The Conservation Status of the World’s Reptiles

Running title: Conservation Status of Reptiles

1 Institute of Zoology, Zoological Society of London, Regent's Park, London, NW1 4RY, UK
2 Conservation Programmes, Zoological Society of London, Regent's Park, London, NW1 4RY, UK
3 Species Programme, IUCN, Rue Mauverney 28, 1196 Gland, Switzerland
4 IUCN - CI Biodiversity Assessment Unit, c/o 130 Weatherall Road, Cheltenham
5 IUCN - CI Biodiversity Assessment Unit, Conservation International, 2011 Crystal
Department of Biological Sciences, Museum of Natural Science, Louisiana State University, 119 Foster Hall, Baton Rouge, LA 70803-3216, USA

Adnan Menderes University, Faculty of Science and Arts, Department of Biology, Aydin, Turkey

Texas A&M University System, AgriLIFE Research, Blackland Research and Extension Center, 720 E Blackland Rd, Temple, TX 76502, USA

The Wetlands Institute, 1075 Stone Harbor Blvd, Stone Harbor, NJ 08247, USA

Departamento Ecologia, Universidade Federal do Rio Grande do Sul - RS, Brazil

Fundación Andigena, PO Box 210, Mérida 5101-A, Mérida, Venezuela

The Katerniaghat Foundation, C-421 Sector-B, Mahanagar, Lucknow, 226006, India

Department of Herpetology, National Museum, P.O. Box 266, Bloemfontein, 9300, South Africa

Department of the Environment - Mato Grosso, Brazil

Department of Biology, Villanova University, 800 Lancaster Avenue, Villanova, Pennsylvania 19085, USA

Mampam Conservation, Glossop, UK

Zoologisches Forschungsmuseum Alexander Koenig (ZFMK), Adenauerallee 160, 53113 Bonn, Germany

Department of Herpetology, Natural History Museum of Zimbabwe, P.O. Box 240, Bulawayo, Zimbabwe

University of Kansas Natural History Museum and Biodiversity Institute, Department of Ecology and Evolutionary Biology, University of Kansas, Dyche Hall, 1345 Jayhawk Blvd, Lawrence, KS 66045-7593, USA

Guana Tolomato Matanzas National Estuarine Research Reserve, Ponte Vedra, FL 32082, USA

3/1 Boat Club Road, Pune 411 001, Maharashtra, India

Sección Zoología Vertebrados, Facultad de Ciencias & Museo Nacional de Historia Natural, Montevideo, Uruguay

Department of Biological Sciences, George Washington University, 2023 G St. NW, Washington, DC 20052, USA

Departamento de Biología, Universidad del Valle, Cali, Colombia

University of California, Berkeley, CA 94720-3160, USA

Instituto Tecnológico de Chetumal, Av. Insurgentes No. 330, C.P. 77013, Col. David Gustavo Gt., Chetumal, Quintana Roo, Mexico

