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DATA ARTICLE

Expert range maps of global mammal distributions harmonised to three taxonomic authorities

Charles J. Marsh[1,2] | Yanina V. Sica[1,2] | Connor J. Burgin[3] | Wendy A. Dorman[1,2] | Robert C. Anderson[1,2] | Isabel del Toro Mijares[1,2] | Jessica G. Vigneron[1,2] | Vijay Barve[4] | Victoria L. Dombrowik[1,2] | Michelle Duong[1,2] | Robert Guralnick[4] | Julie A. Hart[1,2,5] | J. Krish Maypole[1,2] | Kira McCall[1,2] | Ajay Ranipeta[1,2] | Anna Schuerkmann[1,2] | Michael A. Torselli[1,2] | Thomas Lacher Jr[6,7] | Russell A. Mittermeier[7] | Anthony B. Rylands[7] | Wes Sechrest[7] | Don E. Wilson[8] | Agustín M. Abba[9] | Luis F. Aguirre[10] | Joaquín Arroyo-Cabrales[11] | Diego Astúa[12] | Andrew M. Baker[13,14] | Gill Braulik[15] | Janet K. Braun[16] | Jorge Brito[17] | Peter E. Busher[18] | Santiago F. Burneo[19] | M. Alejandra Camacho[19] | Paolo Cavallini[20] | Elisandra de Almeida Chiquito[21] | Joseph A. Cook[22] | Tamás Cserkész[23] | Gábor Csorba[23] | Erika Cuéllar Soto[24] | Valeria da Cunha Tavares[25,26] | Tim R. B. Davenport[27] | Thomas Deméré[28] | Christiane Denys[29] | Christopher R. Dickman[30] | Mark D. B. Eldridge[31] | Eduardo Fernandez-Duque[32] | Charles M. Francis[33] | Greta Frankham[31] | William L. Franklin[34] | Thales Freitas[35] | J. Anthony Friend[36] | Elizabeth L. Gadsby[37] | Guilherme S. T. Garbino[38] | Philippe Gaubert[39] | Norberto Giannini[40] | Thomas Giarla[41] | Jason S. Gilchrist[42] | Jaime Gongora[43] | Steven M. Goodman[44] | Sharon Gursky-Doyen[45] | Klaus Hackländer[46] | Mark S. Hafner[47] | Melissa Hawkins[8] | Kristofer M. Helgen[31] | Steven Heritage[48] | Arlo Hinckley[49] | Stefan Hintsche[50] | Mary Holden[51] | Kay E. Holekamp[52] | Rodney L. Honeycutt[53] | Brent A. Huffman[54] | Tatyana Humle[55] | Rainer Hutterer[56] | Carlos Ibáñez Ulargui[49] | Stephen M. Jackson[57] | Jan Janecka[58] | Mary Janecka[59] | Paula Jenkins[60] | Rimvydas Juškaitis[61] | Javier Juste[49] | Roland Kays[62] | C. William Kilpatrick[63] | Tigga Kingston[64] | John L. Koprowski[65] | Boris Kryštufek[66] | Tyrone Lavery[67] | Thomas E. Lee Jr[68] | Yuri L. R. Leite[69] | Roberto Leonan M. Novaes[70] | Burton K. Lim[71] | Andrey Lissovsky[72] | Raquel López-Antoñanzas[73] | Adrià López-Baucells[74] | Colin D. MacLeod[75] | Fiona G. Maisels[76,77] | Michael A. Mares[16] | Helene Marsh[78] | Stefano Mattioli[79] | Erik Meijaard[80] | Ara Monadjem[81,82] | F. Blake Morton[83] | Grace Musser[84] | Tilo Nadler[85] | Ryan W. Norris[86] | Agustina Ojeda[87] | Nicté Ordóñez-Garza[17] |

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[1]Department of Ecology and Evolutionary Biology, Yale University, New Haven, Connecticut, USA

[2]Center for Biodiversity and Global Change, Yale University, New Haven, Connecticut, USA

[3]Department of Biology, University of New Mexico, Albuquerque, New Mexico, USA

[4]Florida Museum of Natural History, University of Florida, Gainesville, Florida, USA

[5]New York Natural Heritage Program, State University of New York College of Environmental Science and Forestry, Albany, New York, USA

[6]Department of Ecology and Conservation Biology, Texas A&M University, College Station, Texas, USA

[7]Re:wild, Austin, Texas, USA

[8]National Museum of Natural History, Smithsonian Institution, Washington, District of Columbia, USA

[9]Centro de Estudios Parasitológicos y de Vectores (CEPAVE-UNLP-CONICET), La Plata, Buenos Aires, Argentina

[10]Centro de Biodiversidad y Genética, Universidad Mayor de San Simón, Cochabamba, Bolivia

[11]Laboratorio de Arqueozoologia, INAH, Alcaldia Cuauhtemoc, CdMx, Mexico

[12]Departamento de Zoologia, Universidade Federal de Pernambuco, Recife, Pernambuco, Brazil

[13]School of Biology and Environmental Science, Faculty of Science, Queensland University of Technology, Brisbane, Queensland, Australia

[14]Biodiversity and Geosciences Program, Queensland Museum, Brisbane, Queensland, Australia

[15]School of Biology, University of St. Andrews, St. Andrews, Fife, UK

[16]Sam Noble Museum, University of Oklahoma, Norman, Oklahoma, USA

[17]Instituto Nacional de Biodiversidad (INABIO), Quito, Ecuador

[18]College of General Studies, Boston University, Boston, Massachusetts, USA

[19]Sección Mastozoología, Museo de Zoología, Facultad de Ciencias Exactas y Naturales, Pontificia Universidad Católica del Ecuador, Quito, Ecuador

[20]Faunalia, Pontedera, Pisa, Italy

[21]Núcleo de Pesquisa em Evolução Animal, Universidade Federal do Espírito Santo, São Mateus, Espírito Santo, Brazil

[22]Museum of Southwestern Biology and Department of Biology, University of New Mexico, Albuquerque, New Mexico, USA

[23]Department of Zoology, Hungarian Natural History Museum, Budapest, Hungary

[24]Sultan Qaboos University, Muscat, Oman

[25]Vale Technological Institute, Belém, Pará, Brazil

[26]Laboratório de Mamíferos, Departamento de Sistemática e Ecologia, CCEN/DSE, Universidade Federal da Paraíba, João Pessoa, PB, Brazil

[27]Species Conservation & Science (Africa), Wildlife Conservation Society (WCS), Arusha, Tanzania

[28]Escondido, California, USA

[29]Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum national d'Histoire naturelle (CNRS), Paris, France

[30]Desert Ecology Research Group, School of Life and Environmental Sciences, The University of Sydney, Sydney, New South Wales, Australia

[31]Australian Museum Research Institute, Australian Museum, Sydney, New South Wales, Australia

[32]Department of Anthropology and School of the Environment, Yale University, New Haven, Connecticut, USA

[33]Canadian Wildlife Service, Environment and Climate Change Canada, Ottawa, Ontario, Canada

[34]Deparment of Natural Resource Ecology and Environment, Iowa State University, Ames, Iowa, USA

[35]Departamento de Genética, Universidade Federal do Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil

[36]Department of Biodiversity, Conservation and Attractions, Albany, Western Australia, Australia

