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Lawrence N. Hudson^{1*}  | Tim Newbold^{2,3*} | Sara Contu¹ | Samantha L. L. Hill^{1,2} | Igor Lysenko⁴ | Adriana De Palma^{1,4} | Helen R. P. Phillips^{1,4} | Tamera I. Alhusseini⁵ | Felicity E. Bedford⁶ | Dominic J. Bennett⁴ | Hollie Booth^{2,7} | Victoria J. Burton^{1,8} | Charlotte W. T. Chng⁴ | Argyrios Choimes^{1,4}  | David L. P. Correia⁹ | Julie Day⁴ | Susy Echeverría-Londoño^{1,4} | Susan R. Emerson¹ | Di Gao¹ | Morgan Garon⁴ | Michelle L. K. Harrison⁴ | Daniel J. Ingram¹⁰ | Martin Jung¹⁰  | Victoria Kemp¹¹ | Lucinda Kirkpatrick¹² | Callum D. Martin¹³ | Yuan Pan¹⁴ | Gwilym D. Pask-Hale¹ | Edwin L. Pynegar¹⁵ | Alexandra N. Robinson⁵ | Katia Sanchez-Ortiz¹⁶ | Rebecca A. Senior¹⁴ | Benno I. Simmons⁴ | Hannah J. White¹⁷ | Hanbin Zhang¹⁶ | Job Aben^{18,19} | Stefan Abrahamczyk²⁰ | Gilbert B. Adum^{21,22} | Virginia Aguilar-Barquero²³ | Marcelo A. Aizen²⁴ | Belén Albertos²⁵ | E. L. Alcalá²⁶ | María del Mar Alguacil²⁷ | Audrey Alignier^{28,29} | Marc Ancrenaz^{30,31} | Alan N. Andersen³² | Enrique Arbeláez-Cortés^{33,34} | Inge Armbrecht³⁵ | Víctor Arroyo-Rodríguez³⁶ | Tom Aumann³⁷ | Jan C. Axmacher³⁸ | Badrul Azhar^{39,40} | Adrián B. Azpiroz⁴¹ | Lander Baeten^{42,43} | Adama Bakayoko^{44,45} | Andrés Báldi⁴⁶ | John E. Banks⁴⁷ | Sharad K. Baral⁴⁸ | Jos Barlow^{49,50} | Barbara I. P. Barratt⁵¹ | Lurdes Barrico⁵² | Paola Bartolommei⁵³ | Diane M. Barton⁵¹ | Yves Basset⁵⁴ | Péter Batáry⁵⁵ | Adam J. Bates^{56,57} | Bruno Baur⁵⁸ | Erin M. Bayne⁵⁹ | Pedro Beja⁶⁰ | Suzan Benedick⁶¹ | Åke Berg⁶² | Henry Bernard⁶³ | Nicholas J. Berry⁶⁴ | Dinesh Bhatt⁶⁵ | Jake E. Bicknell^{66,67} | Jochen H. Bihn⁶⁸ | Robin J. Blake^{69,70} | Kadiri S. Bobo^{71,72} | Roberto Bóçon⁷³ | Teun Boekhout⁷⁴ | Katrin Böhning-Gaese^{75,76} | Kevin J. Bonham⁷⁷ | Paulo A. V. Borges⁷⁸ | Sérgio H. Borges⁷⁹ | Céline Boutin⁸⁰ | Jérémy Bouyer^{81,82} | Cibele Bragagnolo⁸³ | Jodi S. Brandt⁸⁴ | Francis Q. Brearley⁸⁵ | Isabel Brito⁸⁶ | Vicenç Bros^{87,88} | Jörg Brunet⁸⁹ | Grzegorz Buczkowski⁹⁰ | Christopher M. Buddle⁹¹ | Rob Bugter⁹² | Erika Buscardo^{93,94,95} | Jörn Buse⁹⁶ | Jimmy Cabra-García^{97,98} | Nilton C. Cáceres⁹⁹ | Nicolette L. Cagle¹⁰⁰ | María Calviño-Cancela¹⁰¹ | Sydney A. Cameron^{102,103} | Eliana M. Canello¹⁰⁴ | Rut Caparrós^{25,105} | Pedro Cardoso^{78,106} | Dan Carpenter^{107,108} | Tiago F. Carrijo¹⁰⁹ | Anelena L. Carvalho⁷⁹ | Camila R. Cassano¹¹⁰ | Helena Castro⁵² |

*These authors contributed equally to this work.

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Alejandro A. Castro-Luna¹¹¹ | Rolando Cerda B.¹¹² | Alexis Cerezo¹¹³ |
 Kim Alan Chapman¹¹⁴ | Matthieu Chauvat¹¹⁵ | Morten Christensen¹¹⁶ |
 Francis M. Clarke¹¹⁷ | Daniel F.R. Cleary¹¹⁸ | Giorgio Colombo¹¹⁹ | Stuart P. Connop¹²⁰ |
 Michael D. Craig^{121,122} | Leopoldo Cruz-López¹²³ | Saul A. Cunningham¹²⁴ |
 Biagio D'Aniello¹²⁵ | Neil D'Cruze¹²⁶ | Pedro Giovâni da Silva¹²⁷ | Martin Dallimer¹²⁸ |
 Emmanuel Danquah²¹ | Ben Darvill¹²⁹ | Jens Dauber¹³⁰ | Adrian L. V. Davis¹³¹ |
 Jeff Dawson¹³² | Claudio de Sassi¹³³ | Benoit de Thoisy¹³⁴ | Olivier Deheuvels^{135,136} |
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 Jignasu V. Dolia^{144,145} | Erwin Domínguez¹⁴⁶ | Yamileth Dominguez-Haydar¹⁴⁷ |
 Silvia Dorn¹⁴⁸ | Isabel Draper¹⁰⁵ | Niels Dreber^{149,150} | Bertrand Dumont¹⁵¹ |
 Simon G. Dures^{4,152} | Mats Dynesius¹⁵³ | Lars Edenius¹⁵⁴ | Paul Eggleton¹ |
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 Ignacio C. Fernandez¹⁷² | Catarina C. Ferreira¹⁷³ | Gentile F. Ficetola¹⁷⁴ |
 Cristina Fiera¹⁷⁵ | Bruno K. C. Filgueiras¹⁷⁶ | Hüseyin K. Firincioğlu¹⁷⁷ |
 David Flaspohler¹⁷⁸ | Andreas Floren¹⁷⁹ | Steven J. Fonte^{180,181} | Anne Fournier¹⁸² |
 Robert E. Fowler¹⁰ | Markus Franzén¹⁸³ | Lauchlan H. Fraser¹⁸⁴ |
 Gabriella M. Fredriksson^{185,186} | Geraldo B. Freire-Jr¹⁸⁷ | Tiago L. M. Frizzo¹⁸⁷ |
 Daisuke Fukuda¹⁸⁸ | Dario Furlani¹¹⁹ | René Gaigher¹⁵⁹ | Jörg U. Ganzhorn¹⁸⁹ |
 Karla P. García^{190,191} | Juan C. Garcia-R¹⁹² | Jenni G. Garden^{193,194,195} |
 Ricardo Garilleti²⁵ | Bao-Ming Ge¹⁹⁶ | Benoit Gendreau-Berthiaume¹⁹⁷ |
 Philippa J. Gerard¹⁹⁸ | Carla Gheler-Costa¹⁹⁹ | Benjamin Gilbert²⁰⁰ | Paolo Giordani²⁰¹ |
 Simonetta Giordano¹²⁵ | Carly Golodets²⁰² | Laurens G. L. Gomes²⁰³ |
 Rachele K. Gould²⁰⁴ | Dave Goulson¹⁰ | Aaron D. Gove^{205,206} | Laurent Granjon²⁰⁷ |
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 Doris L. Gutiérrez-Lamus²¹³ | Daniela H. Haarmeyer²¹⁴ | Mick E. Hanley²¹⁵ |
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 Joseph E. Hawes²²⁰ | Matt W. Hayward^{221,222,223} | Christian Hébert²²⁴ |
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 James P. Herrera²²⁸ | Farina Herrmann⁵⁵ | Felix Herzog²²⁹ | Diego Higuera-Diaz²³⁰ |
 Branko Hilje²³¹ | Hubert Höfer²³² | Anke Hoffmann²³³ | Finbarr G. Horgan^{234,235} |
 Elisabeth Hornung²³⁶ | Roland Horváth²³⁷ | Kristoffer Hylander²³⁸ |
 Paola Isaacs-Cubides²³⁹ | Hiroaki Ishida²⁴⁰ | Masahiro Ishitani²⁴¹ | Carmen T. Jacobs¹³¹ |
 Víctor J. Jaramillo²⁴² | Birgit Jauker²⁴³ | F. Jiménez Hernández²⁴⁴ |
 McKenzie F. Johnson¹⁰⁰ | Virat Jolli^{245,246} | Mats Jonsell²⁴⁷ | S. Nur Juliani²⁴⁸ |
 Thomas S. Jung²⁴⁹ | Vena Kapoor²⁵⁰ | Heike Kappes²⁵¹ | Vassiliki Kati²⁵² |

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 Violette Le Féon²⁷⁹ | Gretchen LeBuhn²⁸⁰ | Jean-Philippe Légaré²⁸¹ |
 Valérie Lehouck²⁸² | María V. Lencinas²⁸³ | Pia E. Lentini²⁸⁴ | Susan G. Letcher²⁸⁵ |
 Qi Li²⁸⁶ | Simon A. Litchwark²⁸⁷ | Nick A. Littlewood²⁸⁸ | Yunhui Liu²⁸⁹ |
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 Catrin Westphal⁵⁵ | Edward D. Wiawe⁵⁰² | Christopher D. Williams⁵⁰³ |
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 Volkmar Wolters²⁴³ | Ben A. Woodcock⁵⁰⁷ | Jihua Wu⁵⁰⁸ | Joseph M. Wunderle, Jr⁵⁰⁹ |
 Yuichi Yamaura³⁴¹ | Satoko Yoshikura⁵¹⁰ | Douglas W. Yu^{511,512} | Andrey S. Zaitsev^{243,513} |
 Juliane Zeidler⁵¹⁴ | Fasheng Zou⁵¹⁵ | Ben Collen³ | Rob M. Ewers⁴ |
 Georgina M. Mace³ | Drew W. Purves⁵¹⁶ | Jörn P. W. Scharlemann^{2,10} | Andy Purvis^{1,4}

