

A global reptile assessment highlights shared conservation needs of tetrapods

<https://doi.org/10.1038/s41586-022-04664-7>

Received: 12 April 2021

Accepted: 16 March 2022

Published online: 27 April 2022

Open access

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Comprehensive assessments of species' extinction risks have documented the extinction crisis¹ and underpinned strategies for reducing those risks². Global assessments reveal that, among tetrapods, 40.7% of amphibians, 25.4% of mammals and 13.6% of birds are threatened with extinction³. Because global assessments have been lacking, reptiles have been omitted from conservation-prioritization analyses that encompass other tetrapods^{4–7}. Reptiles are unusually diverse in arid regions, suggesting that they may have different conservation needs⁶. Here we provide a comprehensive extinction-risk assessment of reptiles and show that at least 1,829 out of 10,196 species (21.1%) are threatened—confirming a previous extrapolation⁸ and representing 15.6 billion years of phylogenetic diversity. Reptiles are threatened by the same major factors that threaten other tetrapods—agriculture, logging, urban development and invasive species—although the threat posed by climate change remains uncertain. Reptiles inhabiting forests, where these threats are strongest, are more threatened than those in arid habitats, contrary to our prediction. Birds, mammals and amphibians are unexpectedly good surrogates for the conservation of reptiles, although threatened reptiles with the smallest ranges tend to be isolated from other threatened tetrapods. Although some reptiles—including most species of crocodiles and turtles—require urgent, targeted action to prevent extinctions, efforts to protect other tetrapods, such as habitat preservation and control of trade and invasive species, will probably also benefit many reptiles.

Although comprehensive extinction-risk assessments have been available for birds, mammals and amphibians for well over a decade³, reptiles have, until now, not been comprehensively assessed. Therefore, conservation science and practice has typically relied on the International Union for Conservation of Nature (IUCN) Red List categories and distributions of the other three tetrapod classes to inform policy and guide priorities for investments², despite differing expectations as to how effective common strategies will be across classes^{9,10}. With a high diversity in arid regions and some islands and archipelagos (for example, Antilles, New Caledonia and New Zealand) compared with other tetrapods, reptiles were thought to require different conservation strategies and geographical priorities⁶. In the absence of Red List assessments, researchers have resorted to indirect measures of extinction risk such as range size and human pressure^{6,11}. Here we examine the

results of a comprehensive Red List assessment of reptiles and outline their implications for the conservation needs of reptiles.

Comprising the turtles (Testudines), crocodiles (Crocodylia), squamates (Squamata: lizards, snakes and amphisbaenians) and tuatara (Rhynchocephalia), reptiles are a paraphyletic class representing diverse body forms, habitat affinities and functional roles in their respective ecosystems¹². The largely terrestrial squamates are by far the most speciose group (9,820 species in this assessment), whereas the primarily aquatic turtles and crocodiles are often larger bodied but include only 351 and 24 species, respectively. Rhynchocephalians diverged from the snake and lizard lineage in the Triassic period and include one extant species¹³. Given this diversity of reptiles, threats to their persistence are likely to be equally varied, and so these need to be specified to guide effective conservation action.

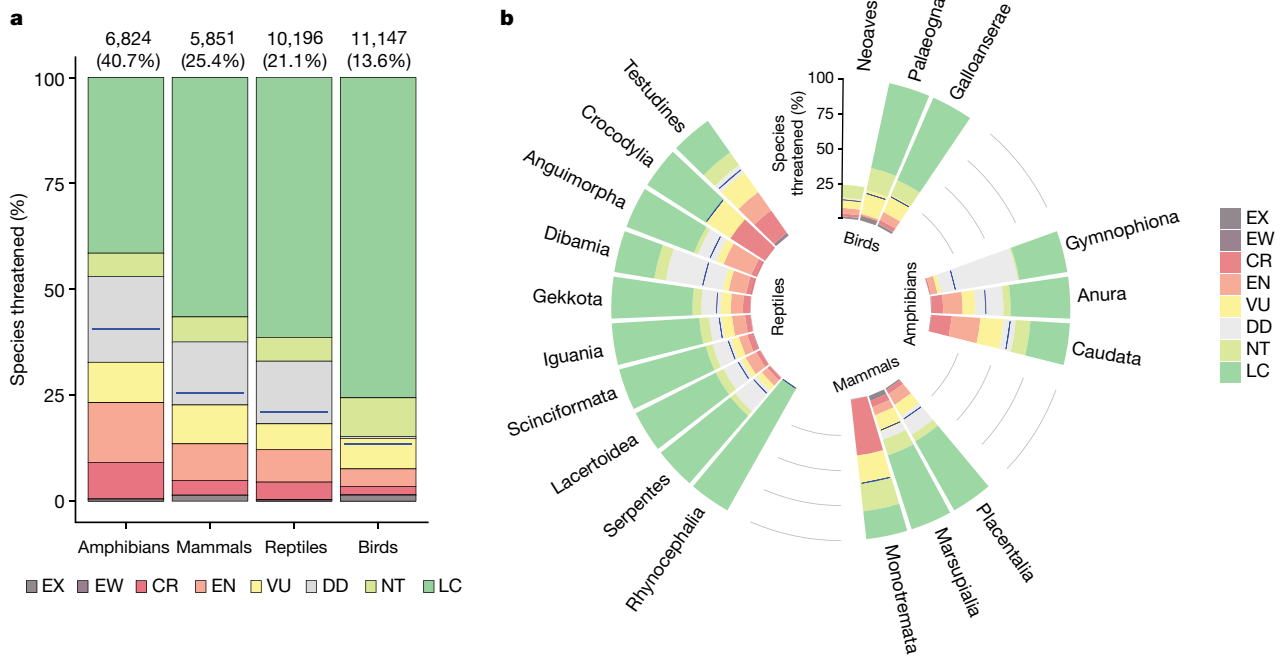


Fig. 1 | Taxonomic patterns of extinction risk in tetrapods. a, Taxonomic patterns organized by class. The numbers above each column refer to the numbers and percentages of species threatened (that is, those categorized as critically endangered, endangered or vulnerable). **b**, Extinction risk by major

taxonomic groups. Blue lines indicate the best estimate of the percentage of species threatened. CR, critically endangered; DD, data deficient; EN, endangered; EW, extinct in the wild; EX, extinct; LC, least concern; NT, near threatened; VU, vulnerable.

Extinction risk and threats

We assessed reptiles globally using the IUCN Red List criteria with input from 961 scientists (Supplementary Note 1) achieved primarily through 48 workshops (Supplementary Table 1). Across all 10,196 species assessed, 21.1% are threatened with extinction (categorized as vulnerable, endangered or critically endangered; Supplementary Table 2).

As a group, a greater number of reptile species are threatened than birds or mammals, but fewer than amphibians. Proportionately more mammals and amphibians are threatened than reptiles (Fig. 1a). The reptile threat prevalence falls within a previous estimate of 15–36% threatened (best estimate 19%) from a random sample of 1,500 reptile species⁸. To our knowledge, this study represents the first global test of a sampled Red List extrapolation. The proportion of turtles and

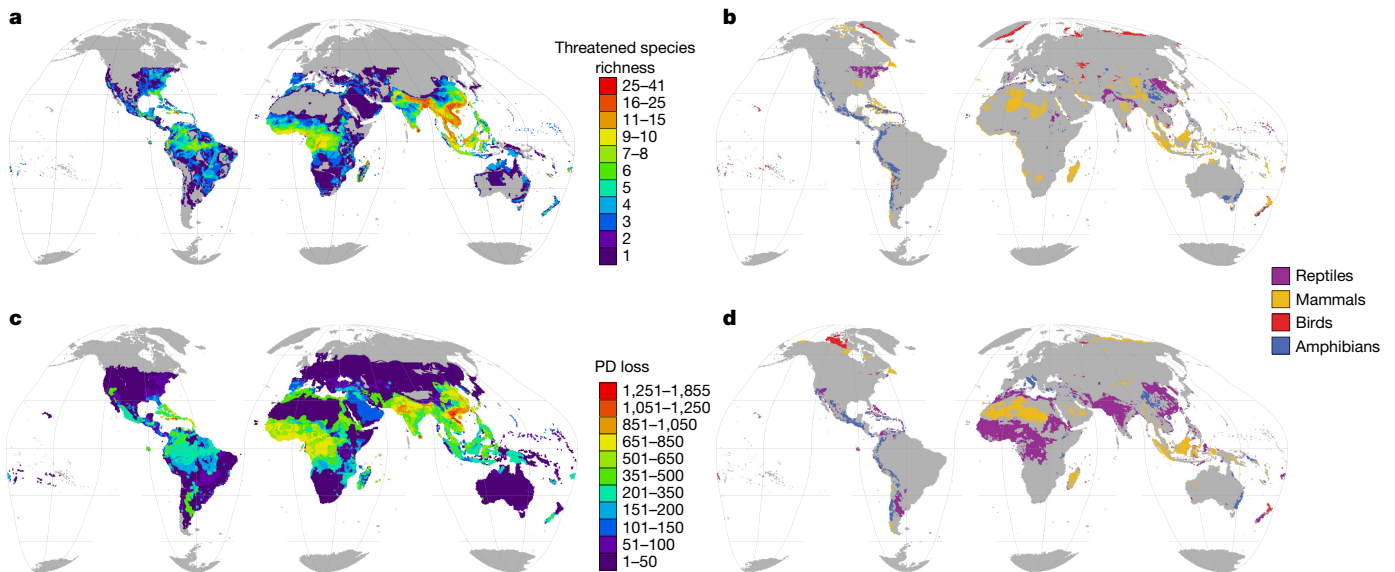


Fig. 2 | Geographical patterns of threat in reptiles and other tetrapods in terrestrial regions. a, Distribution of reptile species that are threatened (critically endangered, endangered or vulnerable). **b**, Regions with disproportionate numbers of threatened species for each tetrapod class (areas for each class where the proportional threat in species diversity is at least twice

the loss for the next-most threatened class). **c**, Loss of reptile phylogenetic diversity (PD) if all threatened species became extinct. **d**, Regions with disproportionate phylogenetic diversity loss for each tetrapod class (calculated as in **b**). Grey, areas with no threatened species (**a**, **c**) or regions in which no class is disproportionately threatened (**b**, **d**). Data are shown at a resolution of 50 km.

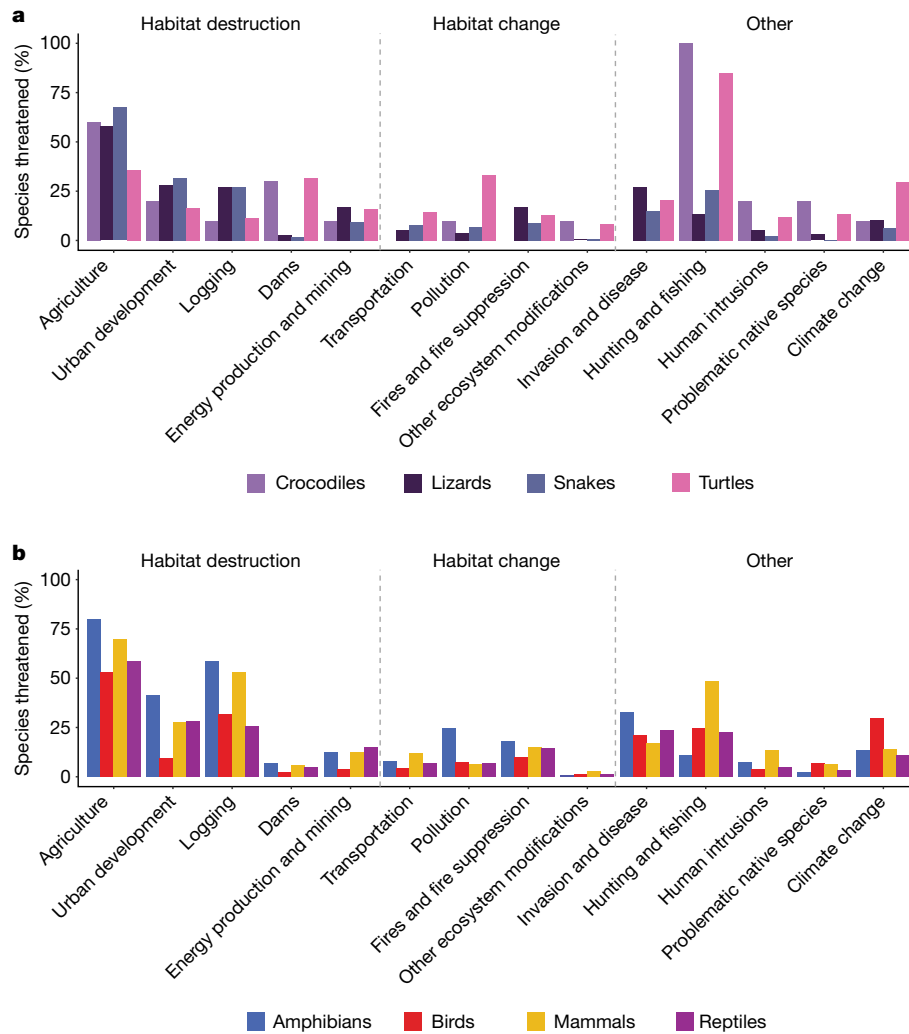


Fig. 3 | Threats to reptiles and other tetrapods. a, Crocodiles, lizards (including amphisbaenians), snakes and turtles. **b**, All tetrapods. Only threats to species categorized as critically endangered, endangered or vulnerable

were included. Some species are subject to more than one threat (mean = 2.4; s.d. = 1.3 threats per species).