[37]Pandrillus Foundation, Portland, Oregon, USA
[38]Departamento de Biologia Animal, Universidade Federal de Viçosa, Viçosa, Minas Gerais, Brazil
[39]Laboratoire Évolution & Diversité Biologique, Université Toulouse III Paul Sabatier, Toulouse, France
[40]Unidad Ejecutora Lillo, CONICET - Fundación Miguel Lillo, San Miguel de Tucumán, Tucumán, Argentina
[41]Department of Biology, Siena College, Loudonville, New York, USA
[42]School of Applied Sciences, Edinburgh Napier University, Edinburgh, UK
[43]Sydney School of Veterinary Science, Faculty of Science, The University of Sydney, Sydney, New South Wales, Australia
[44]Negaunee Integrative Research Center, Field Museum of Natural History, Chicago, Illinois, USA
[45]Department of Anthropology, Texas A&M University, College Station, Texas, USA
[46]Institute of Wildlife Biology and Game Management, University of Natural Resources and Life Sciences, Wien, Austria
[47]Museum of Natural Science, Louisiana State University, Baton Rouge, Louisiana, USA
[48]Duke Lemur Center, Museum of Natural History, Duke University, Durham, North Carolina, USA
[49]Estación Biológica de Doñana-CSIC, Sevilla, Spain
[50]Bruckmühl, Germany
[51]Department of Mammalogy, American Museum of Natural History, New York, New York, USA
[52]Department of Integrative Biology, Michigan State University, East Lansing, Michigan, USA
[53]Natural Science Division, Pepperdine University, Malibu, California, USA
[54]Whitby, Ontario, Canada
[55]Durrell Institute of Conservation and Ecology, School of Anthropology and Conservation, University of Kent, Canterbury, UK
[56]Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany
[57]Australian Museum Research Institute, Sydney, New South Wales, Australia
[58]Department of Biological Sciences, Duquesne University, Pittsburgh, Pennsylvania, USA
[59]Department of Biological Sciences, University of Pittsburgh, Pittsburgh, Pennsylvania, USA
[60]Mammal Group, Vertebrates Division, Department of Life Sciences, The Natural History Museum, London, UK
[61]Institute of Ecology, Nature Research Centre, Vilnius, Lithuania
[62]North Carolina Museum of Natural Sciences, Raleigh, North Carolina, USA
[63]Department of Biology, University of Vermont, Burlington, Vermont, USA
[64]Department of Biological Sciences, Texas Tech University, Lubbock, Texas, USA
[65]Haub School of Environment and Natural Resources, Laramie, Wyoming, USA
[66]Slovenian Museum of Natural History, Ljubljana, Slovenia
[67]Fenner School of Environment and Society, The Australian National University, Acton, Australian Capital Territory, Australia
[68]Department of Biology, Abilene Christian University, Abilene, Texas, USA
[69]Departamento de Ciências Biológicas, Universidade Federal do Espírito Santo, Vitória, Espiríto Santo, Brazil
[70]Instituto de Biologia, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Rio de Janeiro, Brazil
[71]Department of Natural History, Royal Ontario Museum, Toronto, Ontario, Canada
[72]Severtsov Institute of Ecology and Evolution RAS, Moscow, Russia
[73]Institut des Sciences de l'Évolution de Montpellier (ISE-M, UMR 5554, UM/CNRS/IRD/EPHE), Montpellier, France
[74]Natural Sciences Museum of Granollers, Granollers, Spain
[75]GIS In Ecology, Glasgow, UK
[76]Wildlife Conservation Society, Global Conservation Program, New York, New York, USA
[77]Faculty of Natural Sciences, University of Stirling, Stirling, UK
[78]Division of Tropical Environments and Societies, Centre for Tropical Water and Aquatic Ecosystem Research, James Cook University, Townsville, Queensland, Australia
[79]Research Unit of Behavioural Ecology, Ethology and Wildlife Management, Department of Life Sciences, University of Siena, Siena, Italy
[80]Borneo Futures, Bandar Seri Begawan, BA, Brunei Darussalam
[81]Department of Biological Sciences, University of Eswatini, Kwaluseni, Eswatini
[82]Department of Zoology & Entomology, Mammal Research Institute, University of Pretoria, Pretoria, South Africa
[83]Department of Psychology, University of Hull, Hull, UK
[84]Jackson School of Geosciences, University of Texas at Austin, Austin, Texas, USA
[85]Cuc Phuong Commune, Nho Quan District, Ninh BInh, Province, Vietnam
[86]Evolution, Ecology and Organismal Biology, The Ohio State University, Lima, Ohio, USA
[87]Instituto Argentino de Zonas Áridas (IADIZA)-CCT Mendoza-CONICET, Mendoza, Argentina
[88]Instituto de Diversidad y Evolución Austral (IDEAus-CONICET), Chubut, Argentina
[89]Universidade de São Paulo, São Paulo, Brazil

[90]NSW National Parks and Wildlife Service, Queanbeyan, New South Wales, Australia
[91]Rua Terezina, Cascavel, Paraná, Brazil
[92]Orlandia Avenue, Piracicaba, São Paulo, Brazil
[93]Instituto de Desenvolvimento Sustentável Mamirauá – IDSM, Tefé, Amazonas, Brazil
[94]La Conception, Quebec, Canada
[95]Department of Anthropology, San Diego State University, San Diego, California, USA
[96]School of Biological and Chemical Sciences, Queen Mary University of London, London, UK
[97]Department of Ecology and Evolutionary Biology, Princeton University, Princeton, New Jersey, USA
[98]Museo de Historia Natural, Universidad Nacional Mayor de San Marcos, Lima, Lima, Peru
[99]Institut des Sciences de l'Evolution (ISEM, UMR 5554 CNRS-IRD-UM), Université de Montpellier, Montpellier Cedex 5, France
[100]Institute of Wildlife Biology and Game Management, University of Natural Resources and Life Sciences, Vienna, Austria
[101]Department of Geography and the Environment, The University of Texas at Austin, Austin, Texas, USA
[102]Dublin Zoo, Phoenix Park, Dublin, Ireland
[103]Department of Anthropology and Museum Studies, Central Washington University, Ellensburg, WA, USA
[104]Department of Anthropology, Western Washington University, Bellingham, WA, USA
[105]Mitrani Department of Desert Ecology, Jacob Blaustein Institutes for Desert Research, Ben-Gurion University of the Negev, Midreshet Ben-Gurion, Israel
[106]Princess Maha Chakri Sirindhorn Natural History Museum, Prince of Songkhla University, Hatyai, Songkhla, Thailand
[107]Instituto de Biología, Universidad de Antioquia, Medellín, Colombia
[108]Kingscote, South Austalia, Australia
[109]IMBECU, CCT CONICET Mendoza – UNCuyo, Parque Gral. San Martín, Mendoza, Argentina
[110]Forestry Division, Food and Agriculture Organization of the United Nations, Rome, Italy
[111]Laboratório de Ecologia e Conservação da Natureza, Deptartamento de Ciências Ambientais, Universidade Federal de São Paulo (UNIFESP) - Campus Diadema, Diadema, São Paulo, Brazil
[112]University of Venda, Thohoyandou, South Africa
[113]Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, Hanoi, Vietnam
[114]Department of Anthropology, University of Oregon, Eugene, Oregon, USA
[115]Fundación Mamíferos y Conservación, Capelo, Rumiñahui, Ecuador
[116]Institute of Zoology, Zoological Society of London, London, UK
[117]Department of Fish, Wildlife, and Conservation Ecology, New Mexico State University, Las Cruces, New Mexico, USA
[118]Laboratory for Functional Morphology, Biology Department, University of Antwerp, Campus Drie Eiken, Antwerpen (Wilrijk), Belgium
[119]Institut de Systématique, Evolution, Biodiversité (ISYEB), Muséum national d'Histoire naturelle, CNRS, Sorbonne Université, EPHE, Université des Antilles, Paris, France
[120]Kasokwa-Kityedo Forest Project, Masindi, Uganda
[121]Biological Sciences, College of Science and Engineering, Flinders University, Adelaide, South Australia, Australia
[122]BEACON Center for the Study of Evolution in Action, Michigan State University, East Lansing, Michigan, USA
[123]Department of Fish, Wildlife and Conservation Biology, Colorado State University, Fort Collins, Colorado, USA
[124]Research Institute for the Environment and Livelihoods, Charles Darwin University, Casuarina, Northern Territory, Australia
[125]German Primate Center (DPZ), Leibniz Institute for Primate Research, Göttingen, Germany
[126]School of Life Sciences, Arizona State University, Tempe, Arizona, USA