- ¹Department of Life Sciences, Natural History Museum, London, UK
- ²United Nations Environment Programme World Conservation Monitoring Centre, Cambridge, UK
- ³Department of Genetics, Evolution and Environment, Centre for Biodiversity and Environment, Research, University College London, London, UK
- ⁴Department of Life Sciences, Imperial College London, Ascot, UK
- ⁵Imperial College London, South Kensington, London, UK
- ⁶Department of Zoology, Cambridge University, Cambridge, UK
- ⁷Frankfurt Zoological Society, Africa Regional Office, Arusha, Tanzania
- ⁸Science and Solutions for a Changing Planet DTP and the Department of Life Sciences, Imperial College London, South Kensington, London, UK
- ⁹Centre d'étude de la forêt., Université Laval, Laval, QC, Canada
- ¹⁰School of Life Sciences, University of Sussex, Brighton, UK
- ¹¹School of Biological and Chemical Sciences, Queen Mary University of London, London, UK
- ¹²School of Biological and Ecological Sciences, University of Stirling, Stirling, UK
- ¹³School of Biological Sciences, Royal Holloway University of London, Egham, Surrey, UK
- ¹⁴Department of Animal and Plant Sciences, University of Sheffield, Western Bank, Sheffield, UK
- ¹⁵School of Environment, Natural Resources and Geography, Bangor University, Bangor, Gwynedd, UK
- ¹⁶University College London, London, UK
- ¹⁷School of Biological Sciences, Queen's University Belfast, Belfast, UK
- ¹⁸Institute of Biological and Environmental Sciences, University of Aberdeen, Aberdeen, UK
- ¹⁹Evolutionary Ecology Group, University of Antwerp, Antwerp, Belgium
- ²⁰Nees Institute for Plant Biodiversity, University of Bonn, Bonn, Germany
- ²¹Wildlife and Range Management Department, Faculty of Renewable Natural Resources (FRNR), College of Agriculture and Natural Resources (CANR), Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, Ghana
- ²²SAVE THE FROGS! Ghana, Adum-Kumasi, Ghana
- ²³Escuela de Biología, Universidad de Costa Rica, San José, Costa Rica
- ²⁴Laboratorio Ecotono-CRUB, Universidad Nacional del Comahue and INIBIOMA, Río Negro, Argentina
- ²⁵Departamento de Botánica, Facultad de Farmacia, Universidad de Valencia, Burjassot, Valencia, Spain
- ²⁶Marine Laboratory, Silliman University-Angelo King Center for Research and Environmental Management, Silliman University, Dumaguete City, Philippines
- ²⁷Department of Soil and Water Conservation, CSIC-Centro de Edafología y Biología Aplicada del Segura, Murcia, Spain
- ²⁸INRA, UR 0980 SAD-Paysage, Rennes Cedex, France
- ²⁹INRA, UMR 1201 DYNAFOR, Castanet Tolosan Cedex, France
- ³⁰HUTAN – Kinabatangan Orang-utan Conservation Programme, Kota Kinabalu, Malaysia
- ³¹Borneo Futures, Kota Kinabalu, Malaysia
- ³²CSIRO Land & Water Flagship, Winnellie, NT, Australia
- ³³Museo de Zoología, Facultad de Ciencias, Universidad Nacional Autónoma de México, México D.F., Mexico
- ³⁴Colección de Tejidos, Instituto de Investigación de Recursos Biológicos Alexander von Humboldt, Valle del Cauca, Colombia
- ³⁵Biology Department, Universidad del Valle, Cali, Colombia
- ³⁶Instituto de Investigaciones en Ecosistemas y Sustentabilidad, Universidad Nacional Autónoma de México, Morelia, Mexico
- ³⁷College of Science, Engineering & Health, RMIT University, Melbourne, Vic., Australia
- ³⁸UCL Department of Geography, University College London, London, UK
- ³⁹Biodiversity Unit, Institute of Bioscience, Universiti Putra Malaysia, Serdang, Malaysia
- ⁴⁰Faculty of Forestry, Universiti Putra Malaysia, Serdang, Malaysia
- ⁴¹Departamento de Biodiversidad y Genética, Instituto de Investigaciones Biológicas Clemente Estable, Montevideo, Uruguay
- ⁴²Forest & Nature Lab, Department of Forest and Water Management, Ghent University, Gontrode, Belgium
- ⁴³Terrestrial Ecology Unit, Department of Biology, Ghent University, Ghent, Belgium
- ⁴⁴UFR Science de la Nature, Université Naangui Abrogoua, Abidjan, Ivory Coast
- ⁴⁵Centre Suisse de Recherches Scientifiques en Côte d'Ivoire, Abidjan, Ivory Coast
- ⁴⁶MTA Centre for Ecological Research, Vácrátót, Hungary
- ⁴⁷University of Washington Tacoma, Tacoma, WA, USA
- ⁴⁸Northern Hardwoods Research Institute, Edmundston, NB, Canada
- ⁴⁹Lancaster Environment Centre, Lancaster University, Lancaster, UK
- ⁵⁰MCT/Museu Paraense Emílio Goeldi, Belém, Brazil

- ⁵¹AgResearch Limited, Invermay Agricultural Centre, Puddle Alley, Mosgiel, New Zealand
- ⁵²Centre for Functional Ecology, Department of Life Sciences, University of Coimbra, Coimbra, Portugal
- ⁵³COT (Tuscan Ornithological Society), Livorno, Italy
- ⁵⁴Smithsonian Tropical Research Institute, Balboa, Ancon, Panama City, Republic of Panama
- ⁵⁵Agroecology, Department of Crop Sciences, Georg-August University, Göttingen, Germany
- ⁵⁶Biosciences, School of Science & Technology, Nottingham Trent University, Clifton, Nottingham, UK
- ⁵⁷University of Birmingham, Edgbaston, Birmingham, UK
- ⁵⁸Section of Conservation Biology, Department of Environmental Sciences, University of Basel, Basel, Switzerland
- ⁵⁹Department of Biological Sciences, University of Alberta, Edmonton, AB, Canada
- ⁶⁰CIBIO/InBio, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Vairão, Portugal
- ⁶¹Faculty of Sustainable Agriculture, Universiti Malaysia Sabah, Sandakan, Malaysia
- ⁶²The Swedish University of Agricultural Sciences, The Swedish Biodiversity Centre, Uppsala, Sweden
- ⁶³Institute for Tropical Biology and Conservation, Universiti Malaysia Sabah, Jalan UMS, Kota Kinabalu, Malaysia
- ⁶⁴School of Geosciences, University of Edinburgh, Edinburgh, UK
- ⁶⁵Department of Zoology & Environmental Science, Gurukula Kangri University, Haridwar, India
- ⁶⁶Durrell Institute of Conservation and Ecology (DICE), School of Anthropology and Conservation, University of Kent, Canterbury, UK
- ⁶⁷Iwokrama International Centre for Rainforest Conservation and Development, Georgetown, Guyana
- ⁶⁸Department of Ecology-Animal Ecology, Faculty of Biology, Philipps-Universität Marburg, Marburg, Germany
- ⁶⁹Compliance Services International, Pentlands Science Park, Penicuik, Edinburgh, UK
- ⁷⁰Centre for Agri-Environmental Research, School of Agriculture, Policy and Development, University of Reading, Reading, UK
- ⁷¹School for the Training of Wildlife Specialists Garoua, Garoua, Cameroon
- ⁷²Department of Forestry, Faculty of Agronomy and Agricultural Sciences, University of Dschang, Dschang, Cameroon
- ⁷³Mater Natura – Instituto de Estudos Ambientais, Curitiba, Brazil
- ⁷⁴CBS Fungal Biodiversity Centre (CBS-KNAW), Utrecht, The Netherlands
- ⁷⁵Senckenberg Biodiversity and Climate Research Centre (BiK-F), Frankfurt am Main, Germany
- ⁷⁶Institute for Ecology, Evolution & Diversity, Goethe University Frankfurt, Biologicum, Frankfurt am Main, Germany
- ⁷⁷School of Land and Food, University of Tasmania, Sandy Bay, Tas., Australia
- ⁷⁸Departamento de Ciências Agrárias, cE3c – Centre for Ecology, Evolution and Environmental Changes/Azorean Biodiversity Group and Universidade dos Açores, Angra do Heroísmo, Açores, Portugal
- ⁷⁹Instituto Nacional de Pesquisas da Amazônia, Manaus, Brazil
- ⁸⁰Environment and Climate Change Canada, Science & Technology Branch, Carleton University, Ottawa, ON, Canada
- ⁸¹Unité Mixte de Recherche Contrôle des Maladies Animales Exotiques et Emergentes, Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD), Montpellier, France
- ⁸²Unité Mixte de Recherche 1309 Contrôle des Maladies Animales Exotiques et Emergentes, Institut national de la recherche agronomique (INRA), Montpellier, France
- ⁸³Departamento de Zoologia, Instituto de Biociências, Universidade de São Paulo, São Paulo, Brazil
- ⁸⁴Human Environment Systems Center, Boise State University, Boise, ID, USA
- ⁸⁵School of Science and the Environment, Manchester Metropolitan University, Manchester, UK
- ⁸⁶Universidade de Évora – ICAAM, Évora, Portugal
- ⁸⁷Natural Parks Technical Office, Diputació de Barcelona, Barcelona, Spain
- ⁸⁸Natural History Museum of Barcelona, Barcelona, Catalonia, Spain
- ⁸⁹Swedish University of Agricultural Sciences, Southern Swedish Forest Research Centre, Alnarp, Sweden
- ⁹⁰Department of Entomology, Purdue University, West Lafayette, IN, USA
- ⁹¹Department of Natural Resource Sciences, McGill University, Ste-Ann-de-Bellevue, QC, Canada
- ⁹²Alterra, part of Wageningen University and Research, RB Wageningen, The Netherlands
- ⁹³Departamento de Ciências da Vida, Centro de Ecologia Funcional, Universidade de Coimbra, Coimbra, Portugal
- ⁹⁴Departamento de Biologia Vegetal, Instituto de Biologia, Universidade Estadual de Campinas, Campinas, Brazil
- ⁹⁵Department of Botany, School of Natural Sciences, Trinity College Dublin, Dublin 2, Ireland
- ⁹⁶Institute for Environmental Sciences, University Koblenz-Landau, Landau, Germany
- ⁹⁷Departamento de Zoologia, Instituto de Biociências, Universidade de São Paulo, São Paulo, Brazil
- ⁹⁸Departamento de Biología, Grupo de investigación en Biología, Ecología y Manejo de Hormigas, Sección de Entomología, Universidad del Valle, Cali, Colombia