School of Biological Sciences, Monash University, Clayton, Victoria 3800, Australia
69 Laboratório de Zoologia de Vertebrados, Universidade Estadual do Rio de Janeiro (LAZOVERTE - UERJ), Brazil
70 Université Cadi Ayyad, Département de Biologie, BP: 2390, Marrakech, Morocco
71 Fundacion Amigos de la Naturaleza, Santa Cruz de la Sierra, Bolivia
72 Department of Biology, California State University, Northridge, Northridge, California 91330-8303, USA
73 Karumbe, D. Murillo 6334, Montevideo, Uruguay
74 Chengdu Institute of Biology, Chinese Academy of Sciences, P.O. Box 416, Chengdu, Sichuan, China
75 Xuzhou Normal University, Jiangsu Province, China
76 Texas A&M University, 210 Nagle Hall, College Station, TX 77843-2258, USA
77 Museo de Zoología, Fac. De Ciencias, Universidad Nacional Autónoma de México (U.N.A.M.), Mexico
78 Universidade Federal da Paraíba, Rio Tinto, PB, Brazil
79 American Museum of Natural History, Central Park West at 79th St., New York, NY 10024, USA
80 Instituto de Ecología, A. C., Xalapa 91070, Veracruz, Mexico
81 University of Minnesota, Minneapolis, MN 55455, USA
82 Chennai Snake Park, Rajbhavan post, Chennai 600 022, Tamil Nadu, India
83 Department of Natural Resources, Puerto Rico
84 Museo de Zoología, UNELLEZ-Guanare, Venezuela
85 Biology Department, University of San Carlos, Cebu, Philippines
86 GeoBio Center, Ludwig-Maximilians-Universität München, Richard-Wagner-Str. 10, 80333 München, Germany
87 Institute for Applied Ecology, University of Canberra, ACT 2601, Australia
88 Nature Protection Trust of Seychelles, 133 Cherry Hinton Road, Cambridge CB1 7BX, UK
89 Whittier College, Department of Biology, Whittier, CA 90608, USA
90 Edward Grey Institute for Field Ornithology, Department of Zoology, University of Oxford, South Parks Road, Oxford OX1 3PS, United Kingdom
91 Department of Zoology, Natural History Museum, London SW7 5BD, UK
92 San Diego Zoo's Institute for Conservation Research, 15600 San Pasqual Valley Road, Escondido, CA, 92027, USA
93 Department of Biological Sciences, University of Texas at El Paso, 500 West University Avenue, El Paso, TX 79968, USA
94 Istituto per le Piante da Legno e l’Ambiente, corso Casale 476, I-10132 Torino, Italy
95 Yibin University, Sichuan, China
96 Department of Ecology and Evolutionary Biology, University of California, Los Angeles, California 90036, USA
97 University of Otago, 364 Leith Walk, Dunedin 9016. PO Box 56, Dunedin 9054, New Zealand
98 Department of Biology, Pennsylvania State University, University Park, PA, 16802 USA
99 University of the Free State, P.O. Box 339, Bloemfontein 9300, South Africa
100 Species Programme, IUCN, 219c Huntingdon Road, Cambridge, CB3 0DL, UK
101 Department of Conservation, P O Box 10-420, Wellington 6143, New Zealand
102 Department of Herpetology, San Diego Natural History Museum, P.O. Box 121390, San Diego, California 92112, USA
103 South Australian Museum, North Terrace, Adelaide SA 5000, Australia
104 Muséum National d'Histoire Naturelle, UMR CNRS 7205 (Origine, Structure et Evolution de la Biodiversité), Département Systématique et Évolution, CP 30, 25 rue Cuvier, F-75005 Paris, France
105 Department of Biology, Earlham College, Richmond, Indiana 47374, USA
106 Center for Advanced Studies in Ecology and Biodiversity (CASEB), Catholic University of Chile, Santiago, Chile
107 University of Aberdeen, School of Biological Sciences, Aberdeen AB24 2TZ, Scotland
108 State Natural History Museum (Staatliches Naturhistorisches Museum), Pockelsstr. 10, 38106 Braunschweig, Germany
109 Bohol Island State University, Bohol, Philippines
110 Pamukkale University, Department of Biology, Denizli, Turkey
111 Research School of Biology, The Australian National University, Canberra, ACT 0200, Australia
112 Senckenberg Forschungsinstitut und Naturmuseum, Senckenberganlage 25, D-60325 Frankfurt, Germany
113 School of Animal Biology, The University of Western Australia, 35 Stirling Highway, Crawley, Perth, Western Australia 6009, Australia
114 Dokuz Eylül University, Faculty of Education, Department of Biology, Buca, Izmir, Turkey
Staatliches Museum für Naturkunde Stuttgart, Zoologie, Rosenstein 1, D-70191 Stuttgart, Germany

Laboratorio de Biogeografía, Escuela de Geografía, Facultad de Ciencias Forestales y Ambientales, Universidad de Los Andes, Apartado Postal 116, Merida, 5101-A, Venezuela

