higher in PA	118.11	135.93	Higher in PA
14AA	21.79	36.95	35.07	Higher in NPA	231.92	257.41	Higher in PA
14AT	26.41	88.28	83.93	Higher in NPA	368.09	373.72	Higher in PA
14IM	12.80	130.15	125.71	Higher in NPA	392.13	348.12	Higher in NPA
14NT	54.55	61.40	58.36	Higher in NPA	342.61	344.98	Higher in PA
1AA	10.90	39.46	41.36	Higher in PA	233.00	239.98	Higher in PA
1AT	19.21	91.14	100.61	Higher in PA	357.41	358.26	Higher in PA
1IM	8.06	118.75	132.77	Higher in PA	423.05	447.35	Higher in PA
1NT	36.01	106.74	120.08	Higher in PA	483.15	507.43	Higher in PA
1OC	8.37	22.92	20.59	Higher in NPA	82.08	80.27	Higher in NPA
1PA	0.70	64.59	72.06	Higher in PA	339.14	365.47	Higher in PA
2AA	10.31	39.90	38.36	Higher in NPA	240.13	217.42	Higher in NPA
2AT	13.26	48.49	86.29	Higher in PA	211.81	266.96	Higher in PA
2IM	7.03	85.35	122.27	Higher in PA	369.80	404.66	Higher in PA

2NA	5.41	41.68	40.61	Higher in NPA	257.36	256.39	Higher in NPA
2NT	14.48	63.75	70.00	Higher in PA	334.62	371.62	Higher in PA
2OC	8.01	27.15	12.22	Higher in NPA	99.32	101.33	Higher in PA
3IM	4.35	56.73	81.18	Higher in PA	440.89	401.45	Higher in NPA
3NA	17.82	33.45	37.98	Higher in PA	286.36	284.97	Higher in NPA
3NT	14.21	35.39	40.29	Higher in PA	298.47	306.75	Higher in PA
4AA	22.53	43.50	31.00	Higher in NPA	252.91	215.44	Higher in NPA
4IM	8.51	48.19	56.71	Higher in PA	428.07	436.92	Higher in PA
4NA	6.70	15.63	11.93	Higher in NPA	231.60	227.23	Higher in NPA
4NT	49.11	5.93	2.65	Higher in NPA	119.93	102.36	Higher in NPA
4PA	12.30	12.50	8.17	Higher in NPA	217.28	192.55	Higher in NPA
5IM	16.63	36.96	33.98	Higher in NPA	346.04	355.27	Higher in PA
5NA	15.18	13.18	7.47	Higher in NPA	209.41	195.27	Higher in NPA
5PA	16.49	11.33	10.43	Higher in NPA	236.18	223.80	Higher in NPA
6NA	14.40	0.26	0.28	Higher in PA	124.06	124.20	Higher in PA
6PA	10.86	1.55	1.17	Higher in NPA	168.045	154.38	Higher in NPA
7AA	15.40	82.64	93.23	Higher in PA	201.70	211.57	Higher in PA
7AT	16.76	57.47	60.00	Higher in PA	352.38	402.91	Higher in PA
7IM	10.13	122.79	115.08	Higher in NPA	476.13	488.20	Higher in PA
7NA	8.93	37.27	35.94	Higher in NPA	297.22	314.21	Higher in PA
7NT	13.29	93.23	98.84	Higher in PA	394.60	412.96	Higher in PA
7OC	15.88	8.82	9.40	Higher in PA	93.00	77.20	Higher in NPA
8AA	4.74	55.25	52.38	Higher in NPA	217.12	211.35	Higher in NPA
8AT	3.63	31.51	34.30	Higher in PA	155.29	145.7	Higher in NPA
8NA	2.53	13.11	7.77	Higher in NPA	230.53	225.56	Higher in NPA
8NT	5.87	19.19	18.32	Higher in NPA	170.37	150.31	Higher in NPA
8PA	6.15	8.41	7.27	Higher in NPA	233.63	242.56	Higher in PA
9AT	44.72	49.65	54.85	Higher in PA	402.45	431.25	Higher in PA
9IM	3.30	59.19	71.44	Higher in PA	349.41	311.33	Higher in NPA
9NT	19.73	93.61	73.16	Higher in NPA	408.36	357.14	Higher in NPA
9PA	13.31	16.80	19.39	Higher in PA	242.44	194.39	Higher in NPA

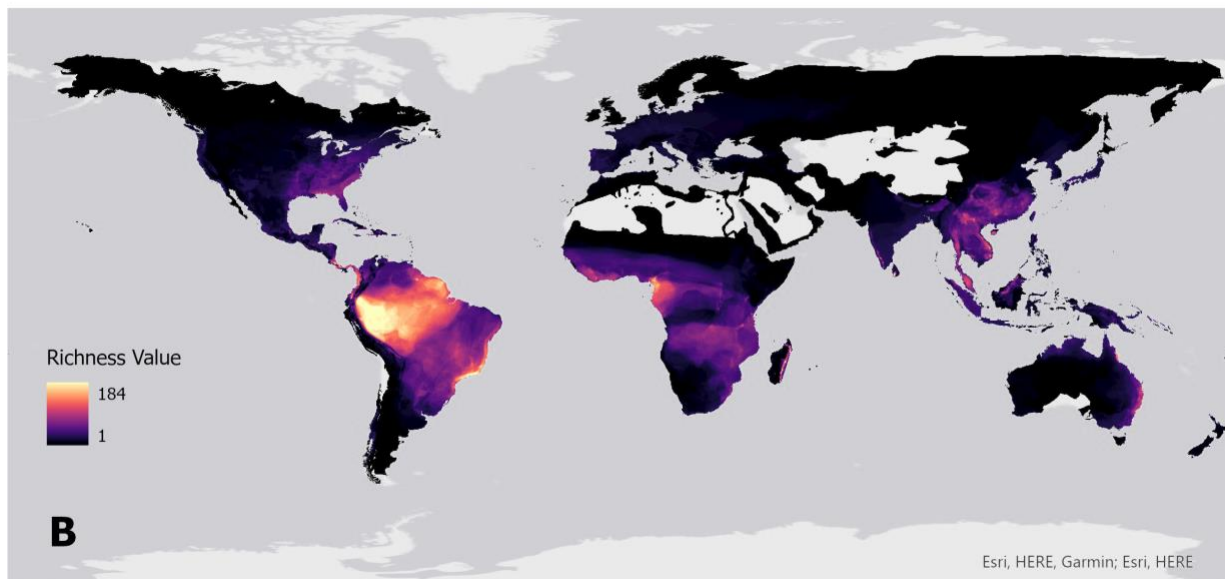
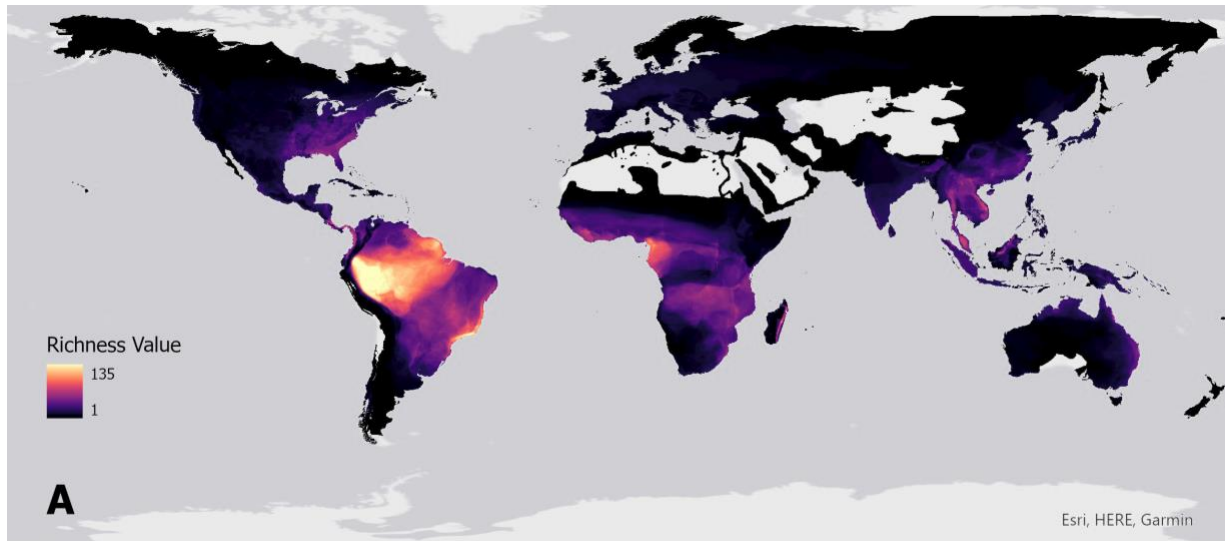