- ⁹⁹Department of Biology, Federal University of Santa Maria, CCNE, Santa Maria, Brazil
- ¹⁰⁰Nicholas School of the Environment, Duke University, Durham, NC, USA
- ¹⁰¹Department of Ecology and Animal Biology, Faculty of Sciences, University of Vigo, Vigo, Spain
- ¹⁰²Department of Entomology, University of Illinois, Urbana, IL, USA
- ¹⁰³Program in Ecology, Evolution and Conservation Biology, University of Illinois, Urbana, IL, USA
- ¹⁰⁴Museu de Zoologia da Universidade de São Paulo, São Paulo, Brazil
- ¹⁰⁵Departamento de Biología (Botánica), Facultad de Ciencias, Universidad Autónoma de Madrid, Madrid, Spain
- ¹⁰⁶Finnish Museum of Natural History, University of Helsinki, Helsinki, Finland
- ¹⁰⁷Parks and Countryside, Bracknell Forest Council, Bracknell, UK
- ¹⁰⁸Soil Biodiversity Group, Life Sciences Department, Natural History Museum, London, UK
- ¹⁰⁹Museu de Zoologia da Universidade de São Paulo, São Paulo, Brazil
- ¹¹⁰Laboratório de Ecologia Aplicada à Conservação, Universidade Estadual de Santa Cruz, Ilhéus, Brazil
- ¹¹¹Instituto de Biotecnología y Ecología Aplicada (INBIOTECA), Universidad Veracruzana, Xalapa, Mexico
- ¹¹²Centro Agronómico Tropical de Investigación y Enseñanza (CATIE), Tropical Agricultural Research and Higher Education Center, Turrialba, Costa Rica
- ¹¹³Department of Quantitative Methods and Information Systems, Faculty of Agronomy, University of Buenos Aires, Buenos Aires, Argentina
- ¹¹⁴Applied Ecological Services, Inc., Prior Lake, MN, USA
- ¹¹⁵Normandie Univ, EA 1293 ECODIV-Rouen, SFR SCALE, UFR Sciences et Techniques, Mont Saint Aignan Cedex, France
- ¹¹⁶MC-Consult, Sorø, Denmark
- ¹¹⁷Institute of Biological and Environmental Sciences, University of Aberdeen, Aberdeen, UK
- ¹¹⁸Department of Biology, CESAM, Universidade de Aveiro, Aveiro, Portugal
- ¹¹⁹Dipartimento di Biologia, Università degli Studi di Milano, Milano, Italy
- ¹²⁰Sustainability Research Institute, University of East London, London, UK
- ¹²¹Centre of Excellence for Environmental Decisions, School of Plant Biology, University of Western Australia, Nedlands, WA, Australia
- ¹²²School of Veterinary and Life Sciences, Murdoch University, Murdoch, WA, Australia
- ¹²³Grupo Ecología de Artrópodos y Manejo de Plagas, El Colegio de la Frontera Sur, Tapachula, Mexico
- ¹²⁴CSIRO Land and Water Flagship, Canberra, ACT, Australia
- ¹²⁵Dipartimento di Biologia, Università di Napoli Federico II, Napoli, Italy
- ¹²⁶Wildlife Conservation Research Unit, Department of Zoology, University of Oxford, Recanati-Kaplan Centre, Tubney, UK
- ¹²⁷Programa de Pós-Graduação em Ecologia, Universidade Federal de Santa Catarina, Florianópolis, Brazil
- ¹²⁸Sustainability Research Institute, School of Earth and Environment, University of Leeds, Leeds, UK
- ¹²⁹British Trust for Ornithology, Stirling, UK
- ¹³⁰Thünen Institute of Biodiversity, Braunschweig, Germany
- ¹³¹Scarab Research Group, Department of Zoology & Entomology, University of Pretoria, Hatfield, South Africa
- ¹³²Durrell Wildlife Conservation Trust, Trinity, Jersey
- ¹³³Center for International Forestry Research, Bogor, Indonesia
- ¹³⁴Kwata NGO, Cayenne, French Guiana
- ¹³⁵CIRAD, UMR System, Montpellier, France
- ¹³⁶ICRAF, Regional Office for Latin America, Lima, Peru
- ¹³⁷UPS, INP, Laboratoire Écologie Fonctionnelle et Environnement, Université de Toulouse, Toulouse, France
- ¹³⁸CNRS – UMR 5245, Ecolab, Toulouse, France
- ¹³⁹CNRS – UMR 8172, Écologie des Forêts de Guyane, Kourou cedex, France
- ¹⁴⁰CNRS – UMR 7206 (retired) CNRS/MNHN, Paris, France
- ¹⁴¹Department of Landscape Ecology, Institute of Natural Resource Conservation, Kiel University, Kiel, Germany
- ¹⁴²Department of Biology, Nature Conservation, University Marburg, Marburg, Germany
- ¹⁴³Institute of Integrative Biology, ETH Zürich, Zürich, Switzerland
- ¹⁴⁴Post Graduate Program in Wildlife Biology and Conservation, National Centre for Biological Sciences, Bangalore, India
- ¹⁴⁵Wildlife Conservation Society (India Program), Centre for Wildlife Studies, Bangalore, India
- ¹⁴⁶Instituto de Investigaciones Agropecuarias – INIA – CRI – Kampenaiké, Punta Arenas, Chile
- ¹⁴⁷Programa de Biología, Universidad del Atlántico, Barranquilla, Colombia
- ¹⁴⁸Applied Entomology, ETH Zürich, Zürich, Switzerland
- ¹⁴⁹Unit for Environmental Sciences and Management, North-West University, Potchefstroom, South Africa

- ¹⁵⁰Department of Ecosystem Modelling, Büsgen-Institute, Georg-August-University of Göttingen, Göttingen, Germany
- ¹⁵¹INRA, UMR 1213 Herbivores, Saint-Genès Champanelle, France
- ¹⁵²Institute of Zoology, Zoological Society of London, Regents Park, London, UK
- ¹⁵³Department of Ecology and Environmental Science, Umeå University, Umeå, Sweden
- ¹⁵⁴Department of Wildlife, Fish and Environmental Studies, Swedish University of Agricultural Sciences, Umea, Sweden
- ¹⁵⁵Centre for Biological Sciences, University of Southampton, Southampton, UK
- ¹⁵⁶MTA-ELTE-MTM Ecology Research Group, Hungarian Academy of Sciences, c/o Biological Institute, Eötvös Lóránd University, Budapest, Hungary
- ¹⁵⁷Hungarian Natural History Museum, Budapest, Hungary
- ¹⁵⁸Institute for Environmental Sciences, University of Koblenz-Landau, Landau, Germany
- ¹⁵⁹Department of Conservation Ecology and Entomology, Stellenbosch University, Matieland, South Africa
- ¹⁶⁰Centre for Invasion Biology, Stellenbosch University, Matieland, South Africa
- ¹⁶¹CE3C – Centre for Ecology, Evolution and Environmental Changes, Faculdade de Ciências, Universidade de Lisboa, Lisboa, Portugal
- ¹⁶²Associação Monte Pico, Monte Café, Mé Zóchi, São Tomé and Príncipe
- ¹⁶³Kew Gardens, Wakehurst, Ardingly, Haywards Heath, Sussex, UK
- ¹⁶⁴Wild Asia, Upper Penthouse, Wisma RKT, Kuala Lumpur, Malaysia
- ¹⁶⁵Conservation Ecology, Faculty of Biology, Philipps-Universität Marburg, Marburg, Germany
- ¹⁶⁶Institute of Entomology, Biology Centre of Academy of Sciences Czech Republic, České Budějovice, Czech Republic
- ¹⁶⁷Institute for Tropical Biology and Conservation, Universiti Malaysia Sabah, Kota Kinabalu, Malaysia
- ¹⁶⁸Dipartimento di Scienze Veterinarie, Università di Pisa, Pisa, Italy
- ¹⁶⁹Swedish University of Agricultural Sciences, Alnarp, Sweden
- ¹⁷⁰Department of Biological Sciences, University of Queensland, St Lucia, Qld, Australia
- ¹⁷¹Queensland Herbarium (DSITIA), Toowong, Qld, Australia
- ¹⁷²School of Sustainability, Arizona State University, Tempe, AZ, USA
- ¹⁷³Department of Biology, Trent University, Peterborough, ON, Canada
- ¹⁷⁴Laboratoire d'Ecologie Alpine (LECA), Université Grenoble Alpes, Grenoble, France
- ¹⁷⁵Institute of Biology Bucharest of Romanian Academy, Bucharest, Romania
- ¹⁷⁶Universidade Federal de Pernambuco – UFPE, Cidade Universitaria, Recife, Brazil
- ¹⁷⁷Tarla Bitkileri Merkez Araştırma Enstitüsü, Yenimahalle-Ankara, Turkey
- ¹⁷⁸School of Forest Resources and Environmental Science, Michigan Technological University, Houghton, MI, USA
- ¹⁷⁹Department of Animal Ecology and Tropical Biology, Biocenter, University of Würzburg, Würzburg, Germany
- ¹⁸⁰Department of Plant Sciences, University of California, Davis, CA, USA
- ¹⁸¹Department of Soil and Crop Sciences, Colorado State University, Fort Collins, CO, USA
- ¹⁸²IRD-UMR 208 PALOC IRD/MNHN, Paris, France
- ¹⁸³Department of Community Ecology, UFZ, Helmholtz Centre for Environmental Research, Halle, Germany
- ¹⁸⁴Department of Natural Resource Sciences, Thompson Rivers University, Kamloops, BC, Canada
- ¹⁸⁵Institute for Biodiversity and Ecosystem Dynamics (IBED), University of Amsterdam, GE Amsterdam, The Netherlands
- ¹⁸⁶PanEco/Yayasan Ekosistem Lestari, Sumatran Orangutan Conservation Programme, Medan, Indonesia
- ¹⁸⁷Programa de Pós Graduação em Ecologia, Universidade de Brasília, Brasília, Distrito Federal, Brazil
- ¹⁸⁸IDEA Consultants Inc., Okinawa Branch Office, Naha, Japan
- ¹⁸⁹Biocentre Grindel, University of Hamburg, Hamburg, Germany
- ¹⁹⁰Departamento de Zoología, Facultad de Ciencias Naturales y Oceanográficas, Universidad de Concepción, Concepción, Chile
- ¹⁹¹Departamento de Planificación Territorial, Facultad de Ciencias Ambientales, Centro EULA-Chile, Universidad de Concepción, Concepción, Chile
- ¹⁹²Hopkirk Institute, Massey University, Palmerston North, New Zealand
- ¹⁹³Seed Consulting Services, Adelaide, SA, Australia
- ¹⁹⁴Environmental Futures Research Institute, Griffith University, Brisbane, Qld, Australia
- ¹⁹⁵Barbara Hardy Institute, University of South Australia, Mawson Lakes, SA, Australia
- ¹⁹⁶Jiangsu Key Laboratory for Bioresources of Saline Soils, Yancheng Teachers University, Yancheng, China
- ¹⁹⁷Département des sciences biologiques, Centre d'études de la forêt Université du Québec à Montréal Succursale Centre-ville, Montréal, QC, Canada
- ¹⁹⁸AgResearch, Ruakura Research Centre, Hamilton, New Zealand
- ¹⁹⁹Ecologia Aplicada/Applied Ecology, Universidade Sagrado Coração (USC), Bauru, Brazil
- ²⁰⁰Department of Ecology and Evolutionary Biology, University of Toronto, Toronto, ON, Canada