crocodiles that are threatened (57.9% and 50.0%, respectively) is much higher than those of squamates (19.6%) and tuatara (0%), and comparable to the most-threatened tetrapod groups, salamanders (57.0%) and monotremes (60.0%) (Fig. 1b). Within squamates, iguanid (73.8%) and xenosaurid (60.0%) lizards and uropeltid (61.1%) and tropidophiid (60.0%) snakes are highly threatened. Since 1500, 31 reptile species (0.3%) have been driven extinct, including 24 squamates and 7 turtles, with 2 squamate species from Christmas Island categorized as extinct in the wild (persisting only as captive populations); 40 critically endangered species are ‘possibly extinct’ (that is, species that are likely to be extinct, but that have a small chance that they may be extant; Extended Data Fig. 1). Additional species probably became extinct before being documented by science¹⁴.

Limited information resulted in 1,507 species (14.8%) being categorized as data deficient, similar to the number in mammals (15.1%) and lower than for amphibians (20.4%), but much higher than for birds (0.5%). Taxonomic groups with fossorial or other secretive habits and/or restricted to poorly studied areas (such as blindsnakes (Gerrhopilidae and Typhlopidae)) had greater proportions of species categorized as data deficient (Supplementary Table 2). The greatest numbers of data-deficient species occur in Asia (585), South America (284) and Africa (271), with fewer data-deficient species in North and Middle America (163), Oceania (124), Australia (55), the Caribbean (34) and Europe (3). Uncertainty about the status of data-deficient species

suggests that the proportion of reptiles threatened with extinction ranges from 18.0% (assuming no data-deficient species are threatened) to 32.8% (assuming all data-deficient species are threatened) with a best estimate of 21.1%.

Concentrations of threatened reptiles are mostly in regions in which other tetrapods are also threatened (Extended Data Fig. 2). Threatened reptiles are concentrated in southeastern Asia, West Africa, northern Madagascar, the northern Andes and the Caribbean, but largely absent from Australian drylands; the Kalahari, Karoo and Sahara deserts; northern Eurasia; and the Rocky Mountains and northern North America (Fig. 2a). In remarkably few regions, however, are reptiles disproportionately threatened relative to other tetrapods (that is, have at least twice the number of species in a threatened category): parts of southern Asia and northeastern USA (Fig. 2b and Extended Data Table 1). Moreover, for most (87%) terrestrial regions in which tetrapods occur, no tetrapod class is disproportionately threatened compared with the other classes.

With deep phylogenetic lineages and high species diversity, reptiles stand to lose a large amount of phylogenetic diversity (a measure of difference within an evolutionary tree¹⁵) if the current extinction crisis continues apace. Assuming all threatened species (and only these species) become extinct, the combined loss of reptile phylogenetic diversity (calculated using existing phylogenetic trees^{16,17}) will be approximately 15.6 billion years. Southeastern Asia, India, West Africa and the Caribbean⁸ (Fig. 2c) comprise the top 15% areas of phylogenetic diversity loss,

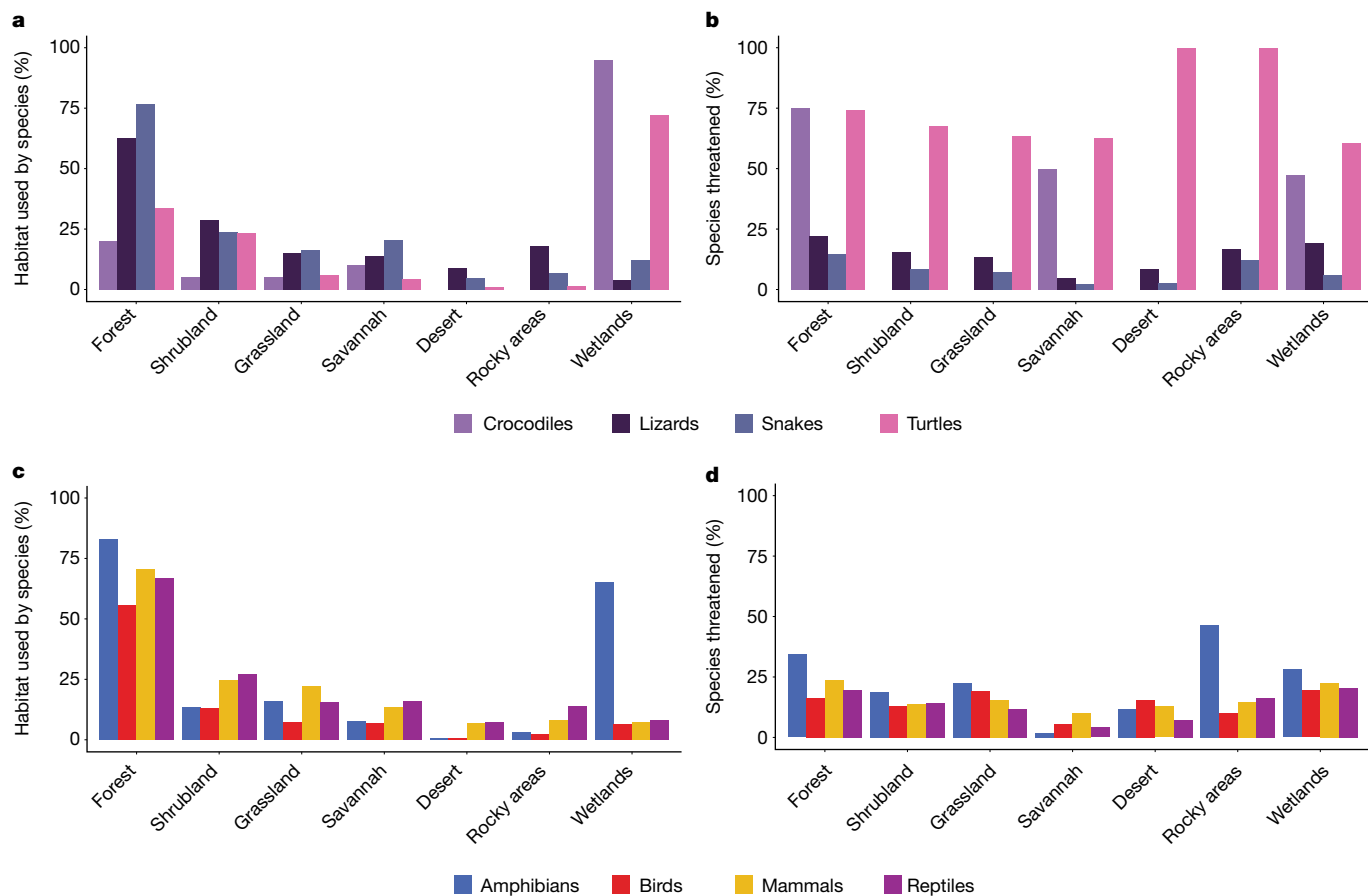


Fig. 4 | Habitat use by reptiles and other tetrapods. a, Habitats used by crocodiles, lizards (includes amphisbaenians), snakes and turtles. **b,** Percentage of reptiles using each habitat that are threatened. **c,** Habitats used

by tetrapods. **d,** Percentage of threatened tetrapod species using each habitat. See Supplementary Table 3 for additional, rarely used habitats not shown here. Artificial habitats are not shown.

with high concentrations of threatened and evolutionarily distinct species (Extended Data Fig. 3). Comparing the distributions of threatened phylogenetic diversity across all four tetrapod groups reveal relatively small geographical areas of disproportionate importance for any class (Fig. 2d and Extended Data Table 2).

The anthropogenic factors increasing extinction risk in reptiles are mainly habitat destruction from agricultural expansion, urban development and logging (Fig. 3a). Other important threats are invasive species and hunting, which includes commercial harvest and trade (Fig. 3a). Among reptile groups, crocodiles and turtles are most frequently affected by hunting and less by agriculture, whereas squamates are most frequently threatened by agriculture (Fig. 3a). The major threats are broadly similar across tetrapods (Fig. 3b). For all tetrapod groups, agriculture threatens the most species, logging is the second or third most prevalent threat, and invasive species and disease are the fourth or fifth most prevalent threat. Threats causing habitat destruction (complete removal of habitat) affect proportionately more species than those causing habitat change (degradation of habitat). The largest differences in relative threat prevalence are for hunting, which threatens mammals much more than the other tetrapods, and urban development, which affects amphibians, reptiles and mammals more than birds.

Climate change is a looming threat to reptiles, for example, by reducing thermally viable windows for foraging¹⁸, skewing offspring sex ratios in species that have temperature-dependent sex determination¹⁹ and contracting ranges²⁰. Given the Red List three-generation horizon for assessments, the lack of long-term studies limits the documentation of climate change as a near-future threat to reptiles²¹, in contrast to, for example, birds (Fig. 3b). Disease is documented as a threat for only 11 species of reptiles (<1% of extant, non-data-deficient species),

although pathogens such as *Ophidiomyces ophiodiicola* (which causes snake fungal disease²²) pose a potential threat and are little studied outside North America. Intentional use of reptiles (local consumption and trade) is an important threat to reptiles²³, and was found to threaten 329 species (3.2%), especially turtles (30.8% of all turtle species).

More than half of all reptile species occur in forested habitats (Fig. 4c). Although some reptiles, particularly lizards, are speciose in arid or seasonally dry habitats such as deserts, grasslands, shrublands and savannahs^{6,24}, these species are less threatened than those occupying forest habitats (13.7% of species restricted to arid habitats versus 26.6% of species restricted to forests; Fisher's exact test, $P = 0.00001$; Fig. 4b). The top threats to reptiles—agriculture, urban development and logging—are also the top threats to species inhabiting forested habitats, affecting 65.9%, 34.8% and 27.9% of forest-dwelling threatened reptiles, respectively, helping to explain the higher extinction risk of forest species. Agriculture and logging are significantly more likely to threaten forest-dwelling than non-forest dwelling reptiles (Fisher's exact test, $P = 0.00001$), whereas urbanization threatens forest-dwelling no differently than non-forest dwelling reptiles (Fisher's exact test, $P = 0.25$). Turtles and crocodiles are much more frequently associated with wetlands than other reptiles (Fig. 4a).

Like reptiles, more than twice as many bird and mammal species occur in forests compared with any other habitat type (Fig. 4c). Forests are also the most common habitat for amphibians, although wetlands are important for many species, especially for breeding (Fig. 4c). Also similar to reptiles, the proportions of forest-inhabiting bird, mammal and amphibian species that are threatened are higher than for species that do not inhabit forests (16.7% versus 13.0%, 27.5% versus 20%, and 42.4% versus 34.4%, respectively; Fisher's exact tests, $P = 0.00001$). Threat levels

for each tetrapod class in arid habitats tend to be lower (less than 23% of species occurring in such regions). Across tetrapods, forests support high diversity and are also subject to widespread threats.