University of Texas at Tyler, 3900 University Blvd., Tyler, TX 75799, USA

Faculty of Veterinary Science, University of Sydney, NSW 2006, Australia

Colorado State University, Fort Collins, Colorado, 80523, USA

Australian Freshwater Turtle Conservation & Research Association (AFTCRA Inc.), 53 Jubilee Road, Carters Ridge, Queensland, Australia

Kadoorie Farm & Botanic Garden, New Territories, Hong Kong SAR

Universidad Autonoma de Ciudad Juarez, Chihuahua, Mexico

Zoo Atlanta, 800 Cherokee Avenue, SE Atlanta, Georgia 30315, USA

Global Viral Forecasting Initiative, Cameroon

Illinois Wesleyan University, Bloomington, Illinois 61702-2900, USA

Environment and Resource Science Division, Department of Environment and Resource Management, Australia

WildScreen, Ground Floor, The Rackhay, Queen Charlotte Street, Bristol BS1 4HJ, UK

Department of Zoology, University of Cambridge, CB2 3EJ, UK

Universidad Juárez Autónoma de Tabasco, División Académica de Ciencias Biológicas, Villahermosa, Tabasco, México

Centre of Environmental Studies Demetra, via Olona 7, 00198 Roma, Italy

University of California, Irvine, California 92697, USA

ARC Centre of Excellence for Coral Reef Studies, James Cook University, Townsville, QLD, 4811, Australia

Staatliche Naturhistorische Sammlungen Dresden, Museum für Tierkunde, Königsbrücker Landstr. 159, D-01109 Dresden, Germany

Natural History Museum of Crete, University of Crete, 71409 Irakleio, Greece

Department of Biology, Merritt College, 12500 Campus Drive, Oakland, CA 94619, USA

Instituto Nacional de Pesquisas da Amazônia, Av. André Araújo, 2936, Aleixo, CEP 69060-001, Manaus, Amazonas, Brazil