Correspondence
Yanina V. Sica, Nathan S. Upham and Walter Jetz, Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT, USA.
Email: yanina.sica@yale.edu, nathan.upham@asu.edu and walter.jetz@yale.edu

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Abstract

Aim: Comprehensive, global information on species' occurrences is an essential biodiversity variable and central to a range of applications in ecology, evolution, biogeography and conservation. Expert range maps often represent a species' only available distributional information and play an increasing role in conservation assessments and macroecology. We provide global range maps for the native ranges of all extant mammal species harmonised to the taxonomy of the Mammal Diversity Database (MDD) mobilised from two sources, the *Handbook of the Mammals of the World* (HMW) and the *Illustrated Checklist of the Mammals of the World* (CMW).

Location: Global.

Taxon: All extant mammal species.

Methods: Range maps were digitally interpreted, georeferenced, error-checked and subsequently taxonomically aligned between the HMW (6253 species), the CMW (6431 species) and the MDD taxonomies (6362 species).
Results: Range maps can be evaluated and visualised in an online map browser at Map of Life (mol.org) and accessed for individual or batch download for non-commercial use.
Main conclusion: Expert maps of species' global distributions are limited in their spatial detail and temporal specificity, but form a useful basis for broad-scale characterizations and model-based integration with other data. We provide georeferenced range maps for the native ranges of all extant mammal species as shapefiles, with species-level metadata and source information packaged together in geodatabase format. Across the three taxonomic sources our maps entail, there are 1784 taxonomic name differences compared to the maps currently available on the IUCN Red List website. The expert maps provided here are harmonised to the MDD taxonomic authority and linked to a community of online tools that will enable transparent future updates and version control.

KEYWORDS
biodiversity, biogeography, conservation planning, GIS, Mammalia, mapping, species distributions

1 | INTRODUCTION

Expert range maps, hand-drawn polygons that demarcate the geographic distributions of species, have a long history in biogeography and ecology. Initially, they were established to visually illustrate the geographic limits of single or multiple species for educational and taxonomic purposes. Over time, they have also taken on an increasing role in conservation assessment and macroecology. The aim of range maps is typically to define the edges of a species' range, with limited scope for identifying 'holes' within that delimited area, which tends to be the focus of other methods for mapping distributions, such as species distribution models or atlases (Jetz et al., 2012).

Range maps represent aggregated expert knowledge and field experience that may implicitly incorporate both coarse and fine-grain information (Figure 1). For example, speciation history and physiographic barriers may provide information on the broad regions that a species occupies, and information on habitat preferences, published or unpublished occurrence records and local knowledge, may be used to delimit the range within that area. The extent to which range maps demarcate populations into separate polygons can also differ. An array of data sources and types may therefore be used to generate any given range map, and the combinations will vary across species and even between different regions of a given species' range. Range maps are particularly important where observation- or specimen-based occurrence records are sparse, such as in the tropics, where they may represent the only distributional knowledge of a species.

Over recent decades, expert range maps have gained further recognition as quantitative spatial objects that can be aggregated to map biogeographic patterns, including taxonomic richness, range size and population genetics (Fritz et al., 2016; Jetz & Rahbek, 2002; Kreft & Jetz, 2010; Lyons et al., 2019; Olalla-Tárraga et al., 2011), and they can be linked with trait or phylogenetic data for further inference (Faurby et al., 2018; Jarzyna et al., 2021; Mazel et al., 2017). Efforts such as Map of Life (MOL) have begun to combine expert range maps with other spatial biodiversity data for a more comprehensive understanding of species distributions (Jetz et al., 2012). They have also been used to identify areas of importance for threatened species and conservation priorities (Schipper et al., 2008), as well as for conservation assessments (Brooks et al., 2019; Pacifici et al., 2020). They are recognised as a central, maximum extent-delimiting data type supporting Species Distribution Essential Biodiversity Variables (SD EBVs), which provide information about the occurrence of species over a specific space–time grid at full taxon extent (Jetz et al., 2019).

However, expert range maps are limited by the somewhat ambiguous temporal scope of the distributions that they are describing (typically characterising recent distributions as records increase towards the present). Below spatial resolutions of ~100 km, they also have a false presence rate (Hurlbert & Jetz, 2007; Hurlbert & White, 2005) that covaries with ecological attributes (Ficetola et al., 2014; Jetz et al., 2008) and with technical aspects of the range map creation. For example, the distribution of a wide-ranging species will usually have a lower level of spatial detail captured within

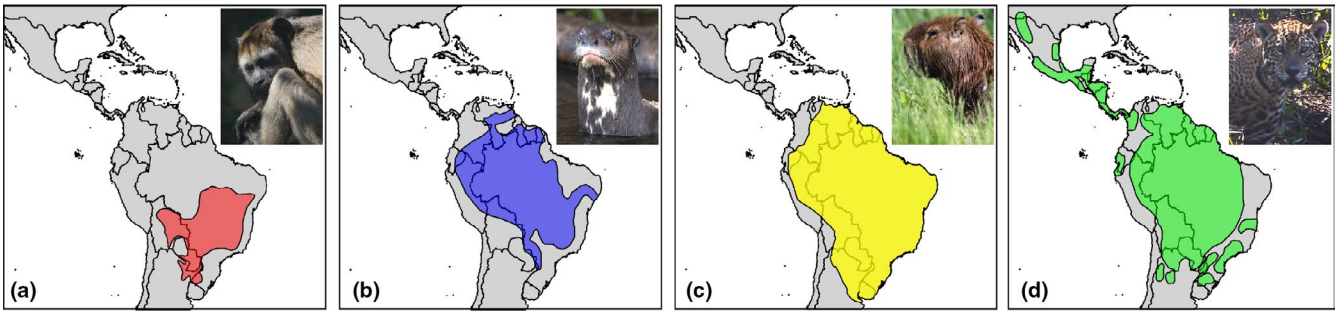

FIGURE 1 Range maps georeferenced from the *Handbook of the Mammals of the World* (HMW) for four South American species, (a) *Alouatta caraya*, (b) *Pteronura brasiliensis*, (c) *Hydrochoerus hydrochaeris* and (d) *Panthera onca*. Different maps species show different levels of precision (i.e., how roughly it approximates the edge of the species' range and how finely they demarcate different populations) and so will differ in their accuracy at different grain sizes