Surrogacy of other tetrapods for reptiles

With numerous threatened tetrapod species (227 birds, 194 mammals, 607 amphibians and 474 reptiles) ranging completely outside formally protected areas, assessing surrogacy is important to gauge the magnitude of efforts needed to conserve these species. We addressed surrogacy using a complementarity representation approach for threatened species, which better addresses the extent to which areas selected for surrogates capture target features than, for example, spatial congruence²⁵. When combined, threatened birds, mammals and amphibians—the tetrapod groups for which comprehensive Red List data were previously available—are good surrogates for the conservation of threatened reptile diversity when prioritizing the richness of rarity-weighted threatened species at both 50-km and 100-km resolution (median species accumulation indices are 0.66 and 0.76, respectively; Extended Data Fig. 4a). Using this same prioritization strategy, birds and mammals individually are reasonable surrogates for reptiles, whereas amphibians are poor surrogates (Extended Data Fig. 4a). By contrast, for a complementarity representation strategy that prioritizes individual threatened species with the smallest ranges, birds, mammals and amphibians are not good surrogates for reptiles (species accumulation indices < 0.40), although combined they are reasonable surrogates at both 50-km and 100-km resolutions (median species accumulation indices are 0.44 and 0.64, respectively; Extended Data Fig. 4b). These results indicate that the smallest-ranged threatened reptiles tend to be isolated from threatened birds, mammals and amphibians. In addition, priority areas for threatened birds and mammals independently, and birds, mammals and amphibians combined, showed high spatial congruence with priority sites for threatened reptiles for both strategies (prioritizing either rarity-weighted threatened species or complementarity representation), although correlations among global portfolios of priority areas were lower (Extended Data Tables 3, 4). Although our results for the smallest ranged threatened species are consistent with previous expectations of low surrogacy⁹, overall, we found reasonably high surrogacy¹⁰.

Discussion

Our discovery of broad similarities in the geography and nature of threats between reptiles and other tetrapods was unexpected given previous arguments about the exceptionalism of reptiles for being particularly diverse in arid habitats⁶. The implications for tetrapod conservation are that geographical prioritizations previously performed for birds, mammals and amphibians overlap broadly with prioritizations for all except the most range-restricted threatened reptiles. The absence of reptiles in many global conservation prioritization analyses to date is unlikely to have left the class less represented than others. Nevertheless, the low surrogacy value of other tetrapods for reptiles with the most restricted ranges suggests that a case-by-case focus is required for these microendemics. Indeed, the ranges of 31 threatened reptiles do not overlap with the ranges of any other threatened tetrapod (among threatened species, 84 birds, 11 mammals and 7 amphibians are similarly isolated from other threatened tetrapods) (Supplementary Table 3).

Researchers have predicted that reptiles are particularly vulnerable to climate change in tropical biomes²⁶ as well as freshwater²⁷ and arid habitats¹⁸, although so far no clear geographical signal in reptile declines due to climate change has been detected²⁸. If such vulnerabilities are found, then—as climate change continues to alter the distributions and extinction risk of species—the surrogacy across tetrapods could unravel with, for example, reptiles in specific habitat types declining swiftly and disproportionately (relative to other tetrapods).

Among the conservation strategies needed to prevent reptile extinction, land protection is critically important to buffer many threatened species from the dual threats of agricultural activities and urban development. The hundreds of threatened reptiles that currently occur completely outside protected areas underscore the need for targeted safeguards of important sites. Beyond place-based strategies, conservation policy and practice must halt unsustainable harvest and stem the spread of invasive disease to prevent many more species from becoming threatened²³. Furthermore, introduced mammals to islands threaten 257 reptile species (2.8% of all reptiles), calling for continued campaigns to eradicate introduced mammals in those places.

With a comprehensive, global assessment of the extinction risk of reptile species now available, these data can be incorporated into the toolbox of conservation practice and policy. At the species level, they can serve as the starting point for 'green status' (formerly 'green list') assessments that define, measure and incentivize species recovery²⁹. More generally, they can be integrated into the calculation of species threat abatement and restoration metrics², the identification of key biodiversity areas³⁰ and resource allocation using systematic conservation planning³¹, all of which have primarily been dependent on data from birds, mammals and amphibians among animals to date. Future reassessments will allow reptile data to be included in the Red List Index³², a widely used indicator of biodiversity trends¹.

Although efforts aimed at protecting other threatened tetrapods probably benefit many of the 1,829 threatened reptiles—especially forest-dwelling species—conservation investments targeted at uniquely occurring reptiles or those requiring tailored policies must also be implemented to prevent extinction. Encouragingly, the First Draft of the Post-2020 Global Biodiversity Framework³³ to be agreed by governments in 2022 explicitly targets safeguarding important sites (target 3), complemented by emergency action for individual threatened species (target 4). This political determination to reverse the slide of species toward extinction bodes well for reptiles.

Online content

Any methods, additional references, Nature Research reporting summaries, source data, extended data, supplementary information, acknowledgements, peer review information; details of author contributions and competing interests; and statements of data and code availability are available at <https://doi.org/10.1038/s41586-022-04664-7>.

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Methods

We used the IUCN Red List criteria^{34,35} and methods developed in other global status-assessment efforts^{36,37} to assess 10,078 reptile species for extinction risk. We additionally include recommended Red List categories for 118 turtle species³⁸, for a total of 10,196 species covered, representing 89% of the 11,341 described reptile species as of August 2020³⁹.

Data compilation

We compiled assessment data primarily through regional in-person and remote (that is, through phone and email) workshops with species experts (9,536 species) and consultation with IUCN Species Survival Commission Specialist Groups and stand-alone Red List Authorities (442 species, primarily marine turtles, terrestrial and freshwater turtles, iguanas, sea snakes, mainland African chameleons and crocodiles). We conducted 48 workshops between 2004 and 2019 (Supplementary Table 1). Workshop participants provided information to complete the required species assessment fields (geographical distribution, population abundance and trends, habitat and ecological requirements, threats, use and trade, literature) and draw a distribution map. We then applied the Red List criteria³⁴ to this information to assign a Red List category: extinct, extinct in the wild, critically endangered, endangered, vulnerable, near threatened, least concern and data deficient. Threatened species are those categorized as critically endangered, endangered and vulnerable.

Taxonomy

We used The Reptile Database³⁹ as a taxonomic standard, diverging only to follow well-justified taxonomic standards from the IUCN Species Survival Commission⁴⁰. We could not revisit new descriptions for most regions after the end of the original assessment, so the final species list is not fully consistent with any single release of The Reptile Database.

Distribution maps

Where data allowed, we developed distribution maps in Esri shapefile format using the IUCN mapping guidelines⁴¹ (1,003 species). These maps are typically broad polygons that encompass all known localities, with provisions made to show obvious discontinuity in areas of unsuitable habitat. Each polygon is coded according to species' presence (extant, possibly extant or extinct) and origin (native, introduced or reintroduced)⁴¹. For some regions covered in workshops (Caucasus, Southeast Asia, much of Africa, Australia and western South America), we collaborated with the Global Assessment of Reptile Distributions (GARD) (<http://www.gardinitiative.org/>) to provide contributing experts with a baseline species distribution map for review. Although refined maps were returned to the GARD team, not all of these maps have been incorporated into the GARD.

Habitat preferences

Where known, species habitats were coded using the IUCN Habitat Classification Scheme (v.3.1) (<https://www.iucnredlist.org/resources/habitat-classification-scheme>). Species were assigned to all habitat classes in which they are known to occur. Where possible, habitat suitability (suitable, marginal or unknown) and major importance (yes or no) was recorded. Habitat data were available for 9,484 reptile species.

Threats

All known historical, current and projected (within 10 years or 3 generations, whichever is the longest; generation time estimated, when not available, from related species for which it is known; generation time recorded for 76.3% of the 186 species categorized as threatened under Red List criteria A and C1, the only criteria using generation length) threats were coded using the IUCN Threats Classification Scheme v.3.2 (<https://www.iucnredlist.org/resources/threat-classification-scheme>), which follows a previously published study⁴². Where possible, the scope

(whole (>90%), majority (50–90%), minority (<50%) of the population; unknown) and severity (causing very rapid (>30%), rapid (>20%), slow but notable (<20%) declines over 10 years or 3 generations, whichever is longer; negligible declines; unknown) of the threat was recorded. Threat data were available for 1,756 of the 1,829 threatened reptile species.

Assessment review

Each assessment underwent two reviews. First, a scientist familiar with the species but not involved in the assessment reviewed the account for biological accuracy and accurate application of the Red List criteria. Once the assessors revised the assessment satisfactorily, staff from the IUCN Red List Unit reviewed the assessment primarily for accurate application of the Red List criteria. The assessors revised the assessment again, if necessary, to satisfy any concerns of the IUCN Red List Unit before the assessment was finalized.

Data limitations

Although we made an extensive effort to complete assessments for all reptiles, some data gaps remain.

Missing species. As of December 2020, 1,145 reptile species, primarily snakes and lizards, were omitted from the present study, including the phylogenetic diversity analyses, because they were described recently and they were described after previous comprehensive assessments from the region. Geographically, they are primarily from tropical regions (as are assessed reptiles) with an underrepresentation of African species (distribution of omitted species: Asia, 41%; Africa, 8%; Australia, 7%; Europe, 3%; North/Central America, 20%; South America, 19%; Caribbean, 5%; Oceania, 4%; percentages sum to greater than 100% because some species occur in two regions). Because they are recently described, many are poorly known, may be rare or occur in a very restricted area, or in poorly surveyed areas that are often subject to high levels of human impacts. As such, recent descriptions are more likely to receive a data-deficient or threatened Red List category than be assigned of least concern⁴¹. The net effect on our analyses is a slight underestimate of the number of threatened snakes and lizards, and plausibly a slight overestimate of least concern species. With tetrapod species described in the future likely to be small-ranged, threatened lizards and amphibians^{43,44}, surrogacy levels may decline from those reported here.

Geographical coverage. Although we made extensive efforts to map the current known distribution for each species, this information is incomplete for some species. Where appropriate, and following expert guidance, we interpolated between known localities if the ecological conditions appeared appropriate. In addition, species occurrence is unlikely to be spread evenly or entirely throughout the area depicted in range maps, with gaps expected, for example, in patches of unsuitable habitat.

Data-deficient species. For species assessed to be data deficient (1,507 reptiles, 14.8%), there was inadequate information on the distribution, population status or threats (historical, current or projected future) of the species (both from published sources and expert knowledge) to make a direct, or indirect, assessment of the risk of extinction. All species were assessed according to their recognized taxonomic circumscription at the time of assessment. Taxonomic uncertainty therefore did not result in a data-deficient assignment, although some species were listed as data deficient because they are morphologically indistinguishable from another species and therefore estimates of distribution and abundance are not feasible.

Time span of assessments. The assessments were completed between 1996 and 2020, with 1,503 assessments completed before 2011. The IUCN Rules of Procedure (<https://www.iucnredlist.org/resources/rules-of-procedure>) recommend reassessment every 10 years and thus,

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as of 2020, 15% of the assessments can be considered outdated. Of the species assessed 1996–2010, slightly more species were threatened (23.0%) than the species assessed more recently (20.7%). This difference is largely explained by the greater percentages of crocodiles and turtles with outdated assessments (29% and 35%, respectively) compared with tuatara, lizards and snakes (0%, 12% and 17%, respectively) and the highly threatened nature of crocodiles and turtles (Supplementary Table 2). The continuing deterioration of biodiversity globally¹ suggests that the species with outdated assessments are more likely to be in higher threat categories today than when they were when last assessed, causing an underestimation of current reptile threat status.

Analyses

Percentage of species threatened with extinction. To estimate the percentage of species threatened with extinction (categories critically endangered, endangered and vulnerable), we used the following formula, which assumes that data-deficient species have the same proportion of threatened species as species that were not data deficient.

$$\text{Prop}_{\text{threat}} = \frac{\text{CR} + \text{EN} + \text{VU}}{N - \text{DD}}$$

where $\text{Prop}_{\text{threat}}$ is the best estimate of the proportion of species that are threatened; CR, EN, VU and DD are the number of species in each corresponding Red List category and N is the number of species assessed (excluding extinct and extinct in the wild species).