Department of Organismic and Evolutionary Biology & Museum of Comparative Zoology, Harvard University, Cambridge, MA 02138, USA
1 School of Biological Sciences, College of Natural Sciences, Bangor University,
Deiniol Road, Bangor LL57 2UW
2 Museum of Natural History, Route de Malagnou 1, 1208 Geneva, Switzerland
3 School of Animal, Plant and Environmental Sciences, University of the
Witwatersrand, P.O. Wits 2050, South Africa
4 Laboratório de Herpetologia, Instituto Butantan, Av. Vital Brazil 1500, São Paulo,
SP, 05503-900, Brazil
5 Fonoteca Zoológica, Dept Biodiversidad y Biologia Evolutiva, Museo Nacional de
Ciencias Naturales (CSIC), José Gutierrez Abascal 2, 28006 Madrid, Spain
6 BIOGES, University of Las Palmas, 35001 Las Palmas, Canary Islands, Spain
7 Zoological Survey of India, North Eastern Regional Centre,
Fruit Garden, Risa Colony, Shillong - 793003, Meghalaya, India
8 Wildlife Trust for India (WTI), Species Recovery Program, India
9 Department of Biological Sciences, University of Wisconsin-Parkside, Kenosha, WI
10 53141, USA
11 Smithsonian Institution Research Associate
12 South African National Biodiversity Institute, Private Bag X7, Claremont 7735, Cape
Town, South Africa
13 Evolutionary Genomics Group, Department of Botany and Zoology, University of
Stellenbosch, Private Bag X1, Matieland 7602, South Africa
14 Instituto Tecnológico de Huejutla, Carr. Huejutla-Chalahuiyapa, A.P. 94, Huejutla de
Reyes, Hidalgo, 43000, Mexico
15 Museo Tridentino di Scienze Naturali, Via Calepina 14, 38122, Trento, Italy
16 Ch. du Bosquet 6, 1967 Bramois, Switzerland
17 CSIRO Marine and Atmospheric Research, PO Box 120, Cleveland 4163
Queensland, Australia
18 Truman State University, Kirksville, MO 63501, USA
19 Universidade Tuiuti do Paraná, Curitiba, Parana State, Brazil
20 Departamento de Biologia e Zoologia, Instituto de Biociências, Universidade Federal
do Mato Grosso, Cuiabá, Brazil
21 El Colegio de la Frontera Sur, Chiapas, México
22 Field Museum of Natural History, 1400 S. Lake Shore Dr, Chicago, IL 60605-2496,
USA
23 Institute of Ecology and Biological Resources, 18 Hoang Quoc Viet St., Hanoi,
Vietnam
1. Göteborg Natural History Museum, Box 7283, SE-402 35 Göteborg, Sweden
2. Departamento de Zoologia, Universidade de Brasilia, ICC Ala Sul - Campus Darcy Ribeiro, Asa Norte, Brasilia-DF, 70910-900, Brazil
3. Museo Nacional de Historia Natural, Interior de la Quinta Normal, Santiago, Chile
4. Institute of Natural and Environmental Sciences, University of Hyogo, Yayoigaoka 6, Sanda, Hyogo 669-1546, Japan
5. Medio Ambiente, Salud & Seguridad Ocupacional, Aerodom SIGLO XXI, Dominican Republic
6. Museum of Vertebrate Zoology, 3101 Valley Life Sciences Building, University of California, Berkeley, CA 94720-3160, USA
7. University of Tennessee, Knoxville, TN 37996, USA
8. Département des Vertébrés Récents, Institut Royal des Sciences naturelles de Belgique, Rue Vautier 29, 1000 Brussels, Belgium
9. Facultad de Biología, Universidad de Salamanca, Salamanca, Spain
10. Universidad de Puerto Rico, Puerto Rico
11. Integrative Biology C0930, The University of Texas at Austin, One University Station, Austin, Texas 78712-0253, USA
12. Dep Animal Biology, Fac Sciences, Granada Univer, E-18071 Granada, Spain
13. Bosque Tropical, A. C., Privada Marlin # 10, Fraccionamiento Roca Azul, Jocotepec 45800, Jalisco, Mexico
14. Department of Biology, Avila University, Kansas City, Missouri 64145, USA
15. Museo Tridentino di Scienze Naturali, Via Marconi 60, Cura Carpignano (PV), 27010, Italy
16. Universidad Autónoma de Aguascalientes, C. P. 20131, Aguascalientes, Mexico
17. School of Biological Sciences A08, University of Sydney, NSW 2006, Australia
18. Indianapolis Zoo, Indianapolis, IN 46222, USA
19. School of Conservation, The Royal Danish Academy of Fine Arts, Esplanaden 34, DK-1263 Copenhagen K, Denmark
20. USGS Patuxent Wildlife Research Center, National Museum of Natural History, Washington, USA
21. Fauna & Flora International – Philippines, 182 Saya St Biga 1, Silang, Cavite 4118 Philippines
22. Department of Invertebrate Zoology, Museo Tridentino di Scienze Naturali, Via Calepina 14, 38122 Trento (Italy)
Abstract
Effective conservation action requires knowledge of the distribution of threatened species and the threat processes affecting them. We present the first global assessment of extinction risk for a random representative sample of 1,500 reptile species. We find strong variation in extinction risk by taxonomic groups and geographic regions, with the most threatened reptiles associated with freshwater environments, tropical regions, and oceanic islands. Extinction risk is predominantly associated with habitat loss and over-exploitation. Our results emphasize the need for research attention to be focussed on tropical areas, which are seeing the highest extinction risk, and fossorial reptiles, for which there is a chronic lack of data.