Figure S1a-b. Unweighted (A) and vulnerability-weighted (B) species richness maps for amphibians. Species range data sourced from IUCN (2021)³⁶.

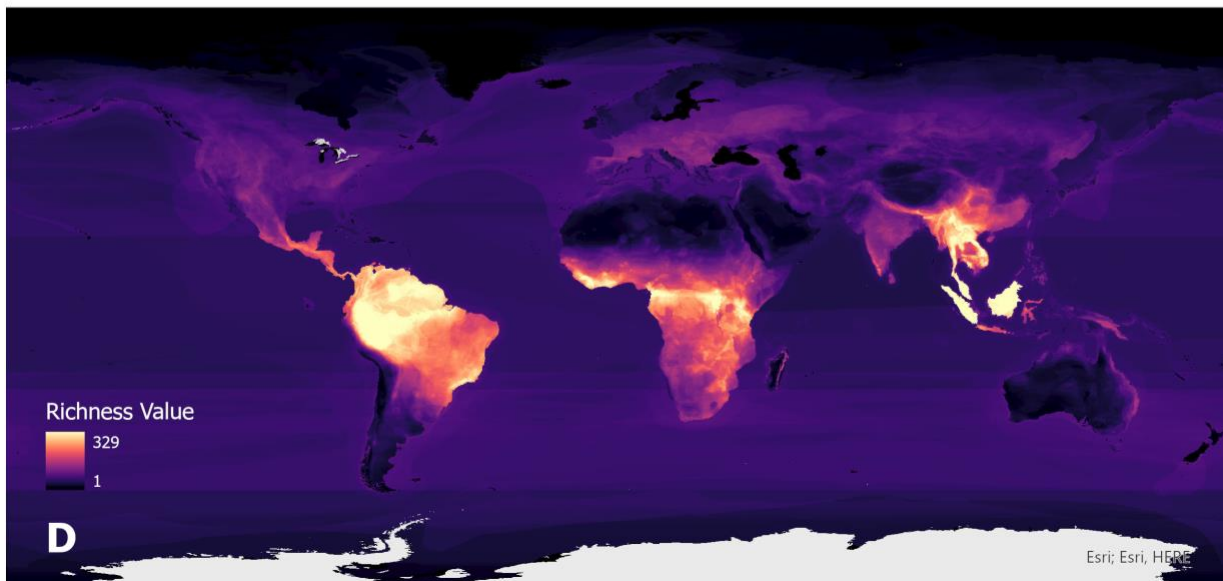
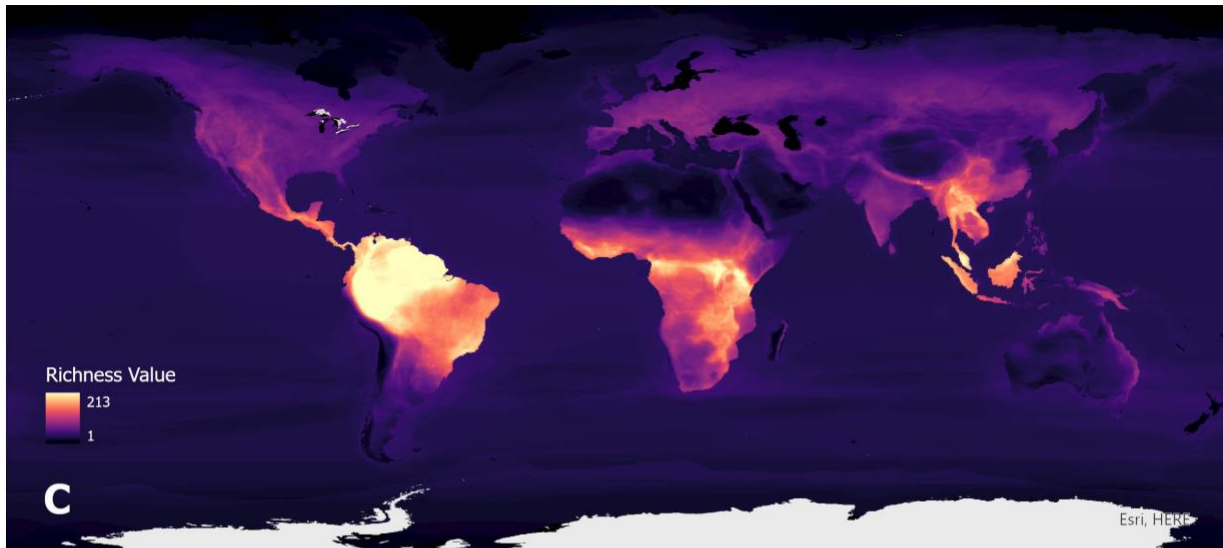


Figure S1c-d. Unweighted (C) and vulnerability-weighted (D) species richness maps for mammals. Marine mammals are also represented in the initial richness maps, but later removed using masking in RStudio. Species range data sourced from IUCN (2021)³⁶.