Data for amphibians, birds and mammals. For all analyses that included data for amphibians, birds and mammals, we used the 2020-1 version³ of the tabular and spatial data downloaded from the IUCN Red List website in May 2020.

Threats. Threats calculations were restricted to species in threatened Red List categories (critically endangered, endangered and vulnerable). Multiple threats can affect a single species. Summaries of threats are for the first level of the IUCN classification scheme. Threats thought to affect only a minority of the global population (<50% of the population) (coded as 'minority') were not included. In addition, we removed threats that were assessed to cause 'no declines' and 'negligible declines' from the analysis (as indicated by the severity coding). We considered all threats without scope or severity scored to be major threats and retained them in the analysis.

Habitat. Analyses of habitat use were restricted to the first level of the IUCN habitat-classification scheme. We excluded habitats for which the major importance to the species was scored 'no' and suitability was scored 'marginal' and considered all habitats without major importance or suitability scored to be suitable and of major importance and included them in the analyses. We did not consider artificial habitats in the analyses.

Only a small number of reptile species inhabits 'caves/subterranean' and 'marine coastal' habitats, so they were not included in Fig. 4 but their threat prevalence is summarized in Supplementary Table 4.

Statistics. Statistical tests were designed to avoid inclusion of multiple observations from the same species (because species can occur in multiple habitats and be threatened by multiple threats). To assess whether arid habitat or forest species were more likely to be threatened, we included only species that were restricted to one of these habitat types. For threats analyses, we compared species that occur in forests (including those that occur in forests and other habitats) to those that do not occur in forests. All tests were two-tailed Fisher's exact tests.

Geographical patterns. The geographical patterns of threat and phylogenetic diversity shown in Fig. 2 are for only terrestrial species (so,

for reptiles, excluding 87 species of marine turtles and sea snakes). Tetrapod classes vary widely in the numbers of pelagic marine species and in the methods used to map distributions. Restricting analyses to terrestrial species ensured more-consistent analyses and avoided wide variation in summary values caused by small numbers of species.

Analyses of the distribution maps used polygons either with the following IUCN map code designations or with no codes indicated:

Presence = extant (code 1) and probably extant (code 2)

Origin = native (code 1), reintroduced (code 2) and introduced (code 6)

Seasonality = resident (code 1), breeding season (code 2), non-breeding season (code 3) and passage (code 4).

Ranges for species categorized as critically endangered (possibly extinct) are coded as possibly extinct (code 4) and excluded from the spatial analyses.

All spatial analyses were conducted on a global 0.5° by 0.5° latitude–longitude grid (approximately 50 km at the Equator). To explore the influence of spatial resolution, we repeated the surrogacy and phylogenetic diversity analyses at a 100-km resolution. We converted polygon range maps (tagged with the appropriate codes as described above) to these grids. We used a global equal-area pseudocylindrical projection, Goode homolosine.

We mapped the distribution of threatened species as a count of the number of species with ranges overlapping each grid cell.

Estimating the spatial distribution of disproportionate threat and phylogenetic diversity loss. We identified global areas in which each tetrapod class is disproportionately threatened compared with all other classes by comparing the species-richness-adjusted level of threat among the four tetrapod classes. First, for each grid cell, we identified the proportional threat level of each class by dividing the number of species in threatened Red List categories (vulnerable, endangered and critically endangered) by the total number of species for the class found in that cell. Second, for all grid cells in which at least five tetrapod species are present, we compared proportional threat values across the four classes and identified a grid cell as having a disproportionate threat level for a given class if: (1) the grid cell had a proportional level of threat equal to 10% or higher for the class; and (2) the grid cell had a proportional level of threat for the class at least twice as high as the proportional level of threat for the next class. We assessed the sensitivity of disproportionate threat patterns to our definition of disproportionate threat by varying the degree of difference in proportional threat level between the highest and second highest class. We identified the number of grid cells with disproportionate threat for each class when the class had a proportional threat level: (1) higher than any other class; (2) 25% or more higher than any other class; (3) 50% or more higher than any other class; (4) 100% or more higher than any other class; and (5) 200% or more higher than any other class. In the main text, we report results for the 100% or more threat level. Results for all thresholds are included in Extended Data Tables 1, 2.

Conservation strategies. We identified global conservation priorities for each tetrapod class using two alternative strategies: strategy 1 prioritized areas containing many threatened species with relatively highly restricted ranges, whereas strategy 2 prioritized areas core to the most range-restricted threatened species globally. We implemented both conservation strategies within the spatial conservation-planning software Zonation⁴⁵ and the R package zonator⁴⁶, using the additive benefit function and the core-area Zonation algorithms for strategies 1 and 2, respectively, at 50-km and 100-km resolutions for threatened reptiles.

The additive benefit function algorithm prioritizes areas by the sum of the proportion of the global range size of all species included in a given grid cell—a quantity similar to weighted species endemism (as defined previously⁴⁷) and endemism richness (as defined⁴⁸). On the

basis of this algorithm, cells with many species occurring only in that cell or few other cells receive the highest priority. The core-area Zonation algorithm prioritizes areas by the maximum proportion of the global range size of all species included in a given grid cell: cells including the highest proportions of the ranges of the most range-restricted species are given the highest priority.

Therefore, comparing the two strategies, strategy 1 gives more importance to the number of species within grid cells (that is, more species = a higher summed proportion), potentially at the expense of the single most-range-restricted species globally, which are instead prioritized directly by strategy 2.

Because complementary representation problems such as these spatial prioritizations often have multiple solutions, we ran five iterations of each algorithm used and summarized variation across those.

Estimating surrogacy. To assess the degree to which conserving the diversity of threatened species of birds, mammals and amphibians (individually or combined) serves as a surrogate for conserving threatened reptile diversity, we calculated a species accumulation index (SAI) of surrogate effectiveness. The SAI is derived from the comparison of three curves: (1) the 'optimal curve' represents the accumulation of the diversity of threatened reptile species when conservation is planned using data for threatened reptiles directly; (2) the 'surrogacy curve' represents the accumulation of the diversity of threatened reptile species when conservation is planned using the diversity of threatened species diversity of a different class as a surrogate; and (3) the 'random curve' represents the accumulation of the diversity of threatened reptile species when conservation areas are selected at random. We estimated optimal, surrogate and random curves based on each reptile-surrogate combination (birds, mammals and amphibians individually and combined). Using 100 sets of approximately random terrestrial grid-cell sequences allowed us to generate 95% confidence intervals around a median 'random curve'. In addition, because we ran five iterations of each spatial prioritization algorithm for each tetrapod class, optimal and surrogate curves were also summarized using the median and 95% confidence intervals across the five iterations.

We then derived the quantitative measure of surrogacy as $SAI = (s - r) / (o - r)$, where s is the area under the surrogate curve, r is the area under the random curve and o is the area under the optimal curve. $SAI = 1$ when the optimal and surrogate curves are the same (perfect surrogacy). It is between 1 and 0 when the surrogate curve lies above the random curve (positive surrogacy), zero when the surrogate and random curves coincide (no surrogacy) and negative when the surrogate curve lies below the random curve (negative surrogacy). We calculated the SAI using R code modified from a previous study⁴⁹. For each reptile-surrogate combination, we report median and 95% confidence intervals across all combinations of optimal, surrogate and random curves (5 target and surrogate curve iterations and 100 random curve iterations).

Although not strictly a measure of surrogacy²⁵, we also calculated the spatial congruence (Spearman's rank correlation, analogous to a previously published approach⁹) of Zonation priorities for each conservation strategy and spatial resolution.

Coverage by protected areas. We overlaid protected areas (polygons, categorized as IUCN I–VI from the World Database of Protected Areas⁵⁰) over the ranges of all threatened tetrapods and classified species with ranges completely outside any protected area as unprotected.

Phylogenetic diversity. To calculate phylogenetic diversity¹⁵, we used published time trees of mammals⁵¹, birds⁵² and amphibians⁵³. For reptiles, we combined two time trees: a comprehensive squamate time tree containing 9,755 squamate species, including the species *Sphenodon punctatus*¹⁶, and a turtle and crocodylian tree containing 384 species¹⁷.

The time trees contain some species lacking genetic data, added by taxonomic interpolation⁵⁴ to maximize taxonomic coverage. In total, we analysed 32,722 tetrapod species including 10,139 reptiles, 5,364 mammals, 9,879 birds and 7,239 amphibians. For squamates, and for turtles and crocodylids, 10,000 fully resolved trees were available. For each group, we randomly sampled 100 trees and combined them to obtain 100 fully resolved reptile time trees, to accommodate for uncertainty. Similarly, we randomly sampled 100 amphibian and 100 mammal time trees over the 10,000 available.

We thoroughly compared the species name mismatches between geographical and phylogenetic data to match synonyms and correct misspelled names. We also imputed species for which the genus (but not the species) was already present in the tree, for example newly described species (262 amphibian, 1,694 bird, 236 mammal and 777 reptile species). Imputed species were randomly attached to a node within the genus subtree. Because polytomies can result in an over-estimation of the phylogenetic diversity, we randomly resolved all polytomies using a previously published method⁵⁴ implemented in R code. This procedure was performed 100 times for birds, and one time for each of the 100 amphibian, 100 mammal and 100 reptile time trees. We included 30,778 tetrapod species, each with geographical and phylogenetic data, in the phylogenetic diversity analyses. This total included 6,641 amphibians, 8,758 birds, 5,550 mammals and 9,829 reptiles. For each class, we estimated phylogenetic diversity¹⁴ for all species and after the removal of threatened species, at 50-km and 100-km resolution. To consider phylogenetic uncertainty (that is, the placement of interpolated species) in phylogenetic diversity calculation for each of the 100 fully resolved trees for each class, we conducted a sensitivity analysis using a previously described method⁵⁵. This method calculates an evolutionary distinctiveness score that (1) increases the total phylogenetic diversity of the clade when including interpolated species and (2) corrects the evolutionary distinctiveness score of species in genera with interpolated species (missing relatives). Following this method, we calculated evolutionary distinctiveness scores⁵⁶ for each cell from the subtree including all species present in the focal cell with the R package *capser*⁵⁷. For genera with interpolated species, the mean evolutionary distinctiveness score of non-interpolated species was assigned to interpolated species of that genus. For those genera, we computed a second evolutionary distinctiveness score corresponding to the mean evolutionary distinctiveness score of the focal genera (including interpolated species). For species belonging to genera with no interpolated species, the first and second evolutionary distinctiveness scores were identical. Next, we calculated the mean of the two evolutionary distinctiveness scores and reported this value as the evolutionary distinctiveness score of each species. Finally, we computed phylogenetic diversity as the sum of evolutionary distinctiveness scores. Therefore, phylogenetic diversity corresponds to Crozier's version of phylogenetic diversity⁵⁸, that is, the sum of the branch lengths connecting all members of a species assemblage without the root. Next, we reported median phylogenetic diversity, computed over 100 fully resolved trees for each class. In the figures, cells with fewer than five species were excluded to avoid outliers.

Reporting summary

Further information on research design is available in the Nature Research Reporting Summary linked to this paper.

Data availability

Taxonomic data for reptiles were from the Reptile Database (<http://www.reptile-database.org/index.html>). All spatial and tabular data for the tetrapod analyses are permanently available at https://transfer.natureserve.org/download/Publications/Global_Reptiles/. Trees used for the phylogenetic diversity analyses are available at Zenodo (<https://>

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zenodo.org/record/5974891). In addition, assessment data, including range maps, for all tetrapods are publicly available on the IUCN Red List of Threatened Species website (<https://iucnredlist.org>). Occasionally, where a species may be threatened because of over-collection, sensitive distribution information is not publicly available. Protected areas boundaries were from the World Database of Protected Areas (<https://www.protectedplanet.net>). Source data are provided with this paper.

Code availability

Python scripts used for the spatial analyses are permanently available at https://transfer.natureserve.org/download/Publications/Global_Reptiles/. No code was used for the Fisher's exact tests, which were performed in Excel and available with the tabular data at https://transfer.natureserve.org/download/Publications/Global_Reptiles/. Code used for the phylogenetic diversity, areas of disproportionate threat and surrogacy analyses are available at Zenodo (<https://zenodo.org/record/5974891>).