- ²⁰¹DIFAR, University of Genova, Genova, Italy
- ²⁰²Tel Aviv University, Tel Aviv, Israel
- ²⁰³World Wildlife Fund, Inc. (WWF) Guianas, Paramaribo, Suriname
- ²⁰⁴Rubenstein School of Natural Resources, University of Vermont, Burlington, VT, USA
- ²⁰⁵Astron Environmental Services, East Perth, WA, Australia
- ²⁰⁶Department of Environment and Agriculture, Curtin University, Perth, WA, Australia
- ²⁰⁷Centre de Biologie pour la Gestion des Populations (CBGP), INRA, IRD, CIRAD, SUPAGRO, Montferrier-sur-Lez cedex, France
- ²⁰⁸Department of Zoology, University of Oxford, Oxford, UK
- ²⁰⁹Department of Biological Sciences, Mount Holyoke College, South Hadley, MA, USA
- ²¹⁰China International Engineering Consulting Corporation, Haidian District, Beijing, China
- ²¹¹CREAF, Cerdanyola del Vallès, Catalonia, Spain
- ²¹²Departamento de Ciencias Ambientales y Recursos Naturales Renovables, Facultad de Ciencias Agronómicas, Universidad de Chile, La Pintana, Chile
- ²¹³Grupos de Fauna, Instituto amazónico de investigaciones científicas Sinchi., Bogotá, Colombia
- ²¹⁴Biodiversity, Evolution and Ecology of Plants (BEE), Biocentre Klein Flottbek and Botanical Garden, University of Hamburg, Hamburg, Germany
- ²¹⁵School of Biological Science, University of Plymouth, Plymouth, UK
- ²¹⁶Friday Harbor, WA, USA
- ²¹⁷International University of Malaya-Wales, Jalan Tun Ismail, Kuala Lumpur, Malaysia
- ²¹⁸Department of Wildlife Management, Sokoine University of Agriculture, Morogoro, Tanzania
- ²¹⁹The Xerces Society for Invertebrate Conservation, Portland, OR, USA
- ²²⁰Animal & Environment Research Group, Department of Life Sciences, Anglia Ruskin University, Cambridge, UK
- ²²¹Walter Sisulu University, Mthatha, Transkei, South Africa
- ²²²Centre for African Conservation Ecology, Nelson Mandela Metropolitan University, Port Elizabeth, South Africa
- ²²³College of Natural Sciences, Bangor University, Bangor, Gwynedd, UK
- ²²⁴Natural Resources Canada, Canadian Forest Service, Laurentian Forestry Centre, Québec, QC, Canada
- ²²⁵Department of Arctic and Marine Biology, University of Tromsø, Tromsø, Norway
- ²²⁶Panthera, New York, NY, USA
- ²²⁷Universidad Nacional Experimental de Guayana, Puerto Ordaz, Venezuela
- ²²⁸Richard Gilder Graduate School, American Museum of Natural History, New York, NY, USA
- ²²⁹Agroscope, Zürich, Switzerland
- ²³⁰Corporación Sentido Natural, Bogotá, Colombia
- ²³¹Earth and Atmospheric Sciences Department, University of Alberta, Edmonton, AB, Canada
- ²³²State Museum of Natural History Karlsruhe (SMNK), Biosciences, Karlsruhe, Germany
- ²³³Museum für Naturkunde – Leibniz Institute for Evolution and Biodiversity Science, Berlin, Germany
- ²³⁴University of Technology Sydney, Sydney, NSW, Australia
- ²³⁵University of New Brunswick, Fredericton, NB, Canada
- ²³⁶Department of Ecology, Faculty of Veterinary Science, SZIE University, Budapest, Hungary
- ²³⁷Department of Ecology, University of Debrecen, Debrecen, Hungary
- ²³⁸Department of Ecology, Environment and Plant Sciences, Stockholm University, Stockholm, Sweden
- ²³⁹Instituto de Investigaciones y Recursos Biológicos Alexander von Humboldt, Bogotá, Colombia
- ²⁴⁰Institute of Natural and Environmental Sciences, University of Hyogo, Hyogo, Japan
- ²⁴¹Hiroshima University Leading-program, Higashihiroshima, Kagamiyama, Japan
- ²⁴²Instituto de Investigaciones en Ecosistemas y Sustentabilidad, Universidad Nacional Autónoma de México, Morelia, México C.P., Mexico
- ²⁴³Department of Animal Ecology, Justus-Liebig-University, Giessen, Germany
- ²⁴⁴Escuela de Biología, Universidad de Costa Rica, San Pedro, Costa Rica
- ²⁴⁵Biodiversity and Environmental Sustainability, Rohini, India
- ²⁴⁶Department of Environmental Studies, Shivaji College (University of Delhi), New Delhi, India
- ²⁴⁷Department of Ecology, Swedish University of Agricultural Sciences, Uppsala, Sweden
- ²⁴⁸School of Biological Sciences, Universiti Sains Malaysia, Minden, Malaysia
- ²⁴⁹Yukon Department of Environment, Whitehorse, YT, Canada
- ²⁵⁰Nature Conservation Foundation, Mysore, India
- ²⁵¹Cologne Biocenter, Zoological Institute, University of Cologne, Köln, Germany

- ²⁵²Department of Environmental & Natural Resources Management, University of Patras, Agrinio, Greece
- ²⁵³Centre for Tropical Environmental and Sustainability Science (TESS) & College of Marine and Environmental Sciences, James Cook University, Cairns, Qld, Australia
- ²⁵⁴School of Science and Technology, Pacific Adventist University, Port Moresby, Papua New Guinea
- ²⁵⁵Unit for Environmental Sciences and Management, North-West University, Potchefstroom, South Africa
- ²⁵⁶Department of Systematic and Evolutionary Botany, University of Zürich, Zürich, Switzerland
- ²⁵⁷Department of Ecology and Evolutionary Biology and Department of Geography and Planning, University of Toronto, Toronto, ON, Canada
- ²⁵⁸The Wilderness & Wildlife Conservation Trust, Colombo, Sri Lanka
- ²⁵⁹School of Biological Sciences, Plymouth University, Plymouth, UK
- ²⁶⁰Institute of Ecology and Evolution, University of Bern, Bern, Switzerland
- ²⁶¹Section Environnement, Développement durable et Territoire, Division Environnement et Territoire, Bundesamt für Statistik, Neuchâtel, Switzerland
- ²⁶²School of Forest Sciences, University of Eastern Finland, Joensuu, Finland
- ²⁶³Institute of Ecology, FB2, University of Bremen, Bremen, Germany
- ²⁶⁴Université Peleforo Gon Coulibaly, Korhogo, Ivory Coast
- ²⁶⁵Station d'Ecologie de Lamto, N'Douci, Ivory Coast
- ²⁶⁶Theoretical Evolutionary Ecology Group, Department of Animal Ecology and Tropical Biology, Biocenter, University of Würzburg, Würzburg, Germany
- ²⁶⁷Wildlife Conservation Society-India, National Centre for Biological Sciences, Bangalore, India
- ²⁶⁸Nature Science Initiative, Dehradun, India
- ²⁶⁹Department of Environmental Science, Policy, and Management, University of California, Berkeley, CA, USA
- ²⁷⁰School of BioSciences, University of Melbourne, Melbourne, Vic., Australia
- ²⁷¹School of Agricultural, Forest and Food Sciences HAFL, Bern University of Applied Sciences, Zollikofen, Switzerland
- ²⁷²Swiss Federal Institute for Forest, Snow and Landscape Research WSL, Birmensdorf, Switzerland
- ²⁷³Instituto Nacional de Tecnología Agropecuaria, EEA Bariloche, Bariloche, Argentina
- ²⁷⁴Department of Biology, Pennsylvania State University, University Park, PA, USA
- ²⁷⁵National Aviary, Allegheny Commons West, Pittsburgh, PA, USA
- ²⁷⁶Centre for Tropical Environmental and Sustainability Sciences, College of Marine and Environmental Science, James Cook University, Cairns, Qld, Australia
- ²⁷⁷Université Pierre-et-Marie-Curie, Paris, France
- ²⁷⁸Institute of Ecology and Environmental Sciences, Paris, France
- ²⁷⁹INRA, UR 406 Abeilles et Environnement, Avignon, France
- ²⁸⁰Department of Biology, San Francisco State University, San Francisco, CA, USA
- ²⁸¹Laboratoire de diagnostic en phytoprotection, Ministère de l'agriculture, des pêcheries et de l'alimentation du Québec, Ville de Québec, QC, Canada
- ²⁸²Research Unit Terrestrial Ecology, Ghent University, Ghent, Belgium
- ²⁸³Laboratorio de Recursos Agroforestales, Centro Austral de Investigaciones Científicas (CADIC), Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Ushuaia, Argentina
- ²⁸⁴School of Biosciences, University of Melbourne, Parkville, Vic., Australia
- ²⁸⁵Purchase College (State University of New York), Purchase, NY, USA
- ²⁸⁶Institute of Applied Ecology, Chinese Academy of Sciences, Shenyang, China
- ²⁸⁷School of Biological Sciences, University of Canterbury, Christchurch, New Zealand
- ²⁸⁸The James Hutton Institute, Aberdeen, UK
- ²⁸⁹College of Resources and Environmental Sciences, China Agricultural University, Beijing, China
- ²⁹⁰Carste Ciência e Meio Ambiente, Floresta, Belo Horizonte, Brazil
- ²⁹¹TEHO Laboratory, Institute of Biology, University of Antioquia, Medellín, Colombia
- ²⁹²International Center for Agricultural Research in the Dry Areas (ICARDA), Amman Office, Amman, Jordan
- ²⁹³Animal and Rangeland Sciences Department, Oregon State University, Corvallis, OR, USA
- ²⁹⁴Department of Agroecology, Flakkebjerg Research Centre, Aarhus University, Slagelse, Denmark
- ²⁹⁵Department of Agroforestry Technology and Science and Genetics, School of Advanced Agricultural Engineering, Castilla La Mancha University, Albacete, Spain
- ²⁹⁶Unidad Académica de Turismo, Coordinación de Investigación y Posgrado, Universidad Autónoma de Nayarit, Tepic, Mexico
- ²⁹⁷Centro de Investigaciones Tropicales, Universidad Veracruzana, Xalapa, Mexico
- ²⁹⁸Graduate School of Agricultural Science, Kobe University, Kobe, Japan
- ²⁹⁹Department of Ecology, University of Debrecen, Debrecen, Hungary
- ³⁰⁰Center for Conservation Innovation, San Jose Tagaytay City, Philippines
- ³⁰¹Biology Department, De La Salle University, Manila, Philippines