Introduction
Throughout their 300 million year history [1], reptiles have adapted to almost every temperate, tropical and marine habitat. They play important roles in natural systems, as prey, predators, and commensal species, serve as important bioindicators for environmental health, and provide the ideal study system to illustrate the biological and evolutionary processes that underlie speciation events [2, 3]. Small ranges and
narrow niche requirements make reptiles particularly susceptible to anthropogenic threat processes, and therefore a group of conservation concern. Regional assessments in Europe and South Africa indicate that between one-tenth and one-fifth of reptile species may be threatened with extinction [4, 5].

More than 9,000 species of reptile have so far been described [6], yet as a group they are poorly-represented on the IUCN Red List of Threatened Species. This limits our understanding of threats to reptiles, and thus the group is often overlooked in conservation decisions. However, a comprehensive global assessment of all reptile species is impractical in a short time frame. We present the results of the first assessment of the conservation status of a randomly selected, representative, and global sample of 1,500 reptile species, as a shortcut for deriving extinction risk patterns on which to base sound conservation action. In this study, we consider reptiles to include the various taxa that make up the informal group of non-avian and non-mammalian amniotes: Crocodylia, Testudines, Squamata (snakes, lizards, amphisbaenians) and Rhynchocephalia (tuataras). We produce the first global species and threatened species richness maps for reptiles. The results highlight key regions, taxa and anthropogenic threat processes which need to be urgently targeted to effectively conserve the world’s reptiles.

Methods

We randomly selected 1,500 species from a list of all described reptile species [6], as set out in [7]. This represents a manageable yet sufficiently large sample size to report on conservation status and trends, while buffering against falsely detecting improvements in extinction risk [7].

Our sample closely reflected the contribution of each taxa towards total reptile diversity: 58% lizards, 37% snakes, 3% turtles/tortoises, 2% amphisbaenians, <1% crocodiles. Overall, 220 of the sample species had been previously assessed by IUCN; new or updated assessments were produced for the remaining 1,280 species, following the IUCN Red List Categories and Criteria [8].

Threats were recorded for each species, and were broadly defined as: habitat loss; invasive alien species; targeted harvesting; accidental mortality (e.g., unintentional trapping); persecution; pollution; natural disasters and climate-related threats; changes in native species dynamics (e.g., predators); intrinsic factors (e.g., restricted range); human disturbance (including fire). Further sub-division allowed the
causes of each to be identified (e.g., habitat loss due to agriculture; targeted harvesting for food; etc.).

Distributions were mapped in ArcGIS for 1,496 species (four species lacked adequate distributional data). We produced maps of global species richness, threatened species richness and Data Deficient species richness, by overlaying a hexagonal grid onto the aggregated species’ distributions. The grid is defined on an icosahedron, projected to the sphere using the inverse Icosahedral Snyder Equal Area (ISEA) Projection, and takes account of the Earth’s spherical nature. We then summed the number of species occurring in each hexagonal grid cell (cell size was approximately 23,300 km$^2$).

We mapped underlying threat processes for all 1,496 mapped species as the number of species within each grid cell affected by the threat process in question. Although coarse in resolution, these aggregations provide an impression of those locations where each threat is affecting a particularly large number of species.

We summarized conservation status across all reptiles and sub-groups (amphisbaenians; crocodiles; lizards; snakes; turtles/tortoises), biogeographical realm, and habitat system (terrestrial; freshwater or marine). We calculated proportions of threatened (Critically Endangered, Endangered and Vulnerable) and Near Threatened species by assuming that Data Deficient species will fall into these categories in the same proportion as non-Data Deficient species. We calculated upper and lower bounds of threat proportions by assuming that (a) no Data Deficient species were threatened (lower margin), and (b) all Data Deficient species were threatened (upper margin).

We followed Bielby et al. [9] to analyse whether extinction risk was randomly distributed across taxonomic families (following Uetz [6], but including some Australasian geckos in the Diplodactylidae [10]), and tested for significant variation in threat levels across families using a chi-square test. Where we detected taxonomically non-random extinction risk, further analyses determined which families deviated from the expected level of threat. Using binomial tests, we calculated the smallest family size necessary to detect a significant deviation from the observed proportion of threatened species and excluded families represented by an insufficient number of species from subsequent analysis. We generated a null frequency distribution of the number of threatened species from 10,000 unconstrained randomizations, by randomly assigning Red List categories to all remaining species.
We then counted the number of threatened species in the focal family and compared this with the null frequency distribution. The null hypothesis (extinction risk is taxonomically random) was rejected if this number fell in the 2.5% at either tail.