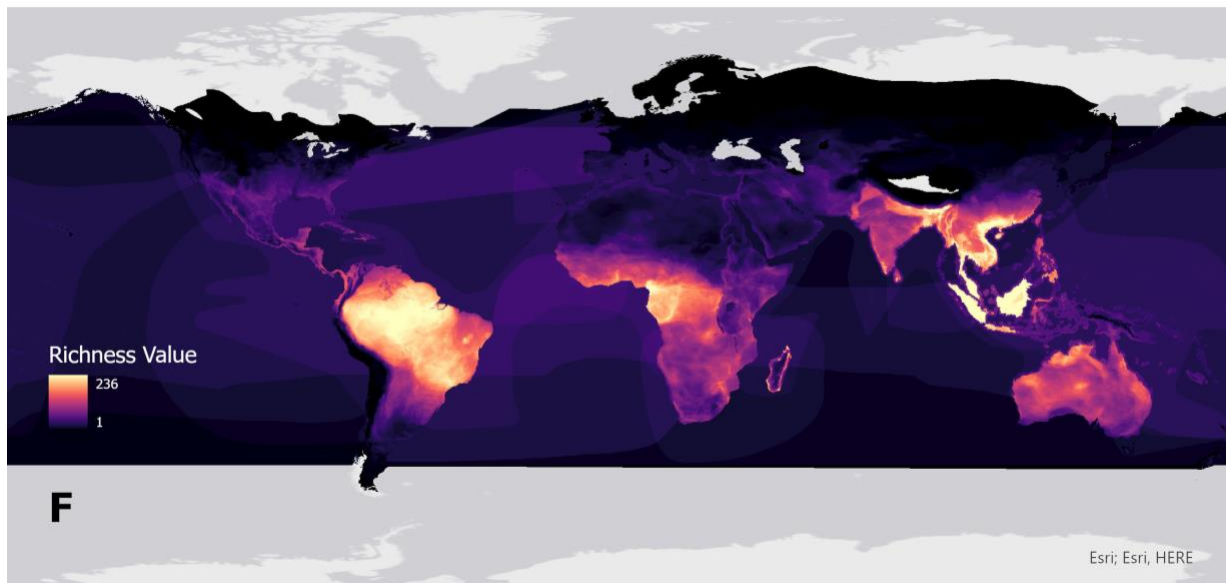
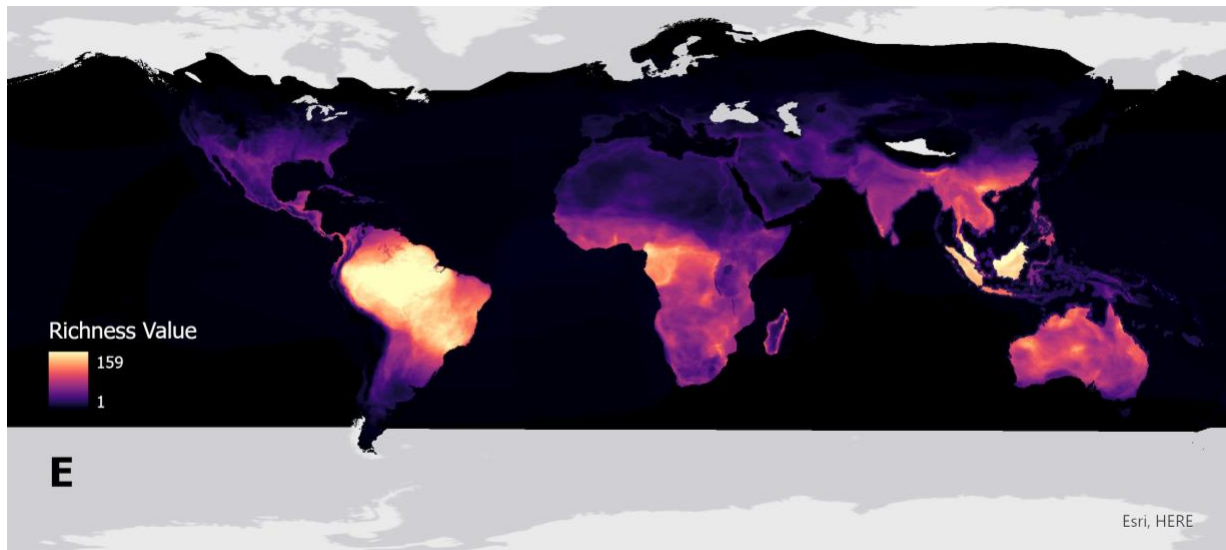


Figure 1e-f. Unweighted (E) and vulnerability-weighted (F) species richness maps for reptiles. Marine reptiles are also represented in the initial richness maps, but later removed using masking in RStudio. Species range data sourced from IUCN (2021)³⁶.