- ³⁰²The New Zealand Institute for Plant & Food Research Limited, Auckland, New Zealand
- ³⁰³National Museums of Kenya, Nairobi, Kenya
- ³⁰⁴Center for Macroecology, Evolution and Climate, Natural History Museum of Denmark, University of Copenhagen, Copenhagen Ø, Denmark
- ³⁰⁵Red de Biología y Conservación de Vertebrados, Instituto de Ecología A.C., Xalapa, Mexico
- ³⁰⁶Department of Geography, University of Bergen, Bergen, Norway
- ³⁰⁷Department of Geography, University of Wisconsin-Madison, Madison, WI, USA
- ³⁰⁸School of Biology, University of Leeds, Leeds, West Yorkshire, UK
- ³⁰⁹Marshall Agroecology Ltd, Barton, Winscombe, UK
- ³¹⁰Universidad Nacional de Colombia, Ciudad Universitaria, Bogotá, Colombia
- ³¹¹Basque Centre for Climate Change – BC3, Bilbao, Spain
- ³¹²School of Biological Sciences, The University of Queensland, Brisbane, Qld, Australia
- ³¹³Associate of Arts Program, University of Delaware – Wilmington, Wilmington, DE, USA
- ³¹⁴Department of Entomology and Wildlife Ecology, University of Delaware, Newark, DE, USA
- ³¹⁵Department of Entomology, University of California, Riverside, CA, USA
- ³¹⁶Centre for Mined Land Rehabilitation, The University of Queensland, Brisbane, Qld, Australia
- ³¹⁷Departamento de Biogeografía y Cambio Global, Museo Nacional de Ciencias Naturales (CSIC), Madrid, Spain
- ³¹⁸Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT, USA
- ³¹⁹Museo de Historia Natural “Vera Alleman Haeghebaert”, Universidad Ricardo Palma, Lima 33, Peru
- ³²⁰Centro Iberoamericano de la Biodiversidad (CIBIO), Universidad de Alicante, Alicante, Spain
- ³²¹Department of Ecology, Swedish University of Agricultural Sciences, Grimsö Wildlife Research Station, Riddarhyttan, Sweden
- ³²²Rainforest Alliance, New York, NY, USA
- ³²³Department of Natural Resources, Cornell University, Ithaca, NY, USA
- ³²⁴Department of Natural Resources & Environmental Sciences, University of Illinois, Urbana, IL, USA
- ³²⁵Universidad Industrial de Santander, Bucaramanga, Colombia
- ³²⁶School of Plant Biology, University of Western Australia, Crawley, WA, Australia
- ³²⁷Lab. Ecotono, INIBIOMA (Universidad Nacional del Comahue-CONICET), Bariloche, Argentina
- ³²⁸Botany Department, National Museums of Kenya, Nairobi, Kenya
- ³²⁹Department of Wildlife Management, University of Eldoret, Eldoret, Kenya
- ³³⁰Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Novi Sad, Serbia
- ³³¹School of Biological Sciences, Universiti Sains Malaysia, Penang, Malaysia
- ³³²El Colegio de la Frontera Sur, Ecología Evolutiva y Conservación, San Cristóbal de las Casas, Mexico
- ³³³Nature Kenya, Nairobi, Kenya
- ³³⁴WWF, Washington, DC, USA
- ³³⁵Independent Research Scholar, New Delhi, India
- ³³⁶Avian Diversity and Bioacoustic Lab, Department of Zoology, Gurukula Kangri University, Haridwar, India
- ³³⁷Graduate School of Bioagricultural Sciences, Nagoya University, Nagoya, Japan
- ³³⁸Key Laboratory of Tropical Forest Ecology, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, Menglun, China
- ³³⁹Environmental Futures Research Institute, and Griffith School of Environment, Griffith University, Nathan, Brisbane, Qld, Australia
- ³⁴⁰College of Bioresource Science, Nihon University, Fujisawa, Japan
- ³⁴¹Forestry and Forest Products Research Institute, Tsukuba, Japan
- ³⁴²Laboratorio de Investigaciones en Abejas (Departamento de Biología), Universidad Nacional de Colombia, Bogotá, Colombia
- ³⁴³Laboratorio de Información Geográfica, El Colegio de la Frontera Sur (ECOSUR), San Cristóbal de las Casas, Mexico
- ³⁴⁴CMRPZ – I.E. Plaza Bonita, San Andrés de Sotavento (Córdoba), Colombia
- ³⁴⁵BirdLife International – Africa Partnership Secretariat, Nairobi, Kenya
- ³⁴⁶Ornithology Section, National Museums of Kenya, Nairobi, Kenya
- ³⁴⁷Department of Zoology, University of British Columbia, Vancouver, BC, Canada
- ³⁴⁸Institut de Systématique, Évolution, Biodiversité, ISYEB – UMR 7205 – CNRS, MNHN, UPMC, EPHE, Muséum national d'Histoire naturelle, Sorbonne Universités, Paris, France
- ³⁴⁹Department of Biology/Biodiversity, Lund University, Lund, Sweden
- ³⁵⁰Department of Biosciences, University of Helsinki, Helsinki, Finland
- ³⁵¹Department of Environmental Sciences, University of Helsinki, Helsinki, Finland