Results and discussion
In this paper, we are starting to close the knowledge gap between the conservation status of reptiles and other better-studied vertebrate groups. We estimate the true percentage of globally threatened reptile species to be 20% (16-36%). A further 6% of species are Near Threatened (4-24%) and likely to become threatened in the future unless causes of threat are mitigated. There were no extinct species in our sample, although three Critically Endangered species may already be extinct.

Threat proportions in terrestrial environments mirrored those recorded for all reptiles, while marine and freshwater reptiles were overall more threatened (28%; Table 1). Overall, 52% of freshwater turtles were classed as threatened (46–57%), thus confirming recent reports of high levels of threat in freshwater habitats (e.g. [11]). As a whole, 49% of turtles and tortoises were estimated as threatened (44–54%; Table 1); another 27% were Near Threatened (24–35%).

Recently reported declines in snake and lizard populations [12, 13] were not all corroborated in our study. While we estimated that 22% of lizards were threatened (18-36%), snakes were overall the least threatened group of reptiles (13% threatened, 11-32%; Table 1). However, the coarse nature of Red List categories may result in time-lags between population declines and changes in Red List status [14], so that recent population changes may not yet reflect in our data. We found some snake families (e.g. vipers, Elapids, Typhlopids) significantly more threatened than expected, while the Colubridae were the only family significantly less threatened than expected (Table 2).

Reptiles are particularly sensitive to habitat degradation because of their comparatively low dispersal ability, morphological specialization on substrate type, relatively small home ranges, and thermoregulatory constraints [23]. Habitat loss from agricultural conversion and logging was by far the predominant threat to terrestrial threatened reptiles, followed by human disturbance, invasive species and targeted harvesting. For marine and freshwater reptiles, targeted harvesting, predominantly for food and the pet trade, was the principle threat, followed by habitat loss, human disturbance and pollution.
High proportions of Data Deficiency can significantly hinder our understanding of threat. Data deficiency was highest in tropical regions (Table 1), especially the Malayan peninsula and Southern India (Fig. 1C), and in exclusively fossorial or semi-fossorial reptiles (e.g., Amphisbaenia: 50% Data Deficient, 7% (3.6–54%) threatened; Table 1). Similarly, in the amphibian assessments, approximately two-thirds of caecilians were classified as Data Deficient [15]. Yet, fossorial species potentially comprise around 20% of the world’s herpetofauna [16]. It is clear that research attention should specifically focus on fossorial and other elusive taxa (e.g. arboreal species).

Conservation priorities often focus on regions of high biodiversity value and/or high threat to effectively target conservation funds [17]. The assessment of biodiversity value is often based on the distribution patterns for certain indicator taxa, (e.g. birds), and the effectiveness of the resulting prioritisation mechanism greatly depends on the degree to which such distribution patterns are congruent with those of other taxa. Amphibians and reptiles are thought to have been greatly overlooked in reserve selection strategies based on such coarse-scale biodiversity surrogate measures [22]. Reptile species richness in our study broadly mirrored species richness patterns observed in mammals, amphibians and birds [18-20], with centres of high species richness and threatened species richness in the tropics of South America, Africa and Southeast Asia (Fig. 1A&B). However, species richness patterns are not always congruent and can vary with given metrics of biodiversity [21]. In addition to these congruent hotspots, parts of Africa (around the Gulf of Guinea and Southern Africa) were also rich in reptile species (Fig. 1A). Islands (e.g., the Caribbean, Sri Lanka, New Caledonia) had high proportions of threatened reptile species (Fig. 1B). Our results provide the opportunity for a more representative view of biodiversity to be compiled, in order to benefit multiple taxa.