the range map than that of a narrow endemic, and geographically variable expert knowledge will result in range maps being more precise in some areas than others. The level of precision and uncertainty and the decisions made during the creation of a map are difficult to quantify and document. They can also quickly become out-of-date, often due to taxonomic revisions (e.g., species splits or merges) or range boundary changes (e.g., range shifts, or the discovery or extinction of subpopulations). Although separate polygons for introduced range components are sometimes included, range maps typically exclude introductions outside of the species' native ranges. Nevertheless, range maps continue to serve an important role, especially in combination with ancillary data such as species habitat preferences and land cover information to further refine species ranges and as one of several inputs into a new generation of model-based species distribution predictions (Merow et al., 2017; Pacifici et al., 2018; Powers & Jetz, 2019; Visconti et al., 2011).

Here, we provide fully georeferenced digital range maps for the native ranges of all extant species of mammals, globally harmonised to three taxonomies: the authoritative mammal taxonomy provided in the Mammal Diversity Database (MDD v1.2; Burgin et al., 2018), the *Handbook of the Mammals of the World* (HMW), which was published across nine volumes (Mittermeier et al., 2013; Wilson et al., 2016, 2017; Wilson & Mittermeier, 2009, 2011, 2014, 2015, 2018, 2019), and the *Illustrated Checklist of the Mammals of the World* (CMW; Burgin et al., 2020a, 2020b). Each of the three datasets are therefore represented by range maps for all species in each taxonomy, tracking any lumps or splits that occurred between them, as well as any name changes, updates to the ranges and newly described species. The maps are based primarily on the HMW and CMW, and, for the MDD, supplemented with spatial information from other primary source materials, where taxonomic revisions have occurred since the publication of the HMW and CMW compendia. The final range maps are not exact replicas of those published in any one source, as changes are introduced during the interpretation and georeferencing stages, as well as other processing steps, such as clipping to coastlines for terrestrial species.

The three taxonomic authorities represent different temporal snapshots of mammal taxonomy. The nine volumes of the HMW were published over the course of a decade. The CMW aimed to unify the HMW taxonomy into a single two-volume publication while providing updates to taxonomy and geographic ranges. The MDD was first published in 2018 as a joint effort of the American Society of Mammalogists and the National Science Foundation-supported VertLife Terrestrial project (vertlife.org) to centralise all published taxonomic changes to mammals as a freely available online database (mammaldiversity.org). The most recent version of the MDD builds upon the CMW and HMW compendia, but provides further updates to taxonomy, synonyms and primary reference information using a wide range of primary literature. The biggest change from the CMW to the MDD is the decision to revert the taxonomy of Bovidae, which follows Groves and Grubb (2011) in the former, to the older taxonomic arrangement presented by Grubb (Grubb, 2005a, 2005b) for the MDD v1.2 (see https://zenodo.org/record/4139818). The rest of the Perissodactyla and non-cetacean Artiodactyla also follow this older arrangement with some modifications (e.g., *Giraffa*; Petzold & Hassanin, 2020). The older arrangement is viewed as more stable and justifiable in the mammalogical community (Gutiérrez & Garbino, 2018; Holbrook, 2013), and results in a reduction of 124 extant species in the MDD taxonomy that had been split in the CMW.

The datasets presented in this publication follow the FAIR principles for data sharing (Wilkinson et al., 2016). They are freely accessible from a recognised formal data repository with no restrictions on reuse for non-commercial purposes, follow data and metadata standards that make them interoperable, and are stored in a well-known format for spatial data (shapefiles) making them fully reusable. The work represents a collaboration with the Mammal Diversity Database (https://www.mammaldiversity.org; Burgin et al., 2018; versions on Zenodo: https://doi.org/10.5281/zenodo.4139722), an authoritative effort to address and curate the global taxonomy of mammals conducted under the auspices of the American Society of Mammalogists.

With regard to the suite of range maps developed by experts as part of Red List assessments of the International Union for the Conservation of Nature (IUCN; https://www.iucnredlist.org/resources/spatial-data-download), the datasets presented in our data paper provide additional range information for many mammal species. The maps available on the IUCN Red List website represent

TABLE 1 Total number of extant, non-domesticated mammal species recognised in each taxonomic source: The *Handbook of the Mammals of the World* (HMW), the *Checklist of the Mammals of the World* (CMW), and version 1.2 of the Mammal Diversity Database (MDD). All species listed as domesticated and extinct have been removed from this summary

	HMW	CMW	MDD v1.2
Species	6253	6431	6362
Genera	1289	1310	1306
Orders	27	27	27
Species lacking georeferenced maps	5	3	2

fewer extant species (5829 species, including 20 species labelled as 'Possibly Extinct'; IUCN, 2021, downloaded 2021-06-03) than presented here (HMW = 6253 species, CMW = 6431 species, MDD = 6362 species; Table 1). This translates to 916, 998, and 946 species names (1227 species names across all three sources combined) in the HMW, CMW, and MDD, respectively, which are absent from the IUCN Red List website, as well as 557 species names within the IUCN taxonomy that are absent from the HMW, CMW, and MDD (total of 1784 differences in species names across sources). The range maps described here therefore provide much complementary material to those available through IUCN, and vice-versa.

We provide the georeferenced range maps as shapefiles with species-level metadata and source information for non-commercial use. Maps are available for bulk download at https://doi.org/10.48600/mol-7r3j-8066 (HMW), https://doi.org/10.48600/mol-zzrs-q778 (CMW) and https://doi.org/10.48600/mol-48vz-p413 (MDD), or all three sources can be accessed from https://mol.org/datasets/?dt=range&sg=Mammals. Maps for individual species can be viewed and downloaded, along with other species-level spatial data, on Map of Life's species pages (https://mol.org/species).

2 | MATERIALS AND METHODS

Range maps were generated by digitally interpreting the maps in the source materials (starting with the HMW), georeferencing them using coastlines, rivers and other geographical features and converting the georeferenced images to vector shapefiles, before quality control and assembling all the species from each source taxonomy into a unified product. To harmonise the HMW and CMW maps, we retained any maps from HMW in which there were no taxonomic or range updates and repeated the digitisation steps with the CMW as source material for any differences. For the MDD dataset, we generated maps for any differences using the HMW or CMW maps as a base along with information from alternative sources, such as published literature.

For the range maps with HMW as the main source, we imaged the maps from each volume, which were then georeferenced using the World Geodetic System projection (WGS84; EPSG: 4326) against the coastlines and political boundaries provided by the Database for Global Administrative Areas v3.6 (GADM; Global Administrative Areas, 2018). Additional spatial data such as rivers and waterbodies were used to determine more exact locations for ground control point placement. For each image, we used a minimum of 10 ground control points that were approximately evenly spaced to ensure constant warping during transformation.