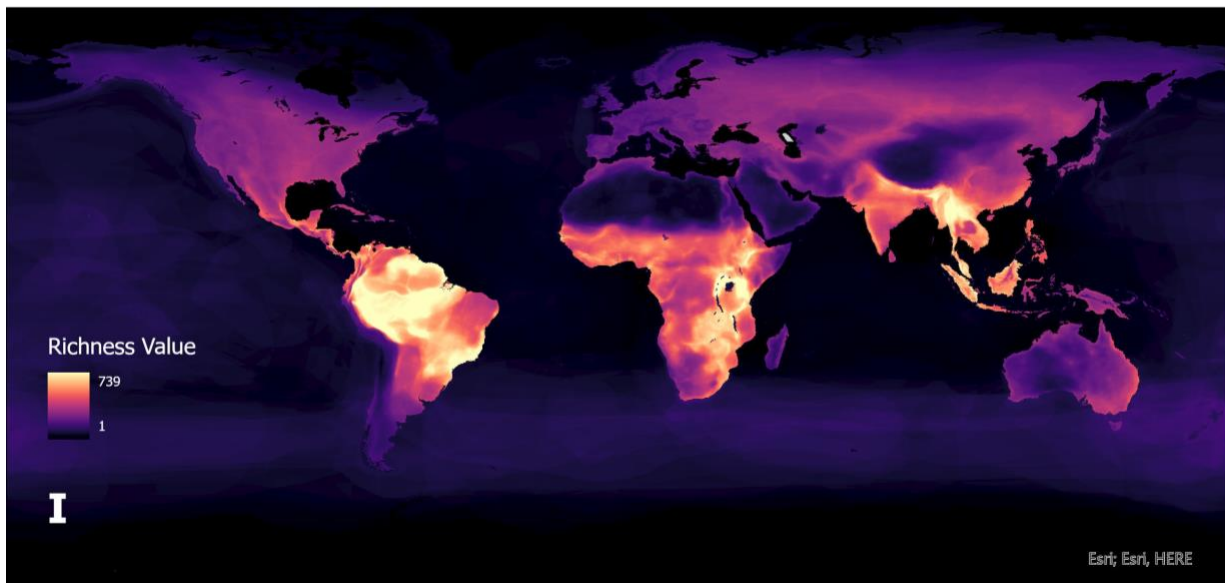
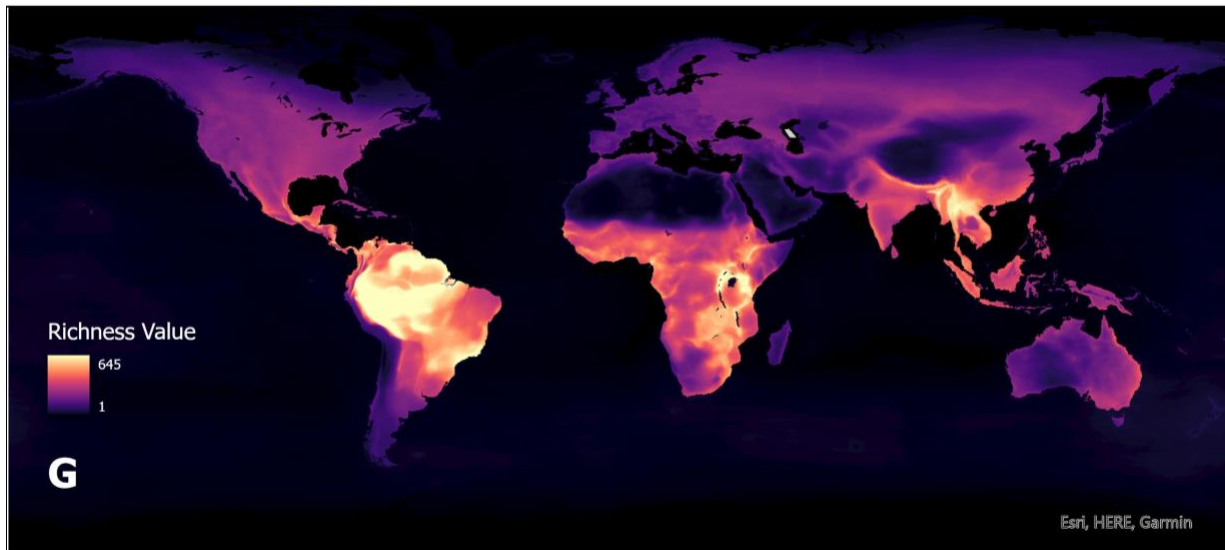
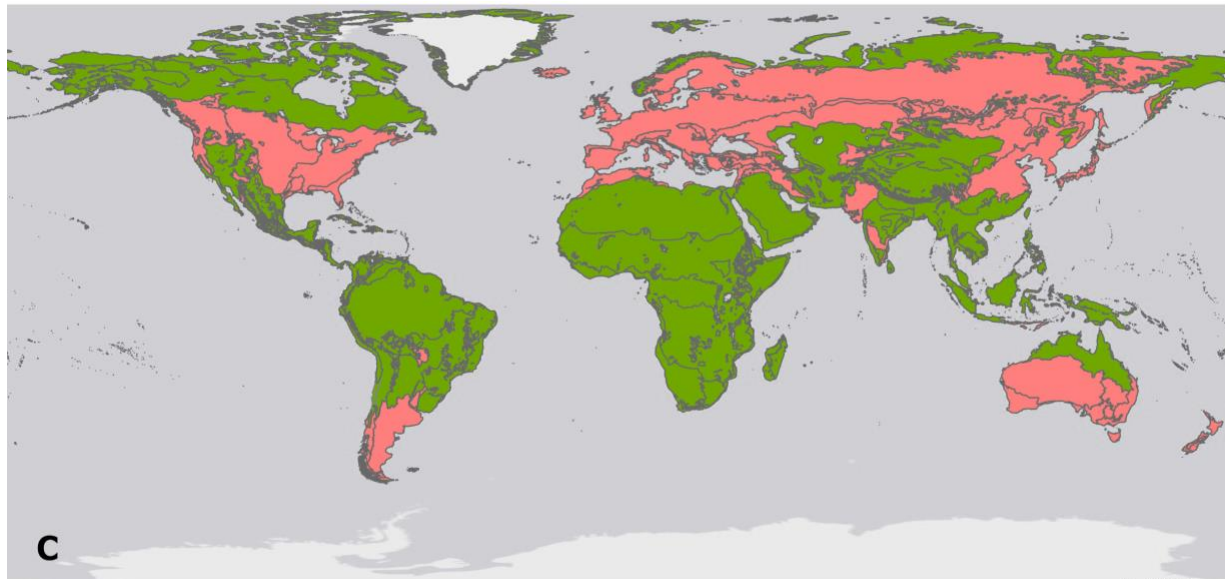
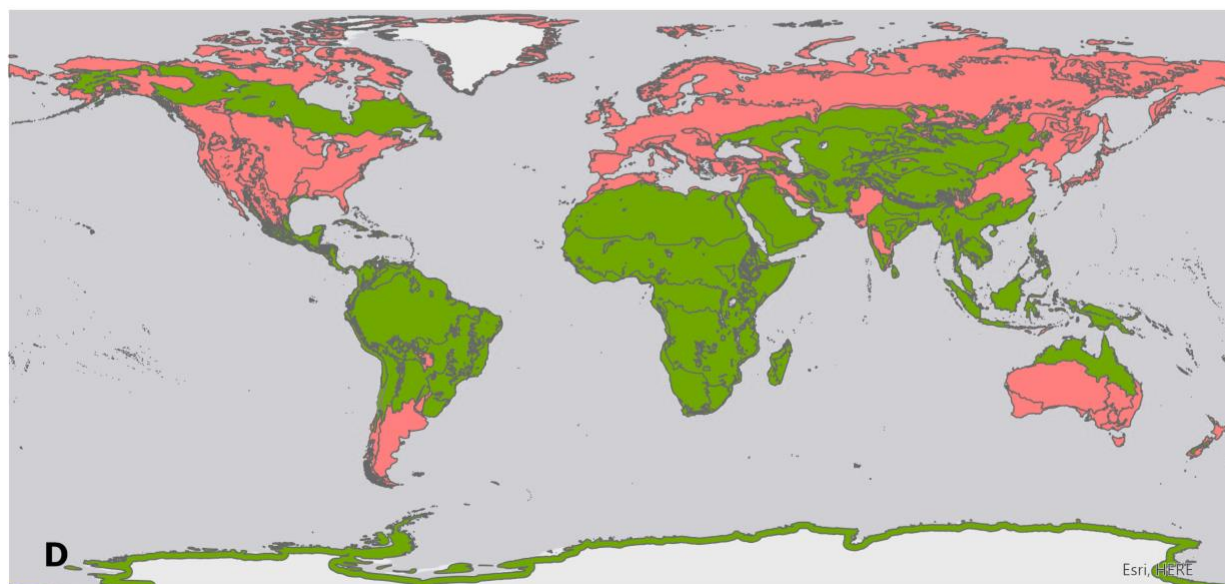


Figure 1g-i. Unweighted (G) and vulnerability-weighted (I) species richness maps for birds. Masking was used during analysis to remove marine species ranges (in the case of birds, migratory patterns and marine seabird ranges). Species range data sourced from IUCN (2021)³⁶.