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Acknowledgements We thank the 961 Red List assessors (listed in Supplementary Note 1); the organizers of workshops in United Arab Emirates (D. Mallon), Fiji (H. Pippard) and Colombia (B. Bock and V. Páez); the co-principal investigators of NSF award 1136586 (G. Costa, C. Graham and V. Radeloff); and J. Chanson, D. Bennett, N. Garcia, H. Hamilton, D. Hole, D. Juhn, A. Kenlan, M. Mascia, R. Mittermeier, M. Ormes, J. P. Ross, J. P. Rodriguez, J. Rodriguez, J. Smart, S. Stuart, P. Uetz and J.-C. Vié. Funding was provided by Agencia Nacional de Promoción Científica y Tecnológica-Fondo para la Investigación Científica y Tecnológica RC 2014-0116 (L.J.A.); the Australian Department of Agriculture, Water and the Environment; the Australian Research Council; B. and G. Moore; Charles Darwin University; Conselho Nacional de Desenvolvimento Científico e Tecnológico; Coordenação de Aperfeiçoamento de Pessoal de Nível Superior; the Environment Agency Abu Dhabi; Environment and Protected Areas Authority of Sharjah; Fundação de Amparo à Pesquisa do Estado de São Paulo grants 2015/20215-7 (C.d.C.N.) and 2020/12658-4 (M.M.); Fundação de Apoio à Pesquisa do Distrito Federal; Global Protected Area Friendly System; IBAT—The Integrated Biodiversity Assessment Tool; Instituto Chico Mendes de Conservação da Biodiversidade; IUCN; Ministério do Meio Ambiente; the Mohamed bin Zayed Species Conservation Fund; Monash University; Museum für Naturkunde; National Science Foundation grants 1136586 (B.E.Y. and T.M.B.), 1455761 (S.B.H.) and 1932765 (S.B.H.); the Rainforest Trust; the Regina Bauer Frankenberg Foundation; the Rufford Foundation; San Diego Zoo Wildlife Alliance; Secretaría de Educación Superior, Ciencia, Tecnología e Innovación; the Society of Entrepreneurs and Ecology Foundation; the South African National Biodiversity Institute; Species Survival Commission; Toyota Motor Corporation through the IUCN-Toyota Red List Partnership; US Fish and Wildlife Service; Universidad del Bio-Bío; Universidad San Francisco de Quito; University of Western Australia; Wildlife Reserves Singapore; World Wildlife Fund; Zoological Institute, St Petersburg theme 122031100282-2; and Zoological Society of London.

Author contributions N.C. and B.E.Y. conceived the original idea. C.H.-T. curated the data. M.F., J.M., G.R. and B.E.Y. ran the analyses. T.M.B., N.C., S.B.H., R.K.B.J. and B.E.Y. secured the principal funding. N.C. and B.E.Y. wrote the first draft and all authors reviewed and edited the manuscript.

Competing interests The authors declare no competing interests.

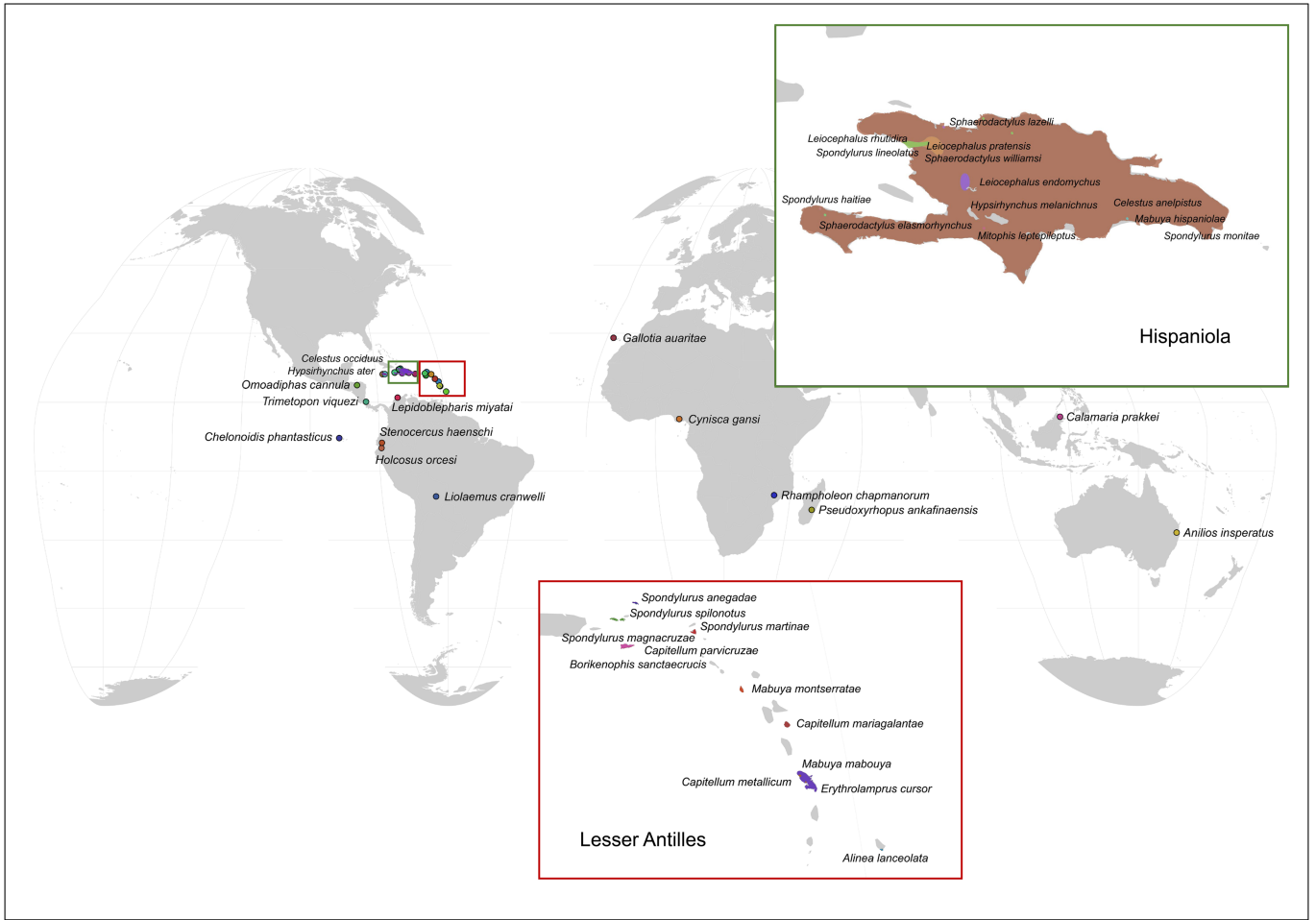
Additional information

Supplementary information The online version contains supplementary material available at <https://doi.org/10.1038/s41586-022-04664-7>.

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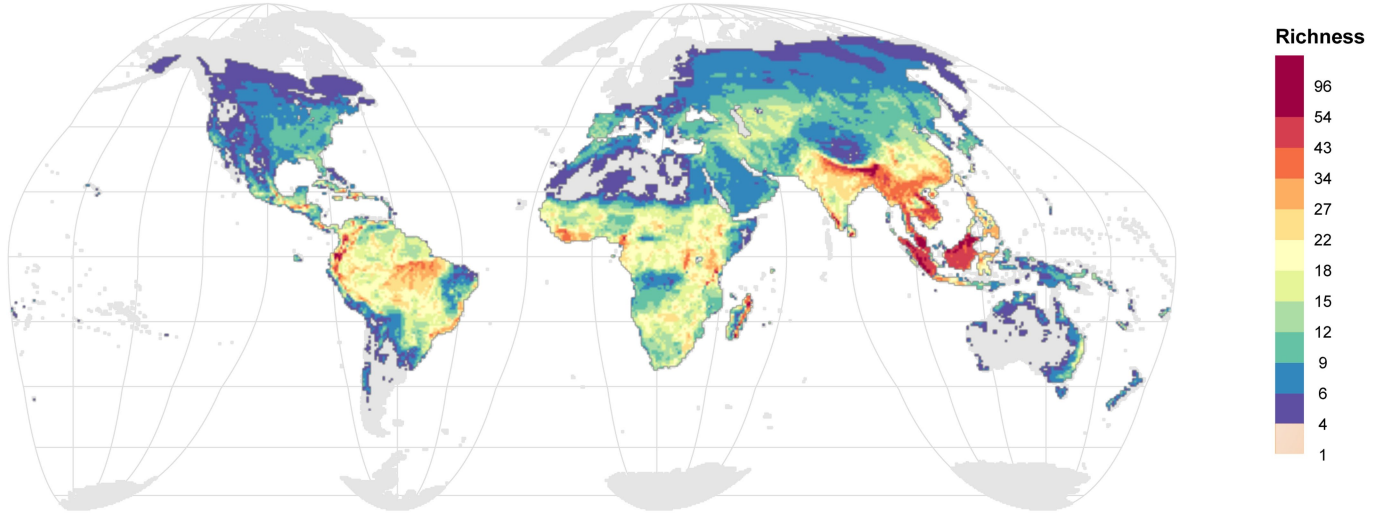
Peer review information *Nature* thanks Céline Bellard, Arne Mooers, Mario Moura and the other, anonymous, reviewer(s) for their contribution to the peer review of this work.

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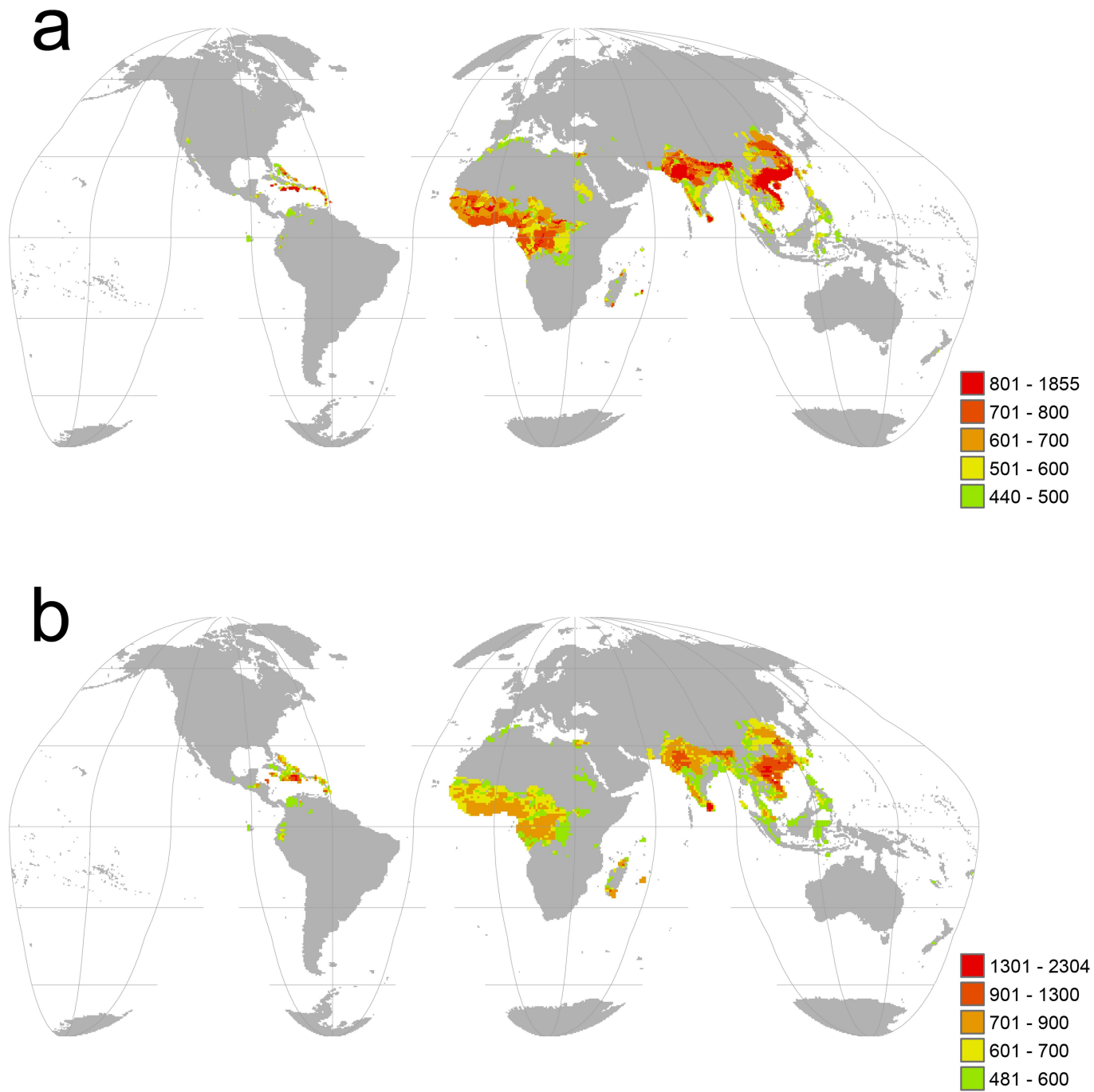


Extended Data Fig. 1 | Locations of critically endangered (possibly extinct) reptiles. Colours depict individual species' ranges. These species were classified as critically endangered (possibly extinct) (CR(PE)) at the time of their assessments. Fortunately, a few species such as *Rhampoleon*

*chapmanorum*⁵⁹ have been recorded subsequent to their assessment publication dates and will no longer be classified as CR(PE) once they are reassessed in the future.