The georeferenced images were converted to GeoTIFFs with cell size equivalent to the resolution of the image using a second-degree polynomial-type transformation with a nearest-neighbour resampling method. These rasters were converted to shapefiles by manually tracing range edges using either the Add Polygon Feature tool in QGIS (QGIS.org, 2020) or the Create Features panel in ArcMap and ArcGIS Pro. In cases where a species range consisted of geographically distinct areas, multipolygons were created. Due to their complexity, coastlines cannot be accurately captured via the tracing method; therefore, coastlines were only roughly outlined manually. Terrestrial species' geometries were subsequently clipped to the coastline of the GADM, while marine species' geometries were clipped to a global map of oceans (Global Administrative Areas, 2018). Species with both terrestrial and marine distributions, such as seals, were not clipped. For each completed species, we then carried out a series of quality controls (described within Technical Validation below).

Once validated, the total number of features in a volume was checked prior to merging. To ensure no geometries were lost during downstream processes, the combined shapefiles were disaggregated so that all geometries were separate before getting clipped, as described above. This clipped file was then merged back together, dissolved by scientific name, and exported as the combined geopackage consisting of range maps for all species. The number of individual features were checked again at the end of the process to confirm that no geometries were lost. Once a volume was completed, we carried out a second quality control to ensure all species in the volume were included, species names were spelled correctly, and that the geometry of each species was valid. Geometry issues were first fixed automatically using the Geospatial Data Abstraction Library (GDAL; GDAL/OGR contributors, 2020) and then using the Check Validity tool in QGIS (QGIS.org, 2020). If necessary, remaining self-intersections and sliver polygons were fixed by hand. In these cases, satellite images were used to verify any potential errors and help inform the decision of how to correct them.

2.1 | Harmonisation between data sources

To create the CMW dataset, range maps for each species in the CMW were compared to those in the HMW volumes. The majority of species did not exhibit range map changes from the HMW to the CMW, but 515 species required some degree of further edits (see the Supplementary Material). These edits fell into one of five categories (Table 2): (1) species that needed to be digitally interpreted from the maps published in the CMW, because they were newly described since the HMW (new species); (2) species that needed to be digitally

TABLE 2 Summary of taxonomic and geographical differences of extant, non-domesticated mammal species recognised in each taxonomic source: The *Handbook of the Mammals of the World* (HMW), the *Illustrated Checklist of the Mammals of the World* (CMW), and version 1.2 of the Mammal Diversity Database (MDD). All species listed as domesticated and extinct have been removed from this summary. Note that multiple categories can apply to a single taxonomic revision

	Differences in CMW from HMW	Differences in MDD v1.2 from CMW
Range changes	44	2
Name changes	146	66
Splits	94 species into 220 species	38 species into 97 species
Lumps	68 species into 32 species	210 species into 59 species
New species	95	20

interpreted directly from the CMW maps because their range changed substantially from the range in the HMW (range changes); (3) species from the HMW that had been taxonomically split into multiple species in the CMW (splits); (4) species in the HMW that had been taxonomically merged into a single species in the CMW (lumps) and (5) species in the HMW that had changes to the scientific name in the CMW taxonomy but no change in geographic range (name changes).

Source interpretation and georeferencing of new species was performed using the same methods as described above for the HMW. For splits, if the split occurred along clear geographical boundaries such as island populations, then the polygons of the original shapefiles were manually separated into child species. However, if the sum of child species was not equal to the range map of the parent species, then each child species was digitally interpreted from the CMW map. The same rule also applied for lumping multiple child species in HMW into a single CMW species. For name changes, the HMW-based shapefiles were simply renamed. The entire CMW dataset was combined into a single geopackage as described above.

Once conversion of shapefiles from the HMW to the CMW was complete, we then harmonised the CMW shapefiles to the MDD taxonomy to create the MDD dataset. The CMW maps were altered in the same way as described above, except using primary taxonomic descriptions to guide the modifications. For newly described species, range maps were derived directly from the source articles. If sources only presented the geocoordinates of a type specimen (type locality), then a range map was generated by buffering the point with a radius of 50 km. If range maps or type localities were not present in source materials, then range maps were hand-drawn following maps from the CMW as well as maps drawn by experts in support of the Red List assessment effort by IUCN (IUCN, 2020; necessary for 63 species or ~1% of the total), followed by error-checking. In all cases, the source materials used to generate each map are recorded in the species-level citation provided in the metadata of the shapefile for each species (see 'Usage notes' section below). Details of all differences between the HMW and CMW, and the CMW and MDD are presented in the supplementary material.

Two species in the CMW, HMW and MDD have no range maps as knowledge of their range is too limited (*Nycticeius aenobarbus* and *Phoniscus aerosus*). Two species have no range map in the HMW, but they have range maps within the CMW and MDD (*Biswamoyopterus laoensis* and *Ctenomys dorsalis*). One species has a range map in the MDD, but not in the CMW or HMW (*Makalata obscura*). Three species that feature in the HMW were considered extinct in the CMW and so were excluded from this dataset and the MDD (*Juscelinomys candango*, *Pipistrellus sturdeei* and *Tonatia saurophila*). In all three datasets, two species considered extinct in the wild are retained as their maps are published (*Elaphurus davidianus* and *Oryx dammah*).

All georeferencing and shapefile creation were carried out in QGIS 3.10.9-A Coruña (QGIS.org, 2020), ArcMap 10.7.1, and ArcGIS Pro 2.5.0. Quality checks and creation of geopackages was carried out in Python 3.8 in Jupyter Notebook 6.0.3 using the fiona (Gillies, 2011), geopandas (Gillies, 2007) and shapely (Jordahl et al., 2020) packages.

3 | TECHNICAL VALIDATION

The HMW maps were quality controlled by published volume. 10%–30% of images per volume were randomly sampled for manual inspection by a team-member other than the individual that had carried out the source interpretation and georeferencing. Images were checked for: (1) appropriate transformations and that the World Geodetic System (WGS84) was the reference coordinate system; (2) that each geometry accurately reflected the information in the raster and that no geometries were lost; (3) all geometries were valid; (4) no features were duplicated and (5) that metadata was complete and without translation errors in the scientific name. If over 15% of sampled species were reported to have errors, then the entire volume of species was checked again, otherwise the dataset was cleared for further processing. As there were fewer species to process for the CMW and MDD maps, all species maps were checked visually against the original source.

We also visually confirmed the aggregated products by generating global maps of species richness across all species of each taxonomic source (Figure 2). The richness maps were created by intersecting the range maps of each species with a global equal-area grid with cell widths of 0.5° and cell height variable by latitude in the Behrmann cylindrical equal-area projection in R 3.6.1 (R Core Team, 2019) using the sf package (Pebesma, 2018).