■ Biome realms where richness is higher INSIDE PAs
■ Biome realms where richness is higher OUTSIDE PAs

Esri, HERE



D

Esri, HERE

Figure S2c-d. For reptiles (C) and birds (D). Biome realms represented in red have higher vulnerability-weighted richness averages outside of protected areas. Biome realms symbolized in green have higher richness values inside of PAs, meaning protected areas are adequately covering richness hotspots within the biome realm. Data used to create biome realms from Olson (2001)⁴⁰.

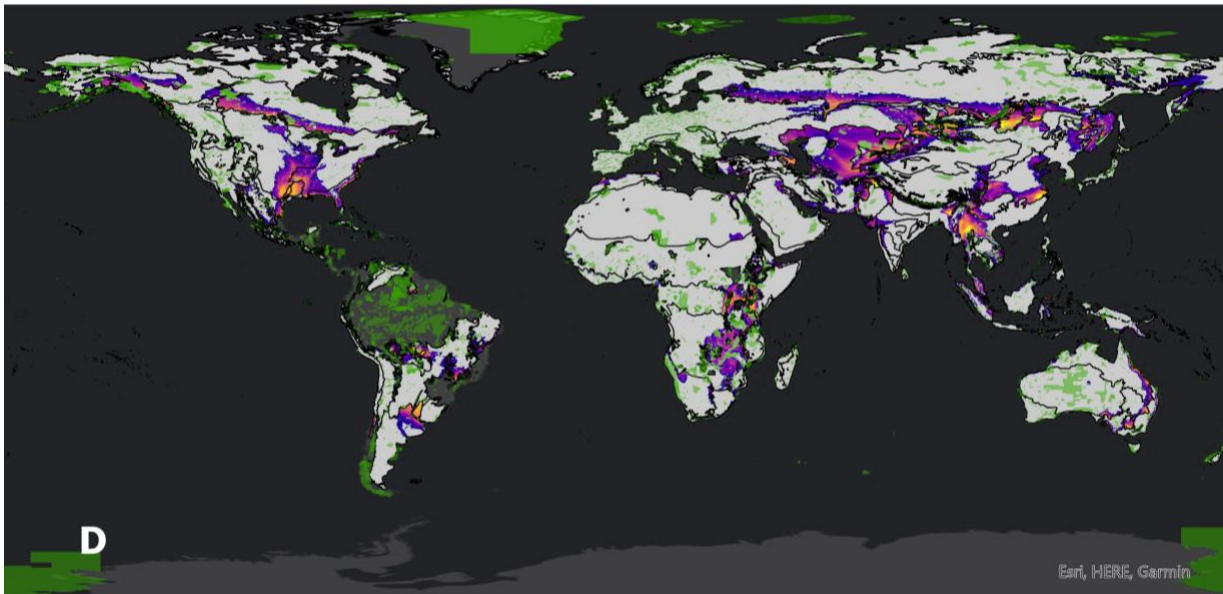
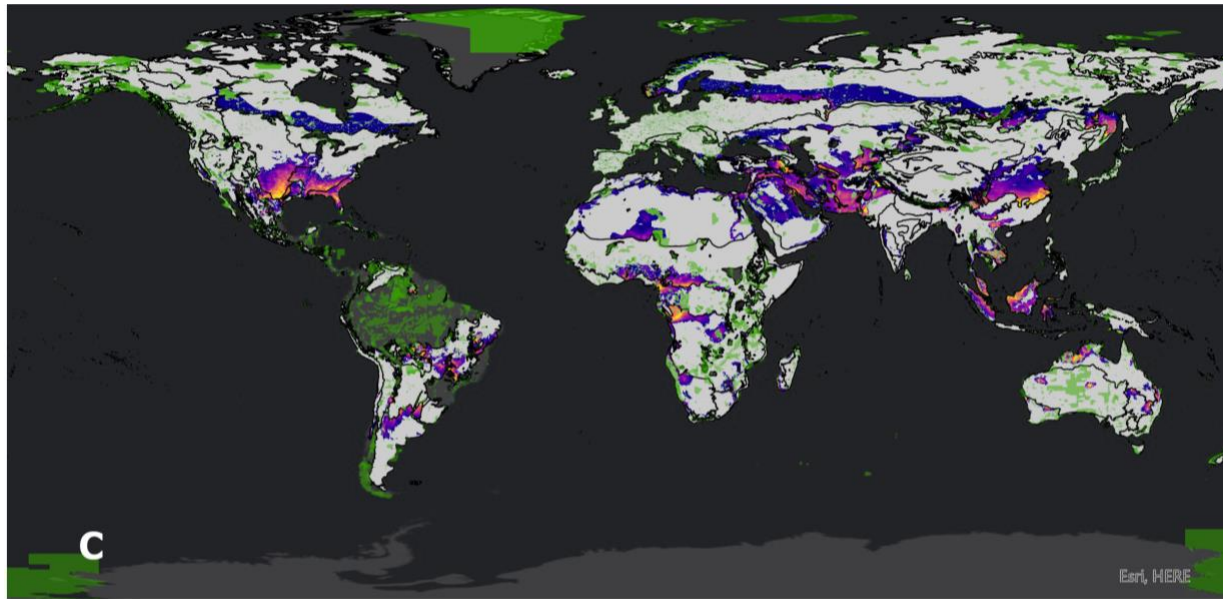


Figure S3c-d. Suggested areas for future protection based on vulnerability-weighted species richness for reptiles (C) and birds (D). Biome realm data is sourced from Olson (2001)⁴⁰, vulnerability-weighted richness data is derived from the IUCN (2021)³⁶, and protected area data is derived from the WDPA (2022)⁴¹.