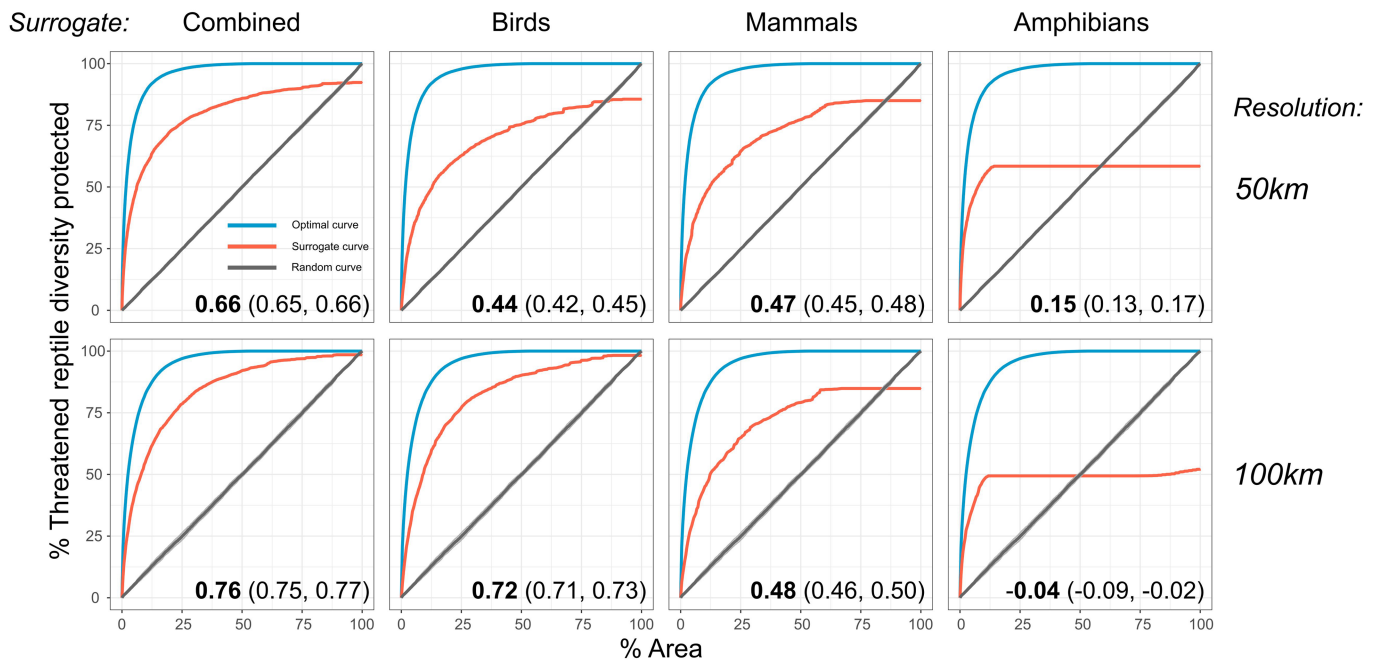


Extended Data Fig. 2 | Richness of threatened (CR, EN, VU) tetrapods (50-km resolution). As in Fig. 2a, only threatened species occurring in terrestrial areas are shown.

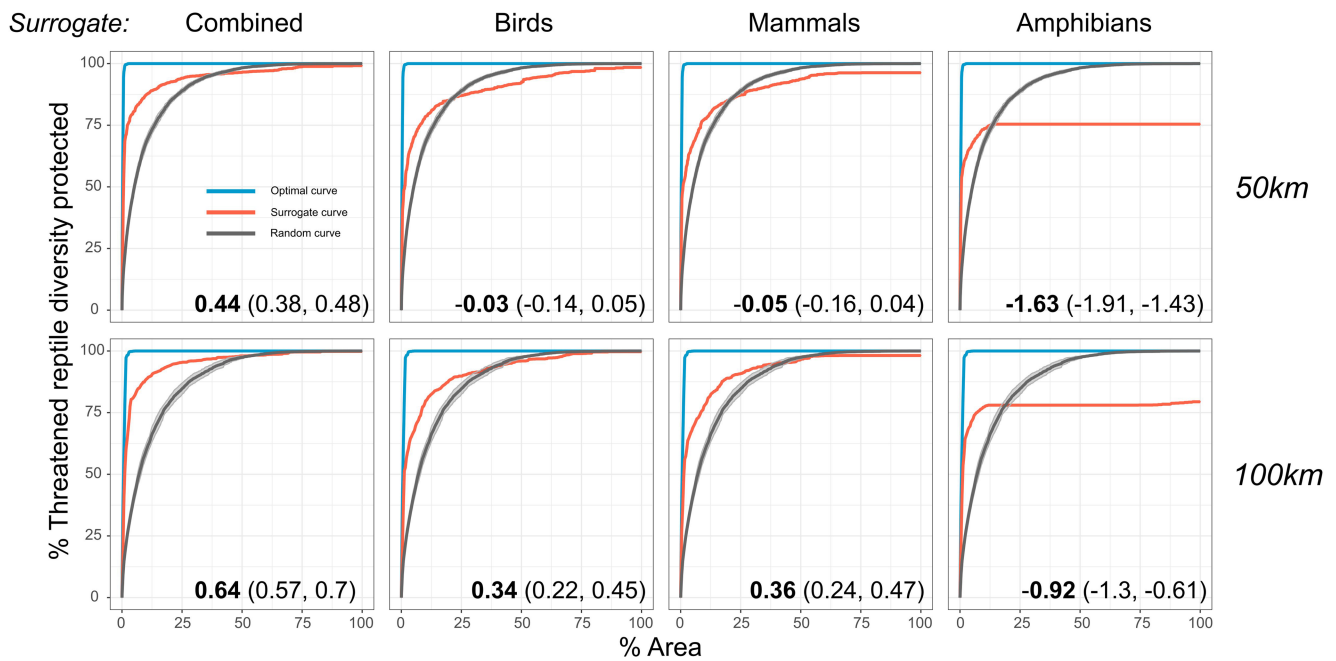


Extended Data Fig. 3 | Areas with the top 15% of PD loss if all threatened reptiles become extinct. a, 50-km resolution, b, 100-km resolution.

a) Conservation Strategy 1: Maximize rarity-weighted richness



b) Conservation Strategy 2: Maximize inclusion of most range-restricted species



Extended Data Fig. 4 | Species Accumulation Index (SAI) values and curves for surrogacy analysis. Effectiveness of threatened birds, mammals, and amphibians – individually or combined – as a surrogate for the conservation of threatened reptile species diversity for two alternative strategies – **a**, Conservation Strategy 1: Maximize rarity-weighted richness, **b**, Conservation Strategy 2: Maximize inclusion of most range-restricted species. See Methods for full explanation of each strategy. Surrogate effectiveness is measured using the Species Accumulation Index (SAI): values range from $-\infty$ to 1, with 1 indicating perfect surrogacy, values between 1 and 0

indicate positive surrogacy, 0 indicating no surrogacy, and values less than 0 indicating negative surrogacy. In each panel, median SAI values are in bold, with lower and upper confidence intervals in brackets. Blue lines are the optimal curves (accumulation of target diversity based on target priority areas); red lines are the surrogate curves (accumulation of target diversity based on surrogate priority areas); and grey lines are the random curves (accumulation of target diversity based on random selection of areas). Confidence intervals (95%, based on 100 randomizations) shown in lighter shading around curves; most are too small to be visible.

Extended Data Table 1 | Sensitivity analysis for proportional threat level differences

Taxon	Number of cells where proportional threat level for species diversity is highest by:				
	Any level	≥25%	≥50%	≥100%	≥200%
Amphibians	2,678 (4%)	2,474 (4%)	2,252 (3%)	1,775 (3%)	1,026 (2%)
Birds	1,919 (3%)	1,209 (2%)	997 (2%)	791 (1%)	554 (1%)
Mammals	6,757 (10%)	6,037 (9%)	5,343 (8%)	3,976 (6%)	2,244 (3%)
Reptiles	4,052 (6%)	3,592 (5%)	3,188 (5%)	2,331 (3%)	1,205 (2%)
NA	51,203 (77%)	53,297 (80%)	54,829 (82%)	57,736 (87%)	61,580 (92%)

Influence of choice of threshold for proportional threat level difference between the most and second most proportionately threatened class on the absolute and relative number of grid cells identified as disproportionately threatened for species diversity across the four tetrapod classes. Provided in brackets are the percentage of all global terrestrial cells (71,605 in total) that are either attributed to the given class or assigned NA if no class is identified as disproportionately threatened using the corresponding threat level. Note that in the main text, we report results for the 100% or more threat level.

Article

Extended Data Table 2 | Sensitivity analysis for proportional threat of phylogenetic diversity loss differences

Taxon	Number of cells where proportional threat level for phylogenetic diversity is highest by:				
	Any level	≥25%	≥50%	≥100%	≥200%
Amphibians	2,761 (4%)	2,542 (4%)	2,307 (3%)	1,935 (3%)	1,422 (2%)
Birds	1,263 (2%)	763 (1%)	512 (1%)	468 (1%)	373 (1%)
Mammals	6,324 (9%)	5,917 (8%)	5,321 (7%)	3,996 (6%)	2,054 (3%)
Reptiles	11,224 (16%)	10,845 (15%)	10,384 (14%)	9,050 (13%)	6,176 (9%)
NA	50,095 (70%)	51,600 (72%)	53,143 (74%)	56,218 (78%)	61,642 (86%)

Influence of choice of threshold for proportional threat level difference between the most and second most proportionately threatened class on the absolute and relative number of grid cells identified as disproportionately threatened for phylogenetic diversity across the four tetrapod classes. Provided in brackets are the percentage of all global cells (71,605 in total) that are either attributed to the given class or assigned NA if no class is identified as disproportionately threatened using the corresponding threat level. Note that in the main text, we report results for the 100% or more threat level.

Extended Data Table 3 | Spatial congruence of Zonation priorities between reptiles and birds, mammals, and amphibians

Spatial Resolution	Strategy 1 (Prioritize assemblages of many species with restricted ranges)			
	Combined	Birds	Mammals	Amphibians
50 km	0.70	0.40	0.35	0.21
100 km	0.75	0.56	0.35	0.26

Strategy 2 (Prioritize areas with the smallest-ranged species)				
Spatial Resolution	Combined	Birds	Mammals	Amphibians
50 km	0.70	0.37	0.29	0.18
100 km	0.74	0.52	0.28	0.23

Shown are Spearman's rank correlation coefficients among priority ranks for each conservation strategy and spatial resolution examined. Note that spatial congruence is not a strict metric of surrogacy because it does not address complementarity among areas²⁴. "Combined" refers to birds, mammals, and amphibians combined.