Even though the presented range maps are provided as polygons and thus not directly tied to a specific spatial resolution, it is vital to recognise the spatial grain limitations of expert range map data. At spatial grains smaller than 200 × 200 km, the presence of errors can be substantial; at grains below ~50–100 km edge length, this issue can render the presence information from these maps uninterpretable. Without further validation or inclusion of

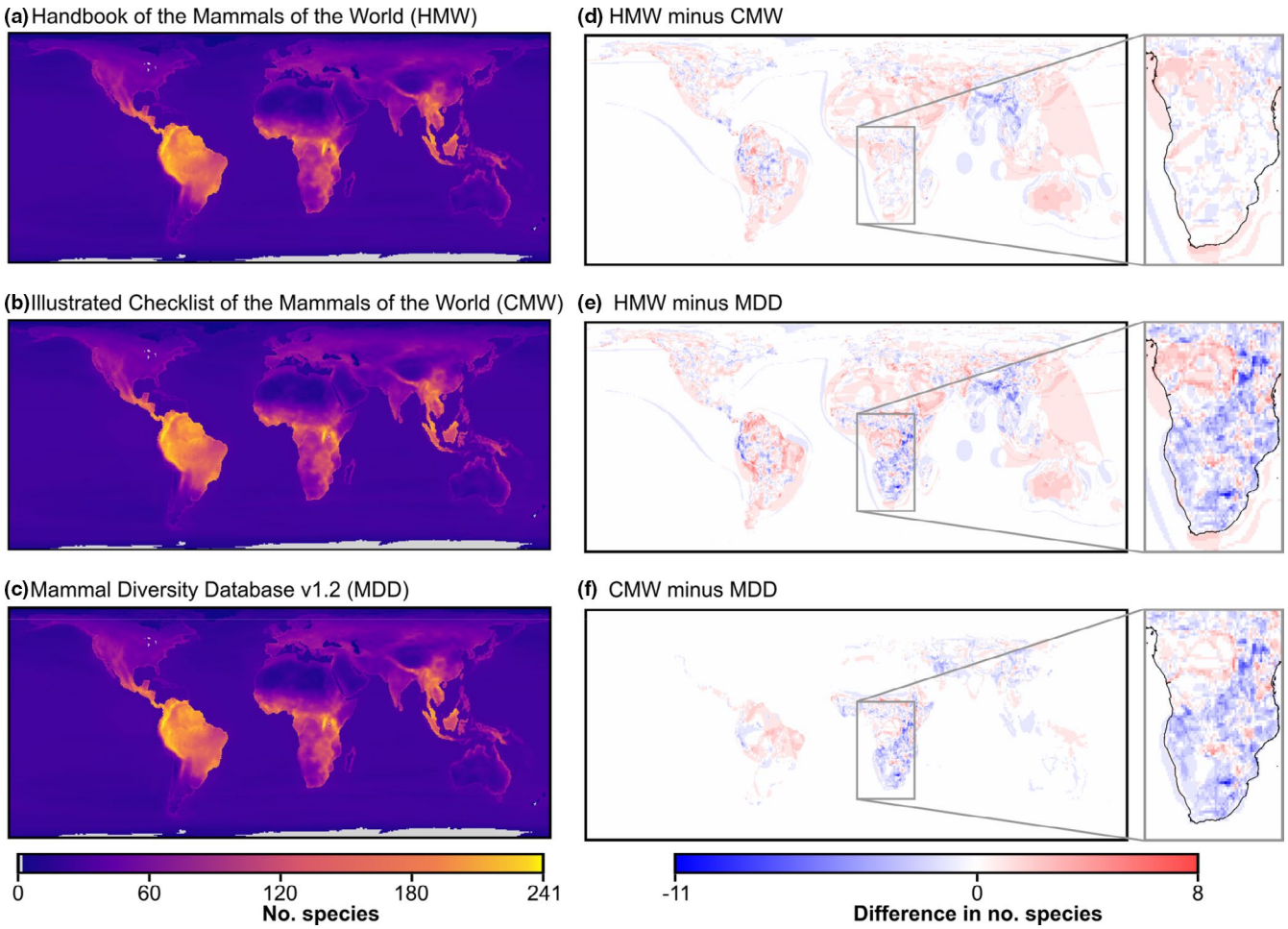

FIGURE 2 Global richness maps of terrestrial mammals generated by all species with digitisable range maps in (a) the *Handbook of the Mammals of the World* (HMW), (b) the *Illustrated Checklist of the Mammals of the World* (CMW) and (c) the CMW harmonised to the latest taxonomy from the Mammal Diversity Database (MDD), as well as the difference in species richness between (d) the HMW minus the CMW, (e) the HMW minus the MDD and (f) the CMW minus the MDD. Detailed regions (sub-Saharan Africa) for each map of difference are presented to the right, with main differences attributed to the inclusion (HMW, CMW) or exclusion (MDD) of ungulate species from Groves and Grubb (2011). Richness maps were generated by intersecting each species' range map with a global equal-area grid with cell widths of 0.5° and cell height variable by latitude in the Behrmann cylindrical equal-area projection

other data, expert range maps should not be analysed in single or aggregated form at grain sizes <200 × 200 km (Hurlbert & Jetz, 2007; Jetz et al., 2008).

3.1 | Comparisons with IUCN range maps

We constructed a richness map for range maps provided by experts to IUCN (6.2, accessed on 25/04/2021; IUCN, 2021) using the same intersections method as above and calculated the difference between the resulting richness map with that of the MDD. IUCN range maps include 30 additional polygon categories for some species based on combinations of information on current status, introductions, reintroductions, seasonality, vagrancy and certainty where possible. Although 90% of species are represented by only one category ('Extant [resident]'), for the remaining 597 species, users will need to pay close attention to subsetting only those categories relevant to their studies. For example, IUCN range maps include eight extinct (or extinct in the wild) species, as well as historical ranges and areas that have not been explored ('Not Mapped') for other species, which would potentially need to be excluded from analyses focussing on current distributions. Therefore, for an accurate comparison with our range maps, which include only native, extant ranges, we removed all polygons labelled as 'Probably Extant & Introduced (resident)', 'Extant & Introduced (resident)', 'Extinct & Introduced', 'Extinct', 'Introduced' and 'Not Mapped'.

There are considerable differences between the range maps provided in this data paper and IUCN (Figure 3), with differences of up to 158 species for a given 0.5° cell. First, there are differences between the range maps themselves due to differences in the information used to generate the maps, as well as considerations on how to treat absences within the wider distribution (i.e., how fine to resolve the boundaries and separate populations into individual polygons). The most appropriate range map will therefore depend not only on the accuracy of the information used to generate the maps but also on