- ³⁵²School of Biology, The University of Nottingham, University Park, Nottingham, UK
- ³⁵³Laboratorio de Zoología y Ecología Acuática – LAZOE, Universidad de Los Andes, Bogotá, Colombia
- ³⁵⁴School of Forestry, University of Canterbury, Christchurch, New Zealand
- ³⁵⁵BIO-Diverse, Bonn, Germany
- ³⁵⁶Department of Wildlife, Fish and Conservation Biology, University of California, Davis, Davis, CA, USA
- ³⁵⁷IUCN-Centre for Mediterranean Cooperation, Campanillas, Málaga, Spain
- ³⁵⁸Oxford University Centre for the Environment, University of Oxford, Oxford, UK
- ³⁵⁹Natural Resources and the Environment, CSIR, Stellenbosch, South Africa
- ³⁶⁰Plant Conservation Unit, Biological Sciences, University of Cape Town, Rondebosch, South Africa
- ³⁶¹International Programme Office (IPO), Vice Chancellor's Office, Kwame Nkrumah University of Science and Technology (KNUST), Kumasi, Ghana
- ³⁶²Naturschutz – Planung und Beratung, Wiesendangen, Switzerland
- ³⁶³Department of Wildlife and Range Management, Kwame Nkrumah University of Science and Technology, Kumasi, Ghana
- ³⁶⁴Forestry Research Institute of Ghana, Kumasi, Ghana
- ³⁶⁵Department of Animal & Environmental Biology, University of Benin, Benin City, Nigeria
- ³⁶⁶Department of Genetics, Evolution and Environment, University College London, London, UK
- ³⁶⁷The Royal Society for the Protection of Birds (RSPB), Sandy, Bedfordshire, UK
- ³⁶⁸Laboratorio de Ecología del Paisaje, Facultad de Ciencias Forestales, Universidad de Concepción, Concepción, Chile
- ³⁶⁹Indian Institute of Science, Bangalore, India
- ³⁷⁰Laboratorio Ecotono, CONICET-INIBIOMA, Universidad Nacional del Comahue, Bariloche, Argentina
- ³⁷¹Laboratorio de Investigaciones en Abejas, LABUN, Universidad Nacional de Colombia, Bogotá D.C., Colombia
- ³⁷²Lancaster Environment Centre, Lancaster University, Lancaster, UK
- ³⁷³Universidade Federal do Pará (UFPA), Núcleo de Altos Estudos Amazonicos (NAEA), Belém, Brazil
- ³⁷⁴German Centre for Integrative Biodiversity Research (iDiv), Halle-Jena-Leipzig, Leipzig, Germany
- ³⁷⁵Department of Plant Biology and Ecology, Faculty of Science and Technology, University of the Basque Country, Leioa, Spain
- ³⁷⁶IKERBASQUE. Basque Foundation for Science, Bilbao, Spain
- ³⁷⁷Instituto de Diversidad y Ecología Animal (IDEA, CONICET-UNC) and Centro de Zoología Aplicada, FCEfYN, Universidad Nacional de Córdoba, Córdoba, Argentina
- ³⁷⁸IRD, UMR AMAP, TA A51/PS2, Montpellier cedex 05, France
- ³⁷⁹French Institute of Pondicherry, UMIFRE 21 CNRS-MAEE, Puducherry, India
- ³⁸⁰School of Environmental Sciences, University of East Anglia, Norwich, UK
- ³⁸¹National Institute of Agricultural Technology (INTA), Río Gallegos, Argentina
- ³⁸²National University of Southern Patagonia (UNPA), Río Gallegos, Argentina
- ³⁸³National Commission of Scientist Research and Technology (CONICET), Buenos Aires, Argentina
- ³⁸⁴Laboratory of Biogeography & Ecology, Department of Geography, University of the Aegean, Mytilene, Greece
- ³⁸⁵Department of Animal Ecology and Tropical Biology, Biocenter, University of Würzburg, Würzburg, Germany
- ³⁸⁶University of Cambridge, Cambridge, UK
- ³⁸⁷Conservation Science Group, Department of Zoology, University of Cambridge, Cambridge, UK
- ³⁸⁸Systematics and Evolution Laboratory, Department of Biology, Western Kentucky University, Bowling Green, KY, USA
- ³⁸⁹Department of Natural Resource Ecology and Management, Iowa State University, Ames, IA, USA
- ³⁹⁰Facultad de Recursos Naturales, Escuela de Ciencias Ambientales, Laboratorio de Planificación Territorial, Universidad Católica de Temuco, Temuco, Chile
- ³⁹¹Biología y Conservación de Vertebrados, Instituto de Ecología A.C., El Haya, Xalapa, Mexico
- ³⁹²Universitat Autònoma de Barcelona, Cerdanyola del Vallès, Spain
- ³⁹³Laboratorio de Entomología Ecológica, Departamento de Biología, Facultad de Ciencias, Universidad de La Serena, La Serena, Chile
- ³⁹⁴Albertine Rift Program, Wildlife Conservation Society, Kampala, Uganda
- ³⁹⁵IFEVA/Cátedra de Producción Vegetal, Departamento de Producción Vegetal, Facultad de Agronomía, Universidad de Buenos Aires/CONICET., Buenos Aires, Argentina
- ³⁹⁶Directora del Programa Conservación de Biodiversidad en Bosques Subtropicales, Cátedra de Desarrollo Sustentable y Biodiversidad, Facultad de Ciencias Agrarias, Universidad Nacional de Jujuy, CIT-Jujuy CONICET, Fundación CEBio, San Salvador de Jujuy, Argentina
- ³⁹⁷Departament de Ciències Ambientals, Universitat de Girona, Girona, Spain
- ³⁹⁸Entomology, Cornell University, Ithaca, NY, USA
- ³⁹⁹Botany, School of Natural Sciences, Trinity College Dublin, Dublin 2, Ireland

- ⁴⁰⁰Center for Environmental Sciences and Engineering & Department of Ecology and Evolutionary Biology, University of Connecticut, Storrs, CT, USA
- ⁴⁰¹MARETEC, Instituto Superior Técnico, Universidade de Lisboa, Lisbon, Portugal
- ⁴⁰²CREA-ABP, Consiglio per la ricerca in agricoltura e l'analisi dell'economia agraria, Centro di ricerca per l'agrobiologia e la pedologia, Firenze, Italy
- ⁴⁰³Ecosystem Management, School of Environment and Rural Science, University of New England, Armidale, NSW, Australia
- ⁴⁰⁴Escuela de Biología, Universidad Industrial de Santander, Bucaramanga, Colombia
- ⁴⁰⁵National Center for Ecological Analysis and Synthesis, University of California, Santa Barbara, Santa Barbara, CA, USA
- ⁴⁰⁶Department of Bioscience, Aarhus University, Aarhus C, Denmark
- ⁴⁰⁷The Royal Society for the Protection of Birds (RSPB), Edinburgh Park, Edinburgh, UK
- ⁴⁰⁸Center for Conservation and Sustainable Development, Missouri Botanical Garden, Saint Louis, MO, USA
- ⁴⁰⁹Departamento de Biologia, Universidade Federal de Sergipe, São Cristóvão/Se, Brazil
- ⁴¹⁰Life Sciences Department, University of Alcalá, Alcalá de Henares, Spain
- ⁴¹¹Entomology Collection, Systematics and Biogeography Laboratory, School of Biology, Industrial University of Santander, Bucaramanga, Colombia
- ⁴¹²Percy FitzPatrick Institute of African Ornithology, DST/NRF Centre of Excellence, University of Cape Town, Rondebosch, Cape Town, South Africa
- ⁴¹³School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, Wits, South Africa
- ⁴¹⁴Centro de Ciências Biológicas e da Saúde, Universidade Federal de Mato Grosso do Sul, Campo Grande, Brazil
- ⁴¹⁵Department of Biological Sciences, Brock University, St. Catharines, ON, Canada
- ⁴¹⁶Edinburgh, UK
- ⁴¹⁷Luquillo LTER, Institute for Tropical Ecosystem Studies, College of Natural Sciences, University of Puerto Rico at Rio Piedras, San Juan, PR, USA
- ⁴¹⁸Escuela Nacional de Estudios Superiores, Universidad Nacional Autónoma de México, Morelia, Mexico
- ⁴¹⁹Science and Conservation Division, Department of Parks and Wildlife, Manjimup, WA, Australia
- ⁴²⁰PROPLAME-PRHIDEB-CONICET, Departamento de Biodiversidad y Biología Experimental, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Ciudad Universitaria, (CP1428EHA) Ciudad Autónoma de Buenos Aires, Argentina
- ⁴²¹ECT Oekotoxikologie GmbH, Flörsheim am Main, Germany
- ⁴²²LOEWE Biodiversity and Climate Research Centre BiK-F, Frankfurt/Main, Germany
- ⁴²³Facultad de Ciencias Ambientales, Universidad de Ciencias Aplicadas y Ambientales U.D.C.A, Bogotá, Colombia
- ⁴²⁴Catedras CONACYT, CIIDIR, Unidad Oaxaca, IPN, Santa Cruz Xoxocotlán, Mexico
- ⁴²⁵Universidad de Ciencias Aplicadas y Ambientales U.D.C.A., Bogotá, Colombia
- ⁴²⁶School of Natural Resources and Environment, University of Michigan, Ann Arbor, MI, USA
- ⁴²⁷Department of Environmental Sciences, University of Virginia, Charlottesville, VA, USA
- ⁴²⁸Blandy Experimental Farm, Boyce, VA, USA
- ⁴²⁹Département des sciences biologiques (SB), Université du Québec à Montréal (UQÀM), Montréal, QC, Canada
- ⁴³⁰Facultad de Ciencias, Universidad de Chile, Santiago, Chile
- ⁴³¹School of Geography, Earth and Environmental Sciences, University of Birmingham, Birmingham, UK
- ⁴³²Institute of Silviculture and Forest Protection, University of West Hungary, Sopron, Hungary
- ⁴³³Red de Ecología Funcional, Instituto de Ecología A.C. Carretera antigua a Coatepec, El Haya, Xalapa, Mexico
- ⁴³⁴Biology Centre CAS, Institute of Entomology, Ceske Budejovice, Czech Republic
- ⁴³⁵Faculty of Science, University of South Bohemia, Ceske Budejovice, Czech Republic
- ⁴³⁶Bishop's University, Sherbrooke, QC, Canada
- ⁴³⁷CSIRO, Dutton Park, Qld, Australia
- ⁴³⁸Naturalis Biodiversity Center, CR Leiden, The Netherlands
- ⁴³⁹Institute for Tropical Biology and Conservation, Universiti Malaysia Sabah, Jalan UMS, Kota Kinabalu, Malaysia
- ⁴⁴⁰Biocentre Klein Flottbek & Botanical Garden, University of Hamburg, Hamburg, Germany
- ⁴⁴¹Center for Development Research (ZEF), University of Bonn, Bonn, Germany
- ⁴⁴²Chair for Landscape Management, University of Freiburg, Freiburg, Germany
- ⁴⁴³AgResearch Limited, Lincoln Research Centre, Christchurch, New Zealand
- ⁴⁴⁴Institute for Ecology, Evolution and Diversity, Goethe University Frankfurt, Frankfurt am Main, Germany
- ⁴⁴⁵Biology and Biomedical Sciences Division, University of Brighton, Brighton, UK
- ⁴⁴⁶Charles Darwin University, Brinkin, NT, Australia
- ⁴⁴⁷Lawrence University, Appleton, WI, USA
- ⁴⁴⁸School of Natural Resources and Extension, University of Alaska Fairbanks, Fairbanks, AK, USA
- ⁴⁴⁹Center for Ecology, Development and Research, Dehradun, India