Assessing the global distribution of threat processes – current and projected – could become another powerful tool for conservation prioritization. For example, the threat of human-induced climate and land use change does not appear to overlap with areas of endemic or threatened terrestrial vertebrate richness [24], which are currently favoured as priority mechanisms. Clearly, the distribution and severity of threat processes, such as habitat loss and overexploitation, will shape the future fortune of reptiles. We show habitat loss to be the predominant threat in tropical regions, particularly in mainland Southeast Asia, Sri Lanka, Indonesia, the Philippines and
Borneo (Fig. 2A), Central America, the Andean and Tumbes-Choco regions of northwestern South America, the Caribbean and the northeastern rainforests of Madagascar. Harvesting is a major concern in the Indomalayan realm (Fig. 2B). Invasive species increase extinction risk on islands, particularly in New Caledonia, Oceania, New Zealand and on Caribbean islands, yet relatively low frequencies in our sample mask any global-scale patterns. By tackling the origins and effects of anthropogenic threats through targeted projects, particularly in areas affected by multiple threat processes, such as Southeast Asia, we can find the key to securing the future of reptiles.

Acknowledgements

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References


Table 1. Conservation status of a subsample of 1,500 reptiles by order, biogeographic realm and habitat system: DD, Data Deficient; LC, Least Concern; NT, Near Threatened; Thr, threatened, Descr, number of described species. Fossorial reptiles include the families Amphisbaenidae, Trogonophidae, Anomalepididae, Leptotyphlopidae and Typhlopidae, Dibamidae, Uropeltidae and Xenopeltidae.

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<th>NT</th>
<th>Thr</th>
<th>N</th>
<th>Descr</th>
<th>% sampled</th>
<th>% Thr</th>
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<td>235</td>
<td>1500</td>
<td>9247</td>
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<td>19.6</td>
<td>15.7 - 35.7</td>
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### Realm

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<th>% NT</th>
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### Habitat system

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<td>295 875 66 231 1467</td>
<td>19.7</td>
<td>15.7 - 35.9</td>
<td>5.6</td>
<td>4.5 - 24.6</td>
</tr>
<tr>
<td>Freshwater &amp; marine</td>
<td>15 42 14 22 93</td>
<td>28.2</td>
<td>23.7 - 39.8</td>
<td>17.9</td>
<td>15.1 - 31.2</td>
</tr>
<tr>
<td>Fossorial</td>
<td>49 48 3 7 107</td>
<td>12.1</td>
<td>6.5 - 52.3</td>
<td>5.2</td>
<td>2.8 - 48.6</td>
</tr>
</tbody>
</table>
Table 2. Threat distribution across families included in our random sample of 1,500 species: ns, not significant; - significantly under threatened; + significantly over threatened.