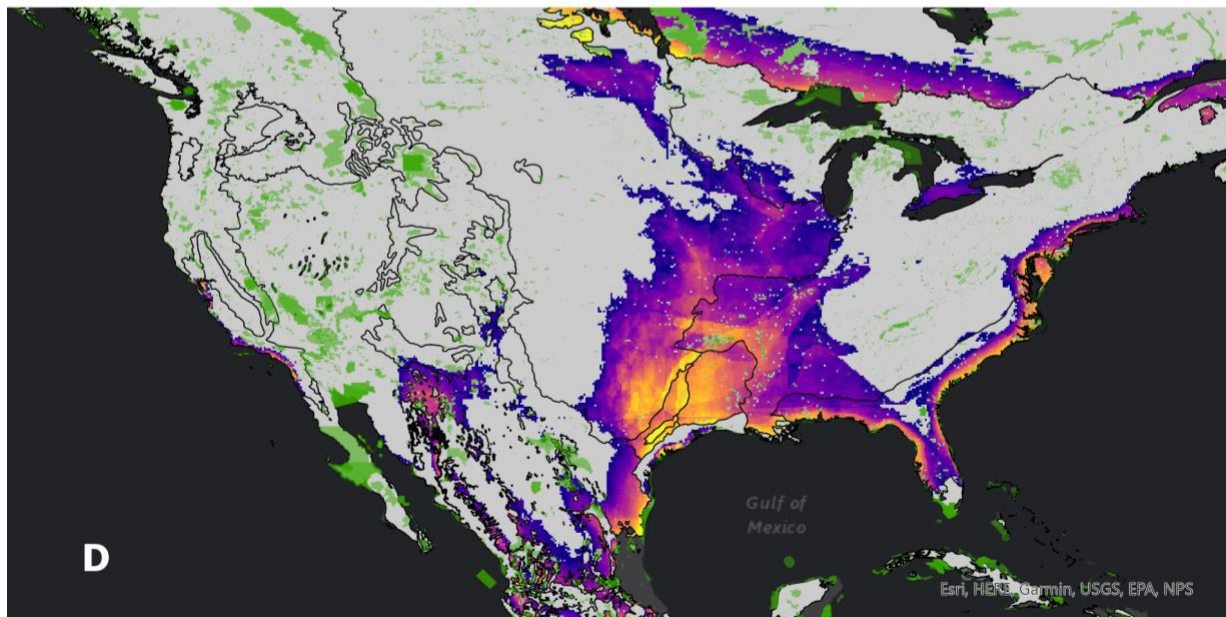
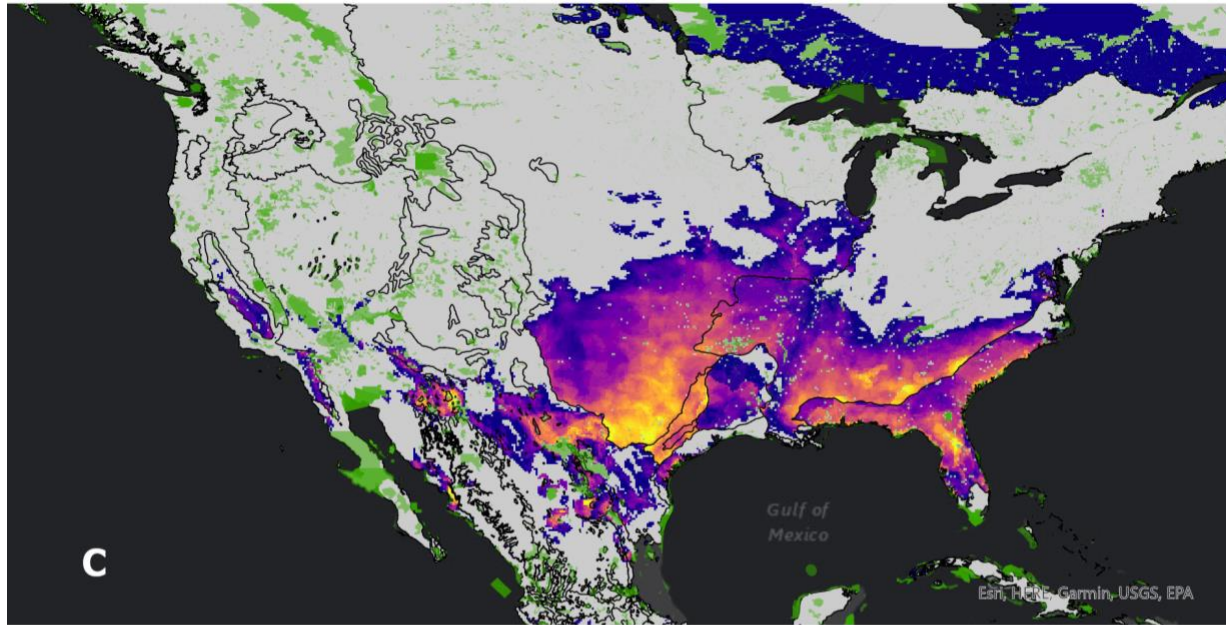


Figure S4c-d. Close up of suggested areas for future protection for reptiles (C) and birds (D) in North America. Biome realm data is sourced from Olson (2001)⁴⁰, vulnerability-weighted richness data is derived from the IUCN (2021)³⁶, and protected area data is derived from the WDPA (2022)⁴¹.

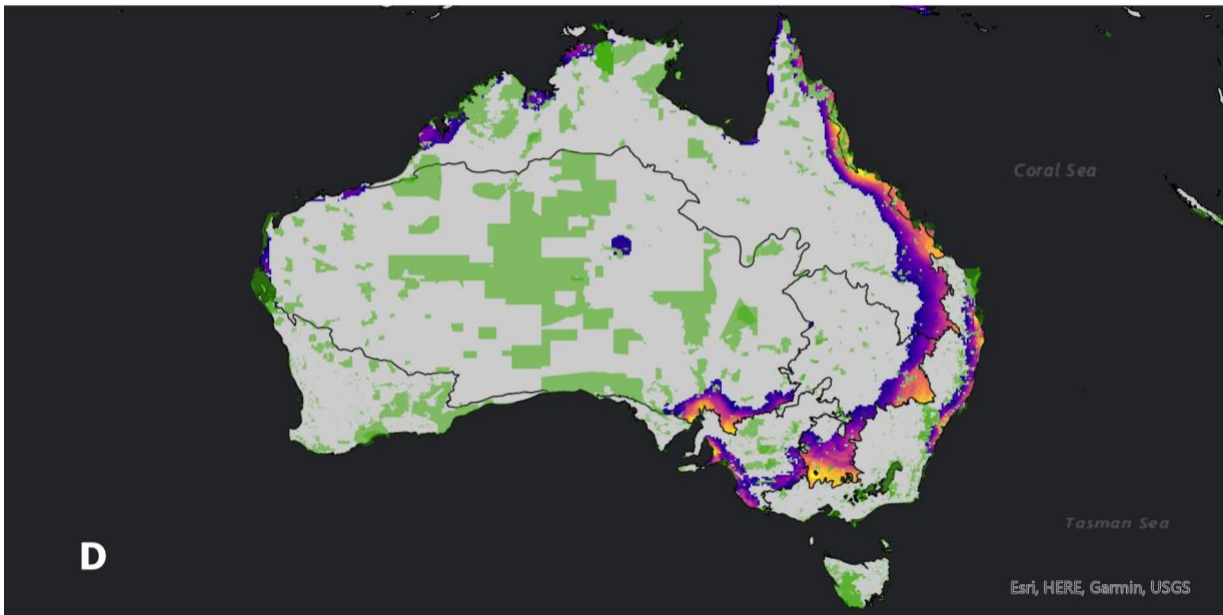
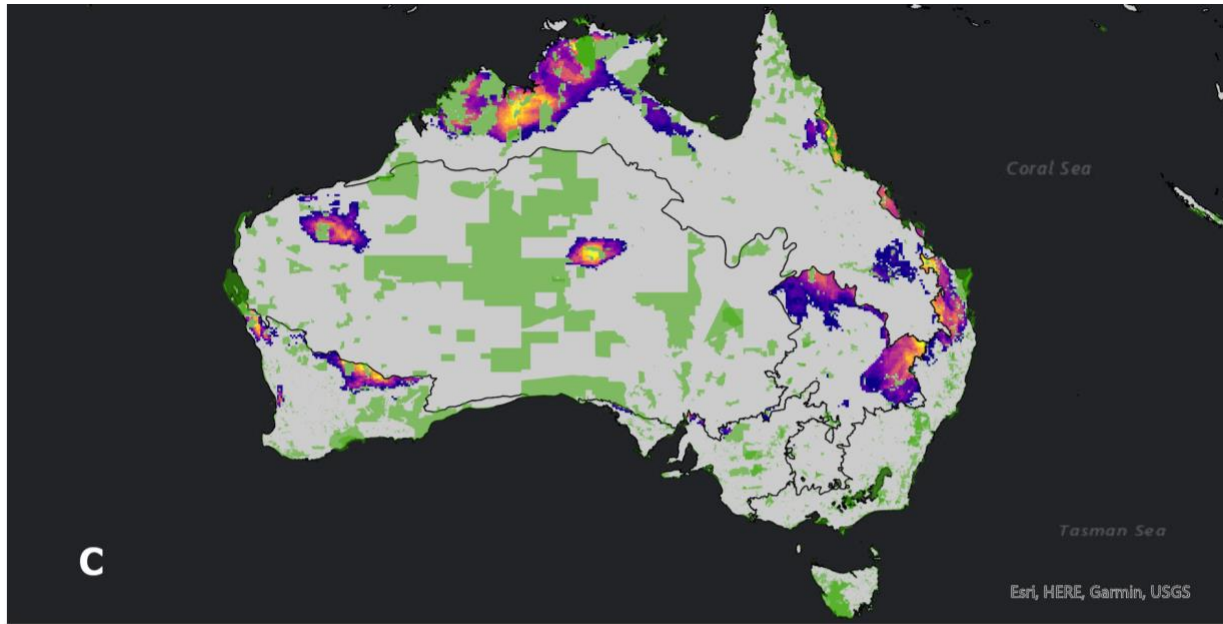