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Extended Data Table 4 | Percentage overlap in highest conservation priority areas between threatened reptiles and threatened birds, mammals, and amphibians, both individually and combined

Strategy 1 (Prioritize assemblages of many species with restricted ranges)

Hotspot definition (percentile of priority areas)

	Spatial Scale	Combined	Birds	Mammals	Amphibians
top 10 th percentile	50 km	54	41	39	17
top 10 th percentile	100 km	55	50	37	14
top 30 th percentile	50 km	68	58	55	18
top 30 th percentile	100 km	71	69	53	16
top 50 th percentile	50 km	79	70	66	19
top 50 th percentile	100 km	83	79	65	17

Strategy 2 (Prioritize areas with the smallest-ranged species)

Hotspot definition	Spatial Scale	Combined	Birds	Mammals	Amphibians
top 10 th percentile	50 km	48	38	34	11
top 10 th percentile	100 km	38	38	30	10
top 30 th percentile	50 km	65	54	52	17
top 30 th percentile	100 km	68	67	50	15
top 50 th percentile	50 km	76	68	62	19
top 50 th percentile	100 km	81	77	61	17

Highest conservation priority areas were defined as the top 10th, 30th or 50th percentile areas ranked in our systematic spatial conservation planning analyses for the respective taxon. Overlap was calculated as the number of highest priority cells shared between taxa divided by the total number of terrestrial cells with threatened reptiles, expressed as a percentage. Percentage overlap is shown at 50 km and 100 km grid cell resolutions.

Supplementary information

A global reptile assessment highlights shared conservation needs of tetrapods

In the format provided by the authors and unedited

Global Reptile Assessment Shows Commonality of Tetrapod Conservation Needs

By Cox, Young, et al.

SUPPLEMENTARY INFORMATION

Supplementary Note 1

List of Assessors

The following people contributed to the assessment of at least one reptile species used in this study. Assessors that are also authors either provided substantial unpublished datasets, hosted assessment workshops and contributed to numerous assessments, and/or served as a reptile Red List Authority.

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Wickramasinghe, N. Wijethilaka, S. Wikramanyake, J. Wilkinson, J. Williams, T. Wilms, S.
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M. Yáñez-Muñoz, J. Yang, C. Yeniyurt, H. Zaher, T. Zamin, G. Zamora, E. Zarza-Franco, A.
Zassi-Boulou, W. Zhao, W. Zhou, Z. Zhou, J. Zichy-Woinarski, T. Ziegler, G. Zug.

Supplementary Table 1.

In-person and remote workshops undertaken as part of the Global Reptile Assessment.

Year	Region	Assessment Type
2004	Mediterranean	Workshop
2005	Mexico	Workshop
2006	Northern and Central Europe	Workshop
2006	Seychelles	Remote assessment
2006	North America	Remote assessment
2008	Caucasus, Iran, and Iraq	Workshop
2008	Philippines	Workshop
2009	Caribbean (iguanas)	Workshop
2011	Madagascar	Workshop
2011	Comoros	Remote assessment
2011	China and Southeast Asia (snakes)	Workshop
2011	Oceania	Workshop
2012	Arabian Peninsula	Workshop
2012	Socotra	Remote assessment
2012	Central America	Workshop
2012	West Africa	Workshop
2012	Cabo Verde	Remote assessment
2012	Brazil (snakes)	ICMBio workshops (two held in 2012)
2013	Northwestern Andes	Workshop
2013	Western Ghats	Workshop
2014	New Guinea	Workshop
2014	East Africa	Workshop
2014	Northern Andes	Workshop
2014	Southeastern South America	Workshop (excluded Brazil)
2014	Widespread species of the Amazon Basin, Guiana Shield, and Venezuela	Workshop
2015	Chile	Workshop
2015	Caribbean	Workshop
2015	Cuba	Remote assessment
2015	Venezuela	Workshop
2016	Aruba, Bonaire and Curaçao	Remote assessment
2016	Central Asia	Workshop
2016	Japan	Remote assessment
2017	Western Australia	Workshop
2017	Eastern Australia	Workshop
2018	Southeast Asia (lizards)	Workshop
2018	China (lizards)	Workshop
2019	Korean Peninsula	Remote assessment
2019	Central and Southern Africa	Workshop
2019	Wallacea	Workshop

Year	Region	Assessment Type
2019	Mainland South Asia	Workshop
2019	Pakistan	Remote assessment
2019	Sri Lanka	Workshop
2010/2017	New Caledonia	IUCN workshop/national assessment workshop
2013/2014	Brazil (lizards)	ICMBio workshops
2013/2018	South Africa	SANBI workshops
2016-2019	Mascarenes	Remote assessment
2018-2019	New Zealand	Hybrid workshop/remote assessment
2017-2019	Horn of Africa	Hybrid remote assessment/meeting

Supplementary Table 2.

Summary of Red List Categories for all families of reptiles. See Methods for calculation of best estimate of percent threatened, which does not include EX or EW species.

Order/Suborder/Family	LC	NT	DD	VU	EN	CR	EW	EX	Total	% DD	% Threatened
Crocodylia	12			5		7			24	0.0%	50.0%
Crocodylia	12			5		7			24	0.0%	50.0%
Alligatoridae	7					1			8	0.0%	12.5%
Crocodylidae	5			5		5			15	0.0%	66.7%
Gavialidae						1			1	0.0%	100.0%
Rhynchocephalia	1								1	0.0%	0.0%
Rhynocephalia	1								1	0.0%	0.0%
Sphenodontidae	1								1	0.0%	0.0%
Squamata	6146	532	1485	557	724	350	2	24	9820	15.1%	19.6%
"Lizards"	3905	386	800	392	545	266	2	20	6316	12.7%	21.9%
Anguimorpha	103	6	28	11	42	8			198	14.1%	35.9%
Anguidae	55	3	17	8	28	7			118	14.4%	42.6%
Anniellidae	1				1				2	0.0%	50.0%
Helodermatidae	1	1							2	0.0%	0.0%
Lanthanotidae					1				1	0.0%	100.0%
Shinisauridae					1				1	0.0%	100.0%
Varanidae	44	2	10	2	9	1			68	14.7%	20.7%
Xenosauridae	2		1	1	2				6	16.7%	60.0%
Dibamia	7	2	10	1	3	1			24	41.7%	35.7%
Dibamidae	7	2	10	1	3	1			24	41.7%	35.7%
Gekkota	994	109	240	117	149	91	1	4	1705	14.1%	24.4%
Carphodactylidae	22	3		2	2	2			31	0.0%	19.4%
Diplodactylidae	89	14	6	13	17	9		1	149	4.0%	27.5%
Eublepharidae	17	1	3	3	9	4			37	8.1%	47.1%
Gekkonidae	635	64	201	84	73	57	1	3	1118	18.0%	23.4%
Phyllodactylidae	81	9	9	6	7	5			117	7.7%	16.7%
Pygopodidae	37	1	3	1	3				45	6.7%	9.5%
Sphaerodactylidae	113	17	18	8	38	14			208	8.7%	31.6%
Iguania	1121	126	162	129	168	68		4	1778	9.1%	22.6%
Agamidae	353	20	61	28	25	10			497	12.3%	14.4%
Chamaeleonidae	79	39	10	22	42	10			202	5.0%	38.5%
Corytophanidae	9								9	0.0%	0.0%
Crotaphytidae	9			1	2				12	0.0%	25.0%
Dactyloidae	215	36	39	20	48	22			380	10.3%	26.4%
Hoplocercidae	11			4	2				17	0.0%	35.3%
Iguanidae	8	3	2	11	12	8		1	45	4.4%	73.8%
Leiosauridae	20	1	4	2	3	2			32	12.5%	25.0%
Liolaemidae	207	12	22	19	21	8			289	7.6%	18.0%
Opluridae	7								7	0.0%	0.0%
Phrynosomatidae	102	7	7	9	6	1			132	5.3%	12.8%
Polychrotidae	5		1	1					7	14.3%	16.7%
Tropiduridae	96	8	16	12	7	7		3	149	10.7%	20.0%

Order/Suborder/Family	LC	NT	DD	VU	EN	CR	EW	EX	Total	% DD	% Threatened
Lacertoidea	574	56	125	33	76	27		2	893	14.0%	17.8%
Amphisbaenidae	98	7	39	6	14	6			170	22.9%	19.8%
Bipedidae	3								3	0.0%	0.0%
Cadeidae	2								2	0.0%	0.0%
Gymnophthalmidae	141	14	47	13	30	5			250	18.8%	23.6%
Lacertidae	220	23	26	8	25	12			314	8.3%	15.6%
Rhineuridae	1								1	0.0%	0.0%
Teiidae	106	12	10	6	7	4		2	147	6.8%	12.6%
Trogonophidae	3		3						6	50.0%	0.0%
Scinciformata	1106	87	235	101	107	71	1	10	1718	13.7%	18.9%
Cordylidae	58	3	4	2	1				68	5.9%	4.7%
Gerrhosauridae	26	3	1	6	2			1	39	2.6%	21.6%
Scincidae	1009	79	222	90	103	71	1	9	1584	14.0%	19.5%
Xantusiidae	13	2	8	3	1				27	29.6%	21.1%
Serpentes ("Snakes")	2241	146	685	165	179	84		4	3504	19.5%	15.2%
Acrochordidae	3								3	0.0%	0.0%
Aniliidae	1								1	0.0%	0.0%
Anomalepididae	7		11						18	61.1%	0.0%
Anomochilidae	1		2						3	66.7%	0.0%
Atractaspidae	63	1	7						71	9.9%	0.0%
Boidae	41	8	2	3	5	1			60	3.3%	15.5%
Bolyeridae				1				1	2	0.0%	100.0%
Calamariidae	41		37	4	4	4			90	41.1%	22.6%
Colubridae	540	24	114	25	23	10			736	15.5%	9.3%
Cylindrophiidae	2	1	7	1		1			12	58.3%	40.0%
Dipsadidae	452	32	154	33	41	24		2	738	20.9%	16.8%
Elapidae	268	15	51	16	9	2			361	14.1%	8.7%
Gerrhopilidae	3		12		1	1			17	70.6%	40.0%
Grayiidae	4								4	0.0%	0.0%
Homalopsidae	20	1	23	2	2				48	47.9%	16.0%
Lamprophiidae	69		9		1				79	11.4%	1.4%
Leptotyphlopidae	72	2	35	3	2	4			118	29.7%	10.8%
Loxocemidae	1								1	0.0%	0.0%
Natricidae	148	11	42	11	12	4			228	18.4%	14.5%
Pareidae	14	1	4						19	21.1%	0.0%
Prosymnidae	14				1	1			16	0.0%	12.5%
Psammophiidae	47	1		1					49	0.0%	2.0%
Pseudoxenodontidae	8		4						12	33.3%	0.0%
Pseudoxyrhophiidae	52	12	7	11	8	2			92	7.6%	24.7%
Pythonidae	24	4	6	6	1				41	14.6%	20.0%
Tropidophiidae	10	4	2	6	9	6			37	5.4%	60.0%
Typhlopidae	120	6	105	7	16	7		1	262	40.1%	19.2%
Uropeltidae	12	2	20	4	12	6			56	35.7%	61.1%
Viperidae	193	20	27	30	32	10			312	8.7%	25.3%
Xenodermidae	9	1	2	1		1			14	14.3%	16.7%
Xenopeltidae	2								2	0.0%	0.0%
Xenophiidae			2						2	100.0%	NA
Testudines	97	39	22	61	56	69		7	351	6.3%	57.8%
Testudines	97	39	22	61	56	69		7	351	6.3%	57.8%
Carettochelyidae					1				1	0.0%	100.0%
Chelidae	27	9	8	4	4	5			57	14.0%	26.5%

Order/Suborder/Family	LC	NT	DD	VU	EN	CR	EW	EX	Total	% DD	% Threatened
Cheloniidae			1	2	1	2			6	16.7%	100.0%
Chelydridae	1	1		3					5	0.0%	60.0%
Dermatemydidae						1			1	0.0%	100.0%
Dermochelyidae				1					1	0.0%	100.0%
Emydidae	16	9	5	15	9	1			55	9.1%	50.0%
Geoemydidae	10	9	2	4	20	26			71	2.8%	72.5%
Kinosternidae	19	6		2		2			29	0.0%	13.8%
Pelomedusidae	13	1	4		1				19	21.1%	6.7%
Platysternidae						1			1	0.0%	100.0%
Podocnemididae				4	1	3			8	0.0%	100.0%
Testudinidae	6	4		17	12	19		7	65	0.0%	82.8%
Trionychidae	5		2	9	7	9			32	6.3%	83.3%
Total	6256	571	1507	623	780	426	2	31	10,196	14.8%	21.1%

Supplementary Table 3.