<table>
<thead>
<tr>
<th>Family</th>
<th>Proportion observed</th>
<th>Proportion expected</th>
<th>Total species (non-DD)</th>
<th>&gt;Expected threat level p-value</th>
<th>&lt;Expected threat level p-value</th>
<th>Over or under threatened</th>
</tr>
</thead>
<tbody>
<tr>
<td>Agamidae</td>
<td>0.065</td>
<td>0.052</td>
<td>62</td>
<td>0.202</td>
<td>0.798</td>
<td>+</td>
</tr>
<tr>
<td>Amphibolidae</td>
<td>0.071</td>
<td>0.012</td>
<td>14</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Anguidae</td>
<td>0.313</td>
<td>0.013</td>
<td>16</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Anomalepididae</td>
<td>0.000</td>
<td>0.002</td>
<td>2</td>
<td>0.363</td>
<td>0.637</td>
<td>ns</td>
</tr>
<tr>
<td>Atractaspidae</td>
<td>0.000</td>
<td>0.006</td>
<td>7</td>
<td>0.785</td>
<td>0.215</td>
<td>ns</td>
</tr>
<tr>
<td>Boidae</td>
<td>0.167</td>
<td>0.010</td>
<td>12</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Chamaeleonidae</td>
<td>0.353</td>
<td>0.029</td>
<td>34</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
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<tr>
<td>Chelidae</td>
<td>0.500</td>
<td>0.008</td>
<td>10</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
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<tr>
<td>Colubridae</td>
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<td>0.226</td>
<td>269</td>
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<td>-</td>
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<tr>
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<td>0.007</td>
<td>9</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Crocodylidae</td>
<td>0.750</td>
<td>0.003</td>
<td>4</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Crotophytidae</td>
<td>0.333</td>
<td>0.002</td>
<td>3</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Diploactylidae</td>
<td>0.231</td>
<td>0.011</td>
<td>13</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Elapidae</td>
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<td>0.043</td>
<td>52</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Emydidae</td>
<td>0.167</td>
<td>0.005</td>
<td>6</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Gekkonidae</td>
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<td>142</td>
<td>0.038</td>
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<tr>
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<td>0.006</td>
<td>8</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
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<td>0.005</td>
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<tr>
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<td>0.028</td>
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<td>+</td>
</tr>
<tr>
<td>Homalopsidae</td>
<td>0.167</td>
<td>0.005</td>
<td>6</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Iguanidae</td>
<td>0.500</td>
<td>0.003</td>
<td>4</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Lacertidae</td>
<td>0.162</td>
<td>0.031</td>
<td>37</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
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<td>Leptotyphlopidae</td>
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<td>0.005</td>
<td>6</td>
<td>0.711</td>
<td>0.289</td>
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<tr>
<td>Pelomedusidae</td>
<td>0.000</td>
<td>0.003</td>
<td>4</td>
<td>0.573</td>
<td>0.427</td>
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<tr>
<td>Phrynosomatidae</td>
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<td>0.025</td>
<td>30</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Polychrotidae</td>
<td>0.302</td>
<td>0.053</td>
<td>63</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Pygopodidae</td>
<td>0.750</td>
<td>0.003</td>
<td>4</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Scincidae</td>
<td>0.230</td>
<td>0.139</td>
<td>165</td>
<td>&lt;0.001</td>
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<tr>
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<td>0.015</td>
<td>18</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
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<tr>
<td>Testudinidae</td>
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<td>0.006</td>
<td>7</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Trionychidae</td>
<td>0.333</td>
<td>0.002</td>
<td>3</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Tropidophiidae</td>
<td>0.333</td>
<td>0.003</td>
<td>3</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
<tr>
<td>Tropiduridae</td>
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<td>0.040</td>
<td>46</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
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<tr>
<td>Typhlopidae</td>
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<td>0.021</td>
<td>25</td>
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<td>1</td>
<td>+</td>
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<td>0.875</td>
<td>0.125</td>
<td>ns</td>
</tr>
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<td>+</td>
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<tr>
<td>Xantusiidae</td>
<td>0.750</td>
<td>0.003</td>
<td>4</td>
<td>&lt;0.001</td>
<td>1</td>
<td>+</td>
</tr>
</tbody>
</table>

The following families were excluded from the analysis (sample size too small): Acrochordidae, Anniellidae, Anomalepidae, Cheloniidae, Corytophanidae, Dibamidae, Helodermatidae, Hoplocercidae, Kinosternidae, Opluridae, Podocnemididae, Trogonophidae, Xenopeltidae.
Figure legends

Figure 1. Species richness of a) all mapped reptiles ($N = 1,496$), b) threatened reptiles in sample ($N = 235$), and c) Data Deficient reptiles in sample ($N = 301$), given as the proportion of species per grid cell. ( ), number of species in sample.

Figure 2. Global distribution of the two major threats to terrestrial and freshwater reptiles, a) habitat loss; b) harvesting, based on the species distributions in our representative sample (all IUCN categories included in analysis), and given as the number of species affected per grid cell.