- ⁴⁵⁰School of Life Sciences, University of KwaZulu-Natal, Durban, South Africa
- ⁴⁵¹Department of Ecology and Natural Resource Management (INA), Norwegian University of Life Sciences (NMBU), Ås, Norway
- ⁴⁵²Museum of Natural Science and Department of Biological Sciences, Louisiana State University, Baton Rouge, LA, USA
- ⁴⁵³Baton Rouge, LA, USA
- ⁴⁵⁴Department of Life Sciences, Ben-Gurion University of the Negev, Be'er Sheva, Israel
- ⁴⁵⁵The Yerucham Center of Ornithology and Ecology, Yerucham, Israel
- ⁴⁵⁶Instituto de Ciências Biológicas, Universidade Federal do Pará, Belém, Brazil
- ⁴⁵⁷Organic Research Centre, Elm Farm, Newbury, UK
- ⁴⁵⁸United States Department of Agriculture, South San Francisco, CA, USA
- ⁴⁵⁹Universidad Nacional de Colombia, Sede Medellín, Medellín, Colombia
- ⁴⁶⁰Department of Biological Sciences, National University of Singapore, Singapore, Singapore
- ⁴⁶¹Ecología de Comunidades Áridas y Semiáridas (EComAS), Departamento de Recursos, Facultad de Ciencias Exactas y Naturales, UNLPam., Santa rosa, La Pampa, Uruguay
- ⁴⁶²Gobierno Autónomo Departamental Santa Cruz, Santa Cruz de la Sierra, Bolivia
- ⁴⁶³Université du Québec à Rimouski, Centre for Northern Research, Centre for Forest Studies, Rimouski, QC, Canada
- ⁴⁶⁴School of Environmental Studies, University of Victoria, Victoria, BC, Canada
- ⁴⁶⁵Museu de Ciències Naturals de Granollers, Granollers, Barcelona, Spain
- ⁴⁶⁶School of Renewable Natural Resources, Louisiana State University Agricultural Center, Baton Rouge, LA, USA
- ⁴⁶⁷Biological Dynamics of Forest Fragments Project, Instituto Nacional de Pesquisas da Amazônia, Manaus, Brazil
- ⁴⁶⁸Department of Natural Resources and Environmental Management, University of Hawaii, Manoa, Honolulu, HI, USA
- ⁴⁶⁹Key Laboratory of Zoological Systematics and Evolution, Institute of Zoology, Chinese Academy of Sciences, Chaoyang District, Beijing, China
- ⁴⁷⁰State Key Laboratory of Urban and Regional Ecology, Research Center for Eco-Environmental Sciences, Chinese Academy of Sciences, Haidian District, Beijing, China
- ⁴⁷¹Institute of Zoology, University of Natural Resources and Life Sciences, Vienna, Austria
- ⁴⁷²Department of Environmental Science and Policy, Drake University, Des Moines, IA, USA
- ⁴⁷³Department of Biology, Hong Kong Baptist University, Kowloon Tong, Hong Kong SAR, China
- ⁴⁷⁴Zoological Division, Research Center For Biology, The Indonesian Institute of Sciences, Cibinong, Bogor, Indonesia
- ⁴⁷⁵Section for Ecoinformatics & Biodiversity, Department of Bioscience, Aarhus University, Aarhus C, Denmark
- ⁴⁷⁶Department of Zoology, Institute of Ecology and Earth Sciences, University of Tartu, Tartu, Estonia
- ⁴⁷⁷School of Ecosystem and Forest Science, Faculty of Science, The University of Melbourne, Richmond, Vic., Australia
- ⁴⁷⁸Department of Biology, Saint Louis University, St. Louis, MO, USA
- ⁴⁷⁹MTA-DE Biodiversity and Ecosystem Services Research Group, Debrecen, Hungary
- ⁴⁸⁰Insect Ecology Group, Department of Zoology, University of Cambridge, Cambridge, UK
- ⁴⁸¹Centre for Integrative Ecology, School of Biological Sciences, University of Canterbury, Christchurch, New Zealand
- ⁴⁸²Instituto Neotropical: Pesquisa e Conservação, Curitiba, Brazil
- ⁴⁸³Department of Ecology and Territory, School of Environmental and Rural Studies, Pontificia Universidad Javeriana, Bogota, Colombia
- ⁴⁸⁴Naturhistorisches Museum Basel, Leiter Biowissenschaften, Basel, Switzerland
- ⁴⁸⁵NERC Centre for Ecology & Hydrology, Bush Estate, Penicuik, Edinburgh, UK
- ⁴⁸⁶Instituto de Biologia, Universidade Federal de Uberlândia (UFU), Uberlândia, Brazil
- ⁴⁸⁷Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Science, Sofia, Bulgaria
- ⁴⁸⁸Division Forest, Nature, and Landscape, Department of Earth & Environmental Sciences, KU Leuven, Leuven, Belgium
- ⁴⁸⁹Museu Nacional de História Natural e da Ciência, Borboletário – Depart. Zoologia, Lisboa, Portugal
- ⁴⁹⁰Departamento de Ciencias Químico-Biológicas, Universidad de las Américas Puebla, Cholula, Mexico
- ⁴⁹¹Departamento de Gestión Agraria, Universidad de Santiago de Chile, Santiago, Chile
- ⁴⁹²Den Haag, The Netherlands
- ⁴⁹³Royal Museum for Central Africa – Joint Experimental Molecular Unit, Tervuren, Belgium
- ⁴⁹⁴Vietnam National Museum of Nature, Vietnam Academy of Science and Technology, Cau Giay, Hanoi, Vietnam
- ⁴⁹⁵Botany Department, University of Otago, Dunedin, New Zealand
- ⁴⁹⁶School for Resource and Environmental Studies, Faculty of Management, Dalhousie University, Halifax, NS, Canada
- ⁴⁹⁷Key Laboratory of Protection and Development Utilization of Tropical Crop Germplasm Resource, Ministry of Education, College of Horticulture and Landscape Agriculture, Hainan University, Haikou, China

⁴⁹⁸College of Life Sciences, Zhejiang University, Hangzhou, China

⁴⁹⁹Department of Biology, John Carroll University, University Heights, OH, USA

⁵⁰⁰The Environment Institute and School of Earth and Environmental Sciences, The University of Adelaide, Adelaide, SA, Australia

⁵⁰¹Environmental Futures Research Institute, Griffith University, Brisbane, Qld, Australia

⁵⁰²Department of Environmental and Natural Resources, Presbyterian University College, Akropong Akuapem, Ghana

⁵⁰³School of Natural Sciences and Psychology, Liverpool John Moores University, Liverpool, UK

⁵⁰⁴Center for Environmental Sciences & Engineering, University of Connecticut, Storrs, CT, USA

⁵⁰⁵Department of Ecology & Evolutionary Biology, University of Connecticut, Storrs, CT, USA

⁵⁰⁶Institute for Biodiversity and Ecosystem Dynamics (IBED), University of Amsterdam, GE Amsterdam, The Netherlands

⁵⁰⁷NERC Centre for Ecology & Hydrology, Crowmarsh Gifford, Wallingford, UK

⁵⁰⁸Institute of Biodiversity Science, School of Life Sciences, Fudan University, Shanghai, China

⁵⁰⁹International Institute of Tropical Forestry, USDA Forest Service, Sabana Field Research Station, Luquillo, PR, USA

⁵¹⁰Tsukuba University, Ibaraki, Japan

⁵¹¹School of Biological Sciences, University of East Anglia, Norwich Research Park, Norwich, UK

⁵¹²State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, China

⁵¹³A. N. Severtsov Institute of Ecology and Evolution, Moscow, Russia

⁵¹⁴Integrated Environmental Consultants Namibia (IECN), Windhoek, Namibia

⁵¹⁵Guangdong Entomological Institute/South China Institute of Endangered Animals, Guangzhou, China

⁵¹⁶Computational Ecology and Environmental Science, Microsoft Research, Cambridge, UK

Correspondence

Lawrence N. Hudson, Department of Life Sciences, Natural History Museum, London, UK.

Email: l.hudson@nhm.ac.uk

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Abstract

The PREDICTS project—Projecting Responses of Ecological Diversity In Changing Terrestrial Systems (www.predicts.org.uk)—has collated from published studies a large, reasonably representative database of comparable samples of biodiversity from multiple sites that differ in the nature or intensity of human impacts relating to land use. We have used this evidence base to develop global and regional statistical models of how local biodiversity responds to these measures. We describe and make freely available this 2016 release of the database, containing more than 3.2 million records sampled at over 26,000 locations and representing over 47,000 species. We outline how the database can help in answering a range of questions in ecology and conservation biology. To our knowledge, this is the largest and most geographically and taxonomically representative database of spatial comparisons of biodiversity that has been collated to date; it will be useful to researchers and international efforts wishing to model and understand the global status of biodiversity.

KEYWORDS

data sharing, global biodiversity modeling, global change, habitat destruction, land use

1 | INTRODUCTION

Many indicators are available for tracking the state of biodiversity through time, for example, in order to assess progress toward goals such as the Convention on Biological Diversity's 2010 target or the newer Aichi Biodiversity Targets (Pereira et al., 2013; Tittensor et al., 2014). Most of the available indicators are taxonomically or ecologically narrow in scope, and many are based on the global status of species (e.g., Butchart et al., 2010; Tittensor et al., 2014), because of

the finality of extinction. However, using a more representative set of taxa and considering local biodiversity offers several advantages. First, average responses of species to human impacts typically vary among higher taxa and ecological guilds (Lawton et al., 1998; McKinney, 1997; Newbold et al., 2014; WWF International, 2014), meaning that indicators need to be broadly based and as representative as possible, if they are to be used as proxies for biodiversity as a whole. Second, the taxa for which most data on trends are available (typically, charismatic groups such as birds or butterflies) are not always the most

important for the continued functioning of ecosystems and delivery of ecosystem services (Norris, 2012). Third, although many of the ultimate drivers behind biodiversity loss are global, the most important pressure mechanisms usually act much more locally (Brook, Ellis, Perring, Mackay, & Blomqvist, 2013). Fourth, most ecosystem services and their underpinning processes are mediated by local rather than global biodiversity (Cardinale et al., 2012; Grime, 1998): It is local rather than global functional diversity, for example, that determines how ecosystems function in a given set of conditions (Steffen et al., 2015). Finally, presence/absence and especially abundance of species at a site respond more rapidly to disturbance than extent of geographic distribution or global/national extinction risk (Balmford, Green, & Jenkins, 2003; Collen et al., 2009; Hull, Darroch, & Erwin, 2015), so local changes are likely to be detected before large global changes or extinction.