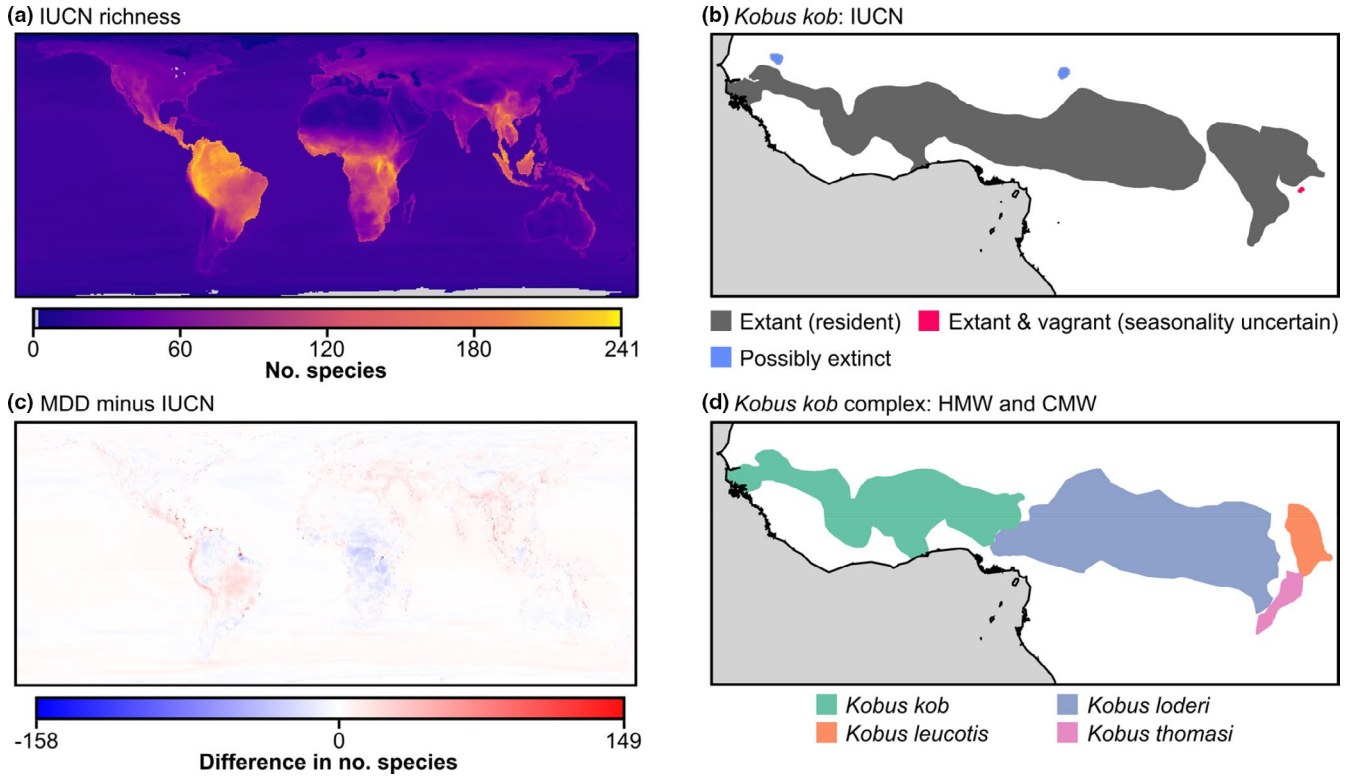

FIGURE 3 Comparisons with expert maps contributed to IUCN assessment. (a and c) Richness patterns and absolute differences with the Mammal Diversity Database (MDD) calculated as MDD minus IUCN (for details see Figure 2). (b and d) Map differences for the antelope *Kobus kob* in West and Central Africa. In the IUCN source (b), it is treated as a single species and includes information on the type of distribution and seasonality, but it is separated into four species in the *Handbook of the Mammals of the World* (HMW) and the *Illustrated Checklist of the Mammals of the World* (CMW) (d)

the user's objectives and study scale. Second, many of the differences can be attributed to differing treatments of coastlines and freshwater bodies. For example, IUCN range maps do not exclude Lake Victoria.

Finally, there are considerable differences in the taxonomic treatments (Table 3; Figure 3). Higher richness will be observed where a parent species has been split into multiple child species, and a given grid cell overlays the boundary between the ranges of the new species. Our data and associated taxonomic sources include more species than IUCN, with 7.2%, 10.3% and 9.1% more extant species in the HMW, CMW and MDD, respectively. Overall, this results in 1784 taxonomic differences from IUCN across the three sources. Taxonomic differences are spread widely across mammal groups. For example, there are differences in 16 out of 27 orders and 73 out of 167 families between the species represented in the MDD and IUCN range maps (Table 3). Of these, 289 are name differences (i.e., synonyms) between the MDD and IUCN, 121 species are present only within IUCN and not MDD, and 615 species are present in MDD and not IUCN, totalling over a thousand taxonomic differences in all (see the Supplementary material for details of all differences per taxonomy).

We therefore do not profess one set of range maps to be superior to another, but instead urge users to consider the most appropriate range map(s) for their specific use-case, based on the taxonomic treatments they wish to use, whether they wish to make modifications with regards to usage permissions, the purposes of the study in relation to the qualities each range map possesses, as well as the region under study. In particular, it is important to recognise the limitations that expert range maps generally have on the spatial grains at which they should be applied (Hurlbert & Jetz, 2007).

4 | DATA RECORDS

All three datasets are hosted primarily in Map of Life (MOL, mol.org), a scalable platform for the integration and use of global species occurrence and environmental data. The aim of MOL is to support effective and global biodiversity monitoring, research, education, and decision-making through the provision of tools and information products addressing global species distributions and their dynamics. MOL is deployed on the Google Cloud Platform, which provides the ability to work with managed, scalable services. The data is hosted within a PostgreSQL database with custom API built for both species information and mapping, which are driven by the need for various unique services that users require.

Individual mammal species maps are publicly available for visualisation and download (e.g., https://mol.org/species/map/Chaetodipus_nelsoni) under the 'Detailed Map' tab for any given species, along

TABLE 3 Differences between range maps of extant, non-domesticated mammal species from the Mammal Diversity Database (MDD) version 1.2 and range maps from the International Union for the Conservation of Nature (IUCN)

Order	Number of families with differences	Name difference	Species in MDD and not in IUCN	Species in IUCN and not in MDD
Afrosoricida	2	5	0	0
Artiodactyla	8	10	16	4
Carnivora	10	22	15	7
Chiroptera	12	81	137	31
Cingulata	1	1	2	1
Dasyuromorphia	1	1	8	2
Didelphimorphia	1	1	36	8
Diprotodontia	5	14	11	1
Eulipotyphla	3	27	65	7
Lagomorpha	2	1	14	1
Macroscelidea	1	2	1	0
Microbiotheria	1	0	2	0
Peramelemorphia	1	0	3	0
Pilosa	1	0	6	0
Primates	7	17	6	10
Rodentia	17	107	293	49

with other sources of spatial information. Each species is represented by a multipolygon that includes dataset- and species-level metadata, as well as the citation information. For convenience, in order to aid the download of large numbers of species, multiple species' shapefiles have also been packaged by taxonomic ranks (order and class). Each dataset is provided with a DOI, which links to the page where they can be accessed and downloaded. The MDD dataset will form the base for version-controlled updates to the range maps provided by Map of Life and a community of experts (see section 'Improvements and a framework for community-driven updates' below).

5 | IMPROVEMENTS AND A FRAMEWORK FOR COMMUNITY-DRIVEN UPDATES

Inevitably, there will be some inaccuracies in the range maps of some species. For example, precision is necessarily limited for wide-ranging species to ensure clarity when printed, and errors can be introduced in the printing and georeferencing procedures that get carried through to the final shapefiles. These errors will be more serious in wide-ranging species, where a small shift in printed pixels translates to larger geographic distances. Both precision and accuracy may be spatially variable as there may be little to no knowledge in parts of a species' range but much in another. Finally, range maps may be drawn using out-of-date knowledge, and the ranges of species may change over time. A larger goal of this data publication, therefore, is to provide a clearly referenced and open basis for future updates, and a transparent, open implementation to track changes in distributions, knowledge, and taxonomy (Jetz et al., 2012).

The data provided has no restriction on the non-commercial use and revision of maps. This might include the updating of maps to an alternative or new taxonomy, or spatial refinements, for example, to allow higher precision coastline and river information. The presented data will undoubtedly require further updates and improvements. We expect a range of such improvements to be provided through Map of Life, where new datasets will also support users with version-control. In order to support this larger vision for transparently and openly improved expert maps, a new tool, soon to be released, will provide an interactive environment for experts to evaluate and improve range maps (https://mol.org/expert-range-mapper-demo/welcome). The new toolset will allow range maps to be updated in a transparent and traceable manner, with all decisions directly attributable. We expect that this will allow users to clearly track version history of any particular range map, download the most appropriate map for their use case and provide additional information currently unavailable from traditional range maps. For example, areas where agreement between experts are low can potentially inform spatial uncertainty in downstream analyses.

The maps provided here only address native ranges and thus do not inform about the sometimes substantial and ongoing alien range expansions (Capinha et al., 2015; Seebens et al., 2017). Work is underway to include alien distribution data on Map of Life, incorporating information from the Global Register of Introduced and Invasive Species database (GRIIS; Pagad et al., 2018) and the global Distribution of Alien Mammals database (DAMA; Biancolini et al., 2021). While a different data type, this will enable timelier accounting for ongoing range dynamics.

Clearly, a variety of different steps are needed to generate, keep up-to-date, and maintain a geospatial resource addressing the

TABLE 4 Details of the metadata fields in the attributes of each species' shapefile

Metadata field	Description
sciname	The scientific name of the species
authors	The authors involved in generating the shapefile. As multiple people have been responsible over many years at multiple stages of georeferencing, processing and quality control, exact attribution of effort at the species-level is not always possible. The author list reflects current and past members of MOL who have been involved in the process in no particular order
year	The year the shapefile was published
rec_source	The original source(s) of the species map if different from the dataset_source, such as a chapter within the HMW or the journal article for more recent taxonomic changes
dataset_source	The main compendia or taxonomic source, i.e., the HMW volume, CMW or MDD

distribution of extant mammals and their changes over time. By drawing on an authoritative effort from mammal experts around the world and offering a fully open data resource to the community, we hope to contribute a useful advance to this larger quest.

6 | USAGE NOTES

There are two forms of citation that we recommend, depending on the usage. For citing at the dataset-level, we recommend a citation of both the dataset and the source (HMW, CMW or MDD), and this information can be found on the download page as well as a text file included with the download. Alternatively, at the species-level, each species' shapefile can be cited independently using the shapefile metadata, which includes the provenance of all information used to generate that species' range map (Table 4).

The recommended full citations are included under the column 'citation'. Where the HMW is the taxonomic source, they have been constructed as: <*sciname*>: <*authors*> (<*year*>) from map published in <*rec_source*> in <*vol_source*>.

Where the CMW is the taxonomic source then there is no species-level rec_source and the citation has been constructed as: <*sciname*>: <*authors*> (<*year*>) from map published in <*dataset_source*>.

Where the MDD is the taxonomic source, if there were no taxonomic revisions necessary from the CMW, then the CMW is also the species-level rec_source: <*sciname*>: <*authors*> (<*year*>) from map published in <*rec_source*> harmonised to <*dataset_source*>.

If taxonomic revisions were necessary and the maps were hand-drawn based on available information such as a journal article(s), then the rec_source reflects all the sources of the information used: <*sciname*>: <*authors*> (<*year*>) using information from <*rec_source*> harmonised to <*dataset_source*>.

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CONFLICT OF INTEREST

The authors declare no competing interests.

DATA AVAILABILITY STATEMENT

All range maps for the three taxonomic sources are openly available for non-commercial use through https://mol.org/datasets or at species-level at https://mol.org/species, or for bulk download at https://doi.org/10.48600/mol-7r3j-8066 (HMW), https://doi.org/10.48600/mol-zzrs-q778 (CMW) and https://doi.org/10.48600/mol-48vz-p413 (MDD).

ORCID

Charles J. Marsh https://orcid.org/0000-0002-0281-3115
Yanina V. Sica https://orcid.org/0000-0002-1720-0127
Valeria da Cunha Tavares https://orcid.org/0000-0003-0966-0139
William L. Franklin https://orcid.org/0000-0003-0767-2806
Guilherme S. T. Garbino https://orcid.org/0000-0003-1701-5930
Thomas Giarla https://orcid.org/0000-0001-7162-7925
Stephen M. Jackson https://orcid.org/0000-0002-7252-0799
Ulyses F. J. Pardiñas https://orcid.org/0000-0001-9496-5433
Bruce D. Patterson https://orcid.org/0000-0002-2249-7260
Ana Pavan https://orcid.org/0000-0002-0653-6186
Joyce Prado https://orcid.org/0000-0002-2025-5479
Nathan S. Upham https://orcid.org/0000-0001-5412-9342
Walter Jetz https://orcid.org/0000-0002-1971-7277

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BIOSKETCH

Charlie Marsh is interested in spatial ecology, focussing on the tropics, and in particular how ecological processes scale with observation and how we can incorporate this scaling into a better understanding of the effects of human disturbance. He is based at Yale University Department of Ecology & Evolutionary Biology (https://eeb.yale.edu/), the Yale Center for Biodiversity and Global Change (https://bgc.yale.edu/), and Map of Life (https://mol.org/).

Author contributions: Conception and Supervision: WJ; writing of initial draft: CJM, YVS, CJB, WAD, RCA, IDTM, JGV, AR, NU & WJ; source interpretation and georeferencing: YVS, WAD, CJB, RCA, IDTM, JGV, VLD, MD, JAH, AL, JKM, KM, MT & LV; taxonomic harmonisation: CJB, VB, JAH & NU; quality control: CJM, YVS, WAD, CJB, RCA, IDTM & JGV; development of protocols and coordination: YVS, CJM, WAD, MD & WJ; infrastructure: YVS, MD, RG, AR, AS & WJ; generation of original source maps: TLaJ, RAM, ABR, WS, DEW, AMA, LFA, JA-C, DA, AMB, GB, JKB, JB, PEB, SFB, MAC, PC, EAC, JAC, TC, GC, ECS, VCT, TRBD, TD, CD, CRD, MDBE, EFD, CMF, GF, WLF, TF, JAF, ELG, GSTG, PG, NG, TG, JSG, JG, SMG, SG-D, KH, MSH, Mha, MHo, KMH, SHe, AH, SHi, KEH, RLH, BAH, TH, RH, CIU, SJ, JJa, MJ, PJ, RJ, JJu, RK, CWK, TK, JLK, BK, TEL, TLeJ, YLRL, RLMN, BKL, AL, RL-A, AL-B, CDM, FGM, MAM, HM, SM, EM, AM, FBM, GM, TN, RWN, AO, NO-G, UFJP, BDP, AP, MP, CP, JP, HLQ, MR, EPR, SJR, DIR, DR, JS-B, SS-B, CJS, CS, LKS, MSh, GS, PS, SS, RS, MSu, ABT, MT, PT, TVD, NT, DGT, ST, STT, RV, VVC, GV, JWa, RW, DW, EAW, GW, JWo & DZ.

SUPPORTING INFORMATION

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