Figure S5c-d. Close up of suggested areas for future protection for reptiles (C) and birds (D) in Australia. Biome realm data is sourced from Olson (2001)⁴⁰, vulnerability-weighted richness data is derived from the IUCN (2021)³⁶, and protected area data is derived from the WDPA (2022)⁴¹.

Source code S1. Calculating weighted/unweighted species richness maps and average richness per biome inside and outside of PAs. Same code used for all taxa with different shapefile sources. Biome realm data is sourced from Olson (2001)⁴⁰, vulnerability-weighted richness data is derived from the IUCN (2021)³⁶, and protected area data is derived from the WDPA (2022)⁴¹.

```
#load data

library(sf)
setwd("D:/Sedona")
reptilepoly <- st_read("IUCN Range Data/REPTILES/REPTILES.shp")

#subset reptiles not extinct

reptilepoly_NE <- subset(reptilepoly, reptilepoly$category!="EX" &
reptilepoly$category!="EW")
unique(reptilepoly_NE$category)

#rasterize

library(raster)
library(fasterize)
ras <- raster()
res(ras) <- 0.10
crs(ras) <- CRS("+proj=longlat +datum=WGS84")
reptilerichness <- fasterize(reptilepoly_NE, ras, fun = "sum")
writeRaster(reptilerichness, "ReptileRichness6.tif")

#add vulnerability weights

reptilepoly_NE$weights <- NA
reptilepoly_NE$weights[which(reptilepoly_NE$category=="LC")]<-1
reptilepoly_NE$weights[which(reptilepoly_NE$category=="NT")]<-2
reptilepoly_NE$weights[which(reptilepoly_NE$category=="VU")]<-4
reptilepoly_NE$weights[which(reptilepoly_NE$category=="EN")]<-6
reptilepoly_NE$weights[which(reptilepoly_NE$category=="CR")]<-8
reptilepoly_NE$weights[which(reptilepoly_NE$category=="DD")]<-2
reptilepoly_NE$weights[which(reptilepoly_NE$category=="LR/cd")]<-4
```

```

unique(reptilepoly_NE$weights)

#plot vulnerability weighted richness

ras <- raster()
res(ras) <- 0.10
crs(ras) <- CRS("+proj=longlat +datum=WGS84")
vulnweighted_richness <- fasterize(reptilepoly_NE, ras, field = "weights",
fun = "sum")
writeRaster(vulnweighted_richness, "VulnWeightedReptileRichness6.tif")

#load ecoregions

ecoregions <- st_read("Ecoregions/wwf_terr_ecos.shp")
ecoregions$BIOMEREALM<-paste(ecoregions$BIOME, ecoregions$REALM, sep="")
sf_use_s2(FALSE) #what consequences does this have on results?

library(dplyr)
ecoregions<-ecoregions %>%
  dplyr::group_by(BIOMEREALM) %>%
  dplyr::summarise(across(geometry, ~ sf::st_union(.)), .groups = "keep")
%>%
  dplyr::summarise(across(geometry, ~ sf::st_combine(.)))

#load protected areas

PA1 <-
st_read("WDPA_Mar2022_Public_shp/WDPA_Mar2022_Public_shp_0/WDPA_Mar2022_Public_shp-polygons.shp")
PA2 <-
st_read("WDPA_Mar2022_Public_shp/WDPA_Mar2022_Public_shp_1/WDPA_Mar2022_Public_shp-polygons.shp")
PA3 <-
st_read("WDPA_Mar2022_Public_shp/WDPA_Mar2022_Public_shp_2/WDPA_Mar2022_Public_shp-polygons.shp")
wdpapoly <- rbind(PA1,PA2,PA3)

sf_use_s2(FALSE)

```

```

vulnweighted_richness[is.na(vulnweighted_richness)]<-0

#loop

dataframe<-data.frame()
n<-length(unique(ecoregions$BIOMERREALM))
for (i in 1:n) {

  BR1<-subset(ecoregions,
ecoregions$BIOMERREALM==unique(ecoregions$BIOMERREALM)[i]) #biome realm subset
  BR1ras<-raster::mask(vulnweighted_richness, BR1) #mask of biome realm vuln
weighted richness values, turns ALL values outside BR into na
  intersect_ft<-st_intersects(BR1, wdpapoly, sparse = T) #list of PA features
that intersect with BR
  wdpa_br1<-wdpapoly[intersect_ft[[1]],] #pulls the 1st feature which is
polygons

  BR1pa<-raster::mask(vulnweighted_richness, wdpa_br1)

  wdpa_br_ras = rasterize(wdpa_br1, ras) #rasterizes the above polygons (TO
USE AS MASK)
  wdpa_br_ras[is.na(BR1ras)]<-NA #makes all values outside of PA na

  #clone vulnrchnras in BR1

  BR1insidePA<-BR1ras
  BR1outsidePA<-BR1ras

  #set values outside PAs to NA

  BR1insidePA[is.na(wdpa_br_ras)]<-NA #set all cells that are NA in
wdpa_br_ras (=outside PAs) to NA in BR1inPA

  #set values inside PAs to NA

  BR1outsidePA[!is.na(wdpa_br_ras)]<-NA #set all cells that are NOT NA in
wdpa_br_ras (=inside PAs) to NA in BR1outPA

```

```

mean(BR1insidePA[!is.na(BR1insidePA)])

mean(BR1outsidePA[!is.na(BR1outsidePA)])

dataframe<-rbind(dataframe,data.frame(BR=unique(ecoregions$BIOMEREALM)[i],
                                       average_br=mean(BR1outsidePA[!is.na(BR1outsidePA)]),
                                       average_pa=mean(BR1insidePA[!is.na(BR1insidePA)]))
))
}

library(writexl)
write_xlsx(dataframe,"D:/Sedona/reptiles.xlsx")

```

Source Code S2. Calculating PA and BR areas. Biome realm data is sourced from Olson (2001)⁴⁰, vulnerability-weighted richness data is derived from the IUCN (2021)³⁶, and protected area data is derived from the WDPA (2022)⁴¹.

```

#calculating PA areas within each BR
dataframe<-data.frame()
n<-length(unique(ecoregions$BIOMEREALM))
for (i in 1:n) {
  print(i)
  BR1<-subset(ecoregions,
ecoregions$BIOMEREALM==unique(ecoregions$BIOMEREALM)[i]) #biome realm subset

  #intersect_ft<-st_intersects(BR1, wdpapoly, sparse = T) #list of PA
features that intersect with BR
  #wdpa_br1<-wdpapoly[intersect_ft[[1]],] #pulls the 1st feature which is
polygons

#retrieve PAs in BR1 while cutting our all parts of the PA outside BR1
intersections_wdpa_br1 <- st_intersection(wdpapoly, BR1)
intersections_wdpa_br1<-st_union(intersections_wdpa_br1)
dataframe<-rbind(dataframe,data.frame(BR=unique(ecoregions$BIOMEREALM)[i],

```

```

BR_area=sum(st_area(intersections_wdp
a_br1))))
}

#calculating BR areas
library(sf)
setwd("D:/Sedona")
ecoregions <- st_read("Ecoregions/wwf_terr_ecos.shp")
ecoregions$BIOMERREALM<-paste(ecoregions$BIOME, ecoregions$REALM, sep="")
sf_use_s2(FALSE) #what consequences does this have on results?

library(dplyr)
ecoregions<-ecoregions %>%
  dplyr::group_by(BIOMERREALM) %>%
  dplyr::summarise(across(geometry, ~ sf::st_union(.)), .groups = "keep")
%>%
  dplyr::summarise(across(geometry, ~ sf::st_combine(.)))

dataframe<-data.frame(BR=ecoregions$BIOMERREALM,
                      BR_area=st_area(ecoregions))

```

Source code S3. Create raster of suggested future PAs. Same code was used for each taxa with different source shapefiles. Biome realm data is sourced from Olson (2001)⁴⁰, vulnerability-weighted richness data is derived from the IUCN (2021)³⁶, and protected area data is derived from the WDPA (2022)⁴¹.

```

#load data

library(sf)
library(raster)
library(fasterize)
setwd("D:/Sedona")
mammalpoly <- st_read("IUCN Range Data/MAMMALS/MAMMALS.shp")

#subset mammals not extinct

```

```

mammalpoly_NE <- subset(mammalpoly, mammalpoly$category!="EX" &
mammalpoly$category!="EW")
unique(mammalpoly$category)

#add vulnerability weights

mammalpoly_NE$weights <- NA
mammalpoly_NE$weights[which(mammalpoly_NE$category=="LC")]<-1
mammalpoly_NE$weights[which(mammalpoly_NE$category=="NT")]<-2
mammalpoly_NE$weights[which(mammalpoly_NE$category=="VU")]<-4
mammalpoly_NE$weights[which(mammalpoly_NE$category=="EN")]<-6
mammalpoly_NE$weights[which(mammalpoly_NE$category=="CR")]<-8
mammalpoly_NE$weights[which(mammalpoly_NE$category=="DD")]<-2
unique(mammalpoly_NE$weights)

#plot vulnerability weighted richness

ras <- raster()
res(ras) <- 0.10
crs(ras) <- CRS("+proj=longlat +datum=WGS84")
vulnweighted_richness <- fasterize(mammalpoly_NE, ras, field = "weights", fun
= "sum")

#load ecoregions
ecoregions <- st_read("Ecoregions/wwf_terr_ecos.shp")
ecoregions$BIOMERREALM<-paste(ecoregions$BIOME, ecoregions$REALM, sep="")
sf_use_s2(FALSE) #what consequences does this have on results?

library(dplyr)
ecoregions<-ecoregions %>%
  dplyr::group_by(BIOMERREALM) %>%
  dplyr::summarise(across(geometry, ~ sf::st_union(.)), .groups = "keep")
%>%
  dplyr::summarise(across(geometry, ~ sf::st_combine(.)))

ecoregions <- ecoregions[-c(61:65),]
ecoregions <- ecoregions[-c(1, 3, 6, 24, 28, 43, 61),]

```



```

#load protected areas
PA1 <-
st_read("WDPA_Mar2022_Public_shp/WDPA_Mar2022_Public_shp_0/WDPA_Mar2022_Public_shp-polygons.shp")
PA2 <-
st_read("WDPA_Mar2022_Public_shp/WDPA_Mar2022_Public_shp_1/WDPA_Mar2022_Public_shp-polygons.shp")
PA3 <-
st_read("WDPA_Mar2022_Public_shp/WDPA_Mar2022_Public_shp_2/WDPA_Mar2022_Public_shp-polygons.shp")
wdpapoly <- rbind(PA1,PA2,PA3)

n<-length(unique(ecoregions$BIOMEREALM))
for (i in 1:n) {

BR13<-subset(ecoregions,
ecoregions$BIOMEREALM==unique(ecoregions$BIOMEREALM)[i]) #biome realm subset
BR13ras<-raster::mask(vulnweighted_richness, BR13) #mask of biome realm vuln
weighted richness values, turns ALL values outside BR into na

intersect_ft<-st_intersects(BR13, wdpapoly, sparse = T) #list of PA features
that intersect with BR
wdpa_br13<-wdpapoly[intersect_ft[[1]],] #pulls the 1st feature which is
polygons

wdpa_br_ras = fasterize(wdpa_br13, ras) #rasterizes the above polygons (TO
USE AS MASK)
wdpa_br_ras[is.na(BR13ras)]<-NA #makes all values outside of BR na

#set values inside PAs to NA

BR13FutureAoPs<-BR13ras
BR13FutureAoPs[!is.na(wdpa_br_ras)]<-NA #set all cells that are NOT NA in
wdpa_br_ras (=inside PAs) to NA in BR1outPA
BR13FutureAoPs<-BR13FutureAoPs/maxValue(na.exclude(BR13FutureAoPs))

```

```
BR13FutureAoPs[BR13FutureAoPs<sort((values(BR13FutureAoPs)), decreasing =
TRUE)[cellvalues$`Cell Values`[i]]]<-NA

f <- paste0('FuturePAsBR', i, '.tif')
writeRaster(BR13FutureAoPs, filename = f)
}
```