For these reasons, there is a need to model the response of local biodiversity to human pressures and, thus, to estimate biodiversity changes at local scales, but across a wide spatial domain (ideally globally) and for a wide range of taxa. We therefore need comparable high-quality data on local biodiversity at different levels of human pressure, from many different taxa and regions. At present, spatial comparisons of how biodiversity responds to variation in pressures provide the only feasible way to collate a large, globally representative evidence base and to model responses to human impacts. Although large temporal datasets are available (e.g., Butchart et al., 2004; Collen et al., 2009; Dornelas et al., 2014; Vellend et al., 2013), they may not be sufficiently representative of anthropogenic pressures for the trends they show to be taken at face value (Gonzalez et al., 2016). Furthermore, in the absence of contemporaneous site-specific information about pressures, it is not straightforward to use these data to model how biodiversity responds to pressures or to project changes into the future (but see Visconti et al., 2015). Spatially extensive field data of suitable quality and resolution are time-consuming and expensive to collect. The most convenient and readily available source of suitable biodiversity data is the published literature: Thousands of published papers are based on datasets that would be of value to global modeling efforts. However, it has been rare for such papers to publish data in full, even as supporting information, meaning that many potentially valuable datasets are “dark data” (Hampton et al., 2013), effectively at risk of being lost to science if they have not been lost already.

Since 2012, the PREDICTS project has been collating data on local biodiversity at different levels of human pressure from published papers, where necessary contacting those papers' corresponding authors to request the underlying biodiversity data, species' identities, and precise sampling locations. We have enhanced the collated data by scoring site characteristics relating to human pressures such as the predominant land use and how intensively the land is used by humans. We also used the geographical coordinates of the sites to match them to a number of published spatially explicit datasets. The database has already been used to conduct global (e.g., Newbold et al., 2015; Newbold, Hudson, Arnell, et al., 2016), regional (De Palma et al., 2016) and national (Echeverría-Londoño et al., 2016) analyses of the responses of local biodiversity to land use and related human

pressures. The database was first described by Hudson et al. (2014) who published an interim version (March 2014) of the site-level meta-data along with a detailed description of how the database has been collated and validated. Since that time, the database has nearly doubled in size. Here, we describe the status of the database and make available the full species-level data themselves (not just the site meta-data previously released) to facilitate other research, especially into human impacts on ecological assemblages. We also include suggestions for how the database can be used.

2 | METHODS

We sought datasets describing the abundance or occurrence of species, or the diversity of ecological assemblages of species at multiple sites in different land uses or at different levels of other human pressures (e.g., differing levels of land-use intensity). Data were primarily collated through subprojects on particular regions, land uses, or taxa. We also made general requests for data at conferences and through published articles (Hudson, Newbold, et al., 2013; Hudson et al., 2014; Newbold et al., 2012). Through the course of the project, searches were increasingly targeted toward under- or unrepresented regions, biomes, or taxa, in order to mitigate biased coverage in the literature.

To be included in the database, data were required to meet the following criteria: (1) the dataset was part of a published work, or the sampling methods were published; (2) the same sampling procedure was carried out at each site within each study (sampling effort was permitted to vary so long as it was recorded for each site); and (3) we could acquire the geographical coordinates of each sampled site. Where the author of the original publication was unable to supply the geographical coordinates, sites were georeferenced from maps in the publication (Hudson et al., 2014). Sites' land use—primary vegetation, secondary vegetation (divided according to stage of recovery into mature, intermediate and young; or indeterminate where information on stage was unavailable), plantation forest, cropland, pasture and urban—and, within each land-use class, intensity—minimal, light and intense—were classified from the description given in the source publication or information subsequently provided by data contributors (see Hudson et al., 2014 for full details). These land-use categories were chosen to be as compatible as possible with those used in the harmonized land-use scenarios for 1500–2100 (Hurt et al., 2011) in order to facilitate spatial and temporal projections of modeled land-use effects on biodiversity (e.g., Newbold et al., 2015). For some sites, land use and/or use intensity could not be established, so were given missing values.

The data were arranged in a hierarchical structure. The data from an individual published work, typically a published paper, constituted a “DataSource.” Where different sampling methods were used within a DataSource, for example, because different taxonomic groups were collected, and the data were made available separately, the data were divided into separate “Studies.” Data from a given DataSource were also split into multiple Studies if they covered large geographic areas (e.g., several countries), to reduce the effect of biogeographic differences within Studies. Each Study contained a set of sampled “Sites”

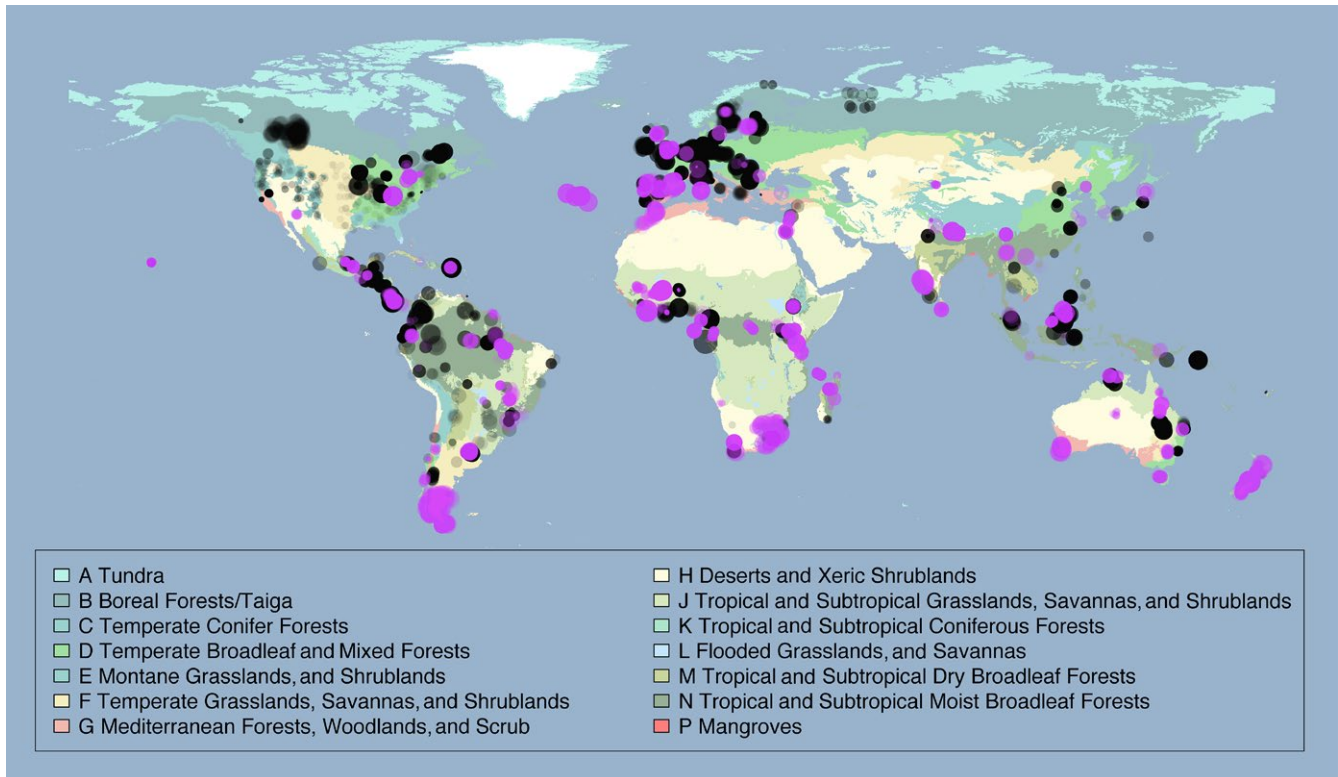


FIGURE 1 Sampling locations. Map colors indicate biomes, taken from the Terrestrial Ecoregions of the World dataset (The Nature Conservancy, 2009), shown in a geographic (WGS84) projection. Circle radii are proportional to \log_{10} of the number of samples at that Site. All circles have the same degree of partial transparency. Sites added to the database since Hudson et al. (2014) are shown in pink

and “Taxa”; at each Site a set of “Measurements” (typically the abundance or occurrence of a set of taxa) were taken. The provided database extracts contain, for each Site, the raw measurement values, the sampling efforts and, where relevant, the effort-corrected abundance values (corrected across Sites within a Study by dividing the abundance measurement by sampling effort, assuming that sampled abundances increase linearly with sampling effort, after first rescaling effort values within each Study to a maximum value of one). The measurements were not corrected for different detectability (Hayward et al., 2015; MacKenzie et al., 2002).

It is important to note that the data in the database are often not exactly the same as those used in the source papers. Numbers of sites may differ because datasets provided may have been partial or included extra sites, or because we have aggregated or disaggregated data differently. Likewise, numbers of taxa may differ because of curation or because more data were provided than had been used in the source paper. Because our focus was to make these data as useful as possible for PREDICTS analyses, rather than to act as a repository for datasets from previous publications, it will often not be possible to use these data to replicate the analyses presented in the source papers.

We were limited by the rate at which we could process new data because so many datasets were contributed. This led to the development of a backlog, which we had to clear by the end of the first phase of funding for PREDICTS. During this stage of the project, in order to process all the datasets in hand within the time available, we focused our

efforts on the fields shown to be most important in our models to that point (De Palma et al., 2015; Newbold et al., 2014, 2015). As a result, DataSources processed since early 2015 often lack data for some fields, including coordinate precision and maximum linear extent; details of the potentially affected fields are listed in Supporting Information.

Team members were trained in how to score datasets received, using written definitions and descriptions of fields and terms, as well as practice datasets. All data underwent basic validation checks to ensure values entered in each field were appropriate (Hudson et al., 2014). Geographical coordinates were visually inspected on a map after entry into the database, and our software automatically detected coordinates falling outside of the expected country (e.g., because latitude and longitude values were accidentally swapped). For the calculation of biodiversity metrics such as species richness, we accepted the identifications of species provided by the authors of the source publications; these were determined at the time of the original research, and so will not reflect subsequent taxonomic changes or re-identifications. We also matched taxonomic names to the Catalogue of Life 2013 checklist (COL; Roskov et al., 2013), allowing us to validate many of the names, assess taxonomic coverage and relate measurements to species-level datasets such as those describing ecological traits. We make available both the original species classifications and those from COL (field names are given in Supporting Information). We reviewed and corrected a number of potential error cases, such as names without a matching COL record, and names for which the higher taxonomic