Threatened (Critically Endangered, Endangered, and Vulnerable) tetrapods with ranges that do not overlap with the ranges of any other threatened tetrapod. Analysis performed using range maps developed as part of the extinction risk assessment process.

Birds

<i>Acrocephalus aequinoctialis</i>	<i>Edolisoma nesiotis</i>	<i>Oreomystis bairdi</i>
<i>Acrocephalus caffer</i>	<i>Elaenia ridleyana</i>	<i>Palmeria dolei</i>
<i>Acrocephalus familiaris</i>	<i>Erythropitta splendida</i>	<i>Paroreomyza montana</i>
<i>Acrocephalus longirostris</i>	<i>Eunymphicus uvaeensis</i>	<i>Passer hemileucus</i>
<i>Acrocephalus rehsei</i>	<i>Fringilla polatzeki</i>	<i>Petroica dannefaerdi</i>
<i>Acrocephalus rimitarae</i>	<i>Gallinula comeri</i>	<i>Petroica traversi</i>
<i>Acrocephalus taiti</i>	<i>Geospiza acutirostris</i>	<i>Pinaroloxias inornata</i>
<i>Acrocephalus vaughani</i>	<i>Geospiza pauper</i>	<i>Pomarea iphis</i>
<i>Aerodramus sawtelli</i>	<i>Geospiza propinqua</i>	<i>Pomarea mendozae</i>
<i>Alopecoenas erythropterus</i>	<i>Geospiza septentrionalis</i>	<i>Pomarea nigra</i>
<i>Alopecoenas rubescens</i>	<i>Hemignathus wilsoni</i>	<i>Pomarea whitneyi</i>
<i>Anas aucklandica</i>	<i>Hemiphaga chathamensis</i>	<i>Pseudonestor xanthophrys</i>
<i>Aphrastura masafucae</i>	<i>Junco insularis</i>	<i>Ptilinopus chalcurus</i>
<i>Atlantisia rogersi</i>	<i>Lewinia muelleri</i>	<i>Ptilinopus chrysogaster</i>
<i>Branta sandvicensis</i>	<i>Loxioides bailleui</i>	<i>Ptilinopus huttoni</i>
<i>Charadrius sanctaehelenae</i>	<i>Loxops caeruleirostris</i>	<i>Ptilinopus insularis</i>
<i>Chasiempis ibidis</i>	<i>Loxops coccineus</i>	<i>Rowettia goughensis</i>
<i>Chasiempis sandwichensis</i>	<i>Magumma parva</i>	<i>Sephanoides fernandensis</i>
<i>Chasiempis sclateri</i>	<i>Manuceria mana</i>	<i>Sittiparus owstoni</i>
<i>Chlorodrepanis flava</i>	<i>Mayornis schistaceus</i>	<i>Symposiachrus ateralbus</i>
<i>Chlorodrepanis stejnegeri</i>	<i>Mimus trifasciatus</i>	<i>Telespiza cantans</i>
<i>Coccyzus ferrugineus</i>	<i>Myadestes obscurus</i>	<i>Todiramphus gambieri</i>
<i>Coenocorypha pusilla</i>	<i>Myadestes palmeri</i>	<i>Todiramphus godeffroyi</i>
<i>Cyanoramphus forbesi</i>	<i>Myiagra cervinicolor</i>	<i>Todiramphus ruficollaris</i>
<i>Cyanoramphus unicolor</i>	<i>Nesospiza acunhae</i>	<i>Vini peruviana</i>
<i>Drepanis coccinea</i>	<i>Nesospiza questi</i>	<i>Vini stepheni</i>
<i>Ducula aurorae</i>	<i>Nesospiza wilkinsi</i>	<i>Vini ultramarina</i>
<i>Ducula galeata</i>	<i>Nesotriccus ridgwayi</i>	<i>Zapornia atra</i>

Mammals

<i>Echymipera davidi</i>	<i>Peromyscus dickeyi</i>	<i>Pteropus rodricensis</i>
<i>Lepus insularis</i>	<i>Peromyscus pseudocrinitus</i>	<i>Rattus nikenii</i>
<i>Mogera uchidai</i>	<i>Peromyscus sejugis</i>	<i>Sorex pribilofensis</i>
<i>Peromyscus caniceps</i>	<i>Phalanger alexandrae</i>	

Reptiles

<i>Alsophis antiquae</i>	<i>Flexiseps valhallae</i>	<i>Oligosoma fallai</i>
<i>Anolis nelsoni</i>	<i>Gongylomorphus bojerii</i>	<i>Phymaturus mallimaccii</i>
<i>Anolis villai</i>	<i>Lepidodactylus tepukapili</i>	<i>Plestiodon longirostris</i>

Aristelliger nelsoni
Aspidoscelis martyr
Bavayia exsuccida
Carinascincus palfreymani
Correlophus belepensis
Cryptoblepharus caudatus
Ctenosaura nolasensis
Cubophis brooksi

Liolaemus famatinae
Liolaemus morenoi
Lygodactylus insularis
Mabuya cochonae
Macrovipera schweizeri
Nactus coindemirensis
Nactus serpensinsula

Podarcis gaigeae
Podarcis levendis
Podarcis milensis
Uta encantadae
Uta lowei
Uta palmeri
Uta tumidarostra

Amphibians

Atelognathus patagonicus
Atelognathus praebasalticus
Atelognathus reverberii

Lyciasalamandra helverseni
Ololygon peixotoi

Pelophylax cerigensis
Pleurodema somuncurensis

Supplementary Table 4.

Numbers of species and percentages of species threatened of major reptile groups (top) and tetrapod classes (bottom) that occur in caves/subterranean and marine coastal habitats. Marine coastal species included are those that make use of coastal terrestrial habitats (e.g., marine iguana); species were not included if they inhabit the ocean for a significant part of their life cycle (e.g., marine turtles).

Habitat	Crocodiles		Lizards		Snakes		Turtles	
	Species	% Threatened	Species	% Threatened	Species	% Threatened	Species	% Threatened
Caves/Subterranean	0	0.0	43	36.8	7	35.0	0	0.0
Marine Coastal	2	50.0	60	24.7	11	21.6	9	60.0

Habitat	Amphibians		Birds		Mammals		Reptiles	
	Species	% Threatened	Species	% Threatened	Species	% Threatened	Species	% Threatened
Caves/Subterranean	102	51.0	24	12.5	485	18.4	50	36.5
Marine Coastal	29	10.3	215	29.8	92	35.9	82	26.2

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n/a Confirmed

- The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- A description of all covariates tested
- A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

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Software and code

Policy information about [availability of computer code](#)

Data collection

Data analysis

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Taxonomic data for reptiles were from the Reptile Database (<http://www.reptile-database.org/index.html>). All spatial and tabular data for the tetrapod analyses are permanently available to the public at https://transfer.natureserve.org/download/Publications/Global_Reptiles/. Trees used for the PD analyses are available at <https://zenodo.org/record/5974891>. In addition, assessment data, including range maps, for all tetrapods are publicly available on the IUCN Red List of Threatened

Species website (<https://iucnredlist.org>). Occasionally, where a species may be threatened from over-collection, sensitive distribution information is not publicly available. Protected areas boundaries were from the World Database of Protected Areas, available at <https://www.protectedplanet.net>.

Field-specific reporting

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Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	This study examined the extinction risk status of reptiles globally. Data were compiled to address the IUCN Red List criteria, including the development of species range maps. The data were analyzed geographically to compare patterns of threat status and potential loss of phylogenetic diversity with other tetrapod groups, as well as with software to address questions about surrogacy of threatened birds, mammals, and amphibians with threatened reptiles. Simple 2x2 contingency tables were used to test for association between habitat use and threat status.
Research sample	<p>For this study, a research sample was an IUCN Red List assessment of a species. Assessments included information about the taxonomic hierarchy, distribution (including a GIS range map), habitats used, threats, and Red List criteria used to assign an extinction risk category.</p> <p>Additional data sets used were:</p> <p>The Reptile Database (2020 version, a taxonomic listing of known reptile species descriptions) IUCN Red List of Threatened Species (version 2020-1, for bird, mammal, and amphibian ranges, habitats, and threats) Squamate phylogenetic tree (Tonini et al. 2016) Turtle and crocodile phylogenetic tree (Colston et al. 2020) Mammal phylogenetic tree (Upham et al. 2019) Bird phylogenetic tree (Hedges et al. 2015) Amphibian phylogenetic tree (Jetz et al. 2018) World Database of Protected Areas (a spatial database of the protected areas in each country)</p>
Sampling strategy	No sampling strategy was used -- we examined all known species of reptiles (aside from some that were described after regional assessments took place).
Data collection	<p>Most data collection took place during regional workshops during which facilitators queried field scientists familiar with species for information about species. Information was entered by the facilitator via computer directly into the Red List database (known as the Species Information Service, or SIS) either in an offline version that was later uploaded to the central version (2004-2013) or directly into the online version (2014-2019). In some cases, the Red List Authority for the IUCN Specialist Group covering a specific group of reptiles completed the assessments for the species in their purview, again via computer to the IUCN Red List database. In all cases, the facilitator or data recorder had previously received training in the proper use of the Red List Categories and Criteria.</p> <p>The data collectors included manuscript authors Bruce Young, Neil Cox, Phil Bowles, Thomas Brooks, Monika Böhm, Mike Hoffmann, Craig Hilton-Taylor, Marcelo Tognelli, Richard Jenkins, Dave Chapple, Carla Eisemberg, Mark Auliya, Tandora Grant, Kate Sanders, and Krystal Tolley. Additional data collectors were: Ana Nieto, Melanie Bilz, Nieves García, Tulia Defex, Jamie Carr, Monni Böhme, Rossana Merizalde, Nicholas Macfarlane, Jing Zhang, Sarah Sutcliffe, S. R. Ganesh, Srinivasulu Chelmala, Janice Chanson, Caroline Pollock, and Naamal De Silva, Jorge Rodriguez, Margaret Ormes, Geoff Hammerson, Matt Foster, Lily Rodriguez, and Penny Langhammer.</p>
Timing and spatial scale	Collection of data for the reptile assessments initiated 13 December 2004 and concluded on 25 October 2019. The spatial scale of the data collection was global, covering all terrestrial and marine areas where reptiles are known to occur (i.e., excluding polar regions). Data collection primarily took place in remote and in-person assessment workshops, which occurred as funding, logistics, and local scientist availability allowed at an average rate of 3 per year (see Supplementary Table 1 for list of assessment events).
Data exclusions	No data were intentionally excluded from the analysis -- assessments of all known species were included. However, because systematists continue to describe new species, some of these recently described species were left out of the analysis.
Reproducibility	<p>Species assessments went through two levels of review post workshop to improve reproducibility and consistency. First, a scientist familiar with the species but not involved in the assessment reviewed the account for biological accuracy and accurate application of the Red List criteria. Once the assessors revised the assessment satisfactorily, staff from the IUCN Red List Unit reviewed the assessment primarily for accurate application of the Red List criteria. The assessors revised the assessment again, if necessary, to satisfy any concerns of the IUCN Red List Unit before the assessment was finalized. These review processes succeeding in verifying the assessment data to the satisfaction of the original assessor(s), reviewer, and IUCN staff.</p> <p>No attempts were made to reproduce the original assessments themselves.</p>
Randomization	No randomized groups were used in this study. The study covered the entire "population" (i.e., not a sample) of reptile species known at the time that the study took place. For this same reason, there were no relevant covariates to consider in the analyses.

Blinding

Blinding was not relevant to this study, which did not involve experimental analysis.

Did the study involve field work? Yes No

Reporting for specific materials, systems and methods

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Materials & experimental systems

n/a	Included in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

Methods

n/a	Included in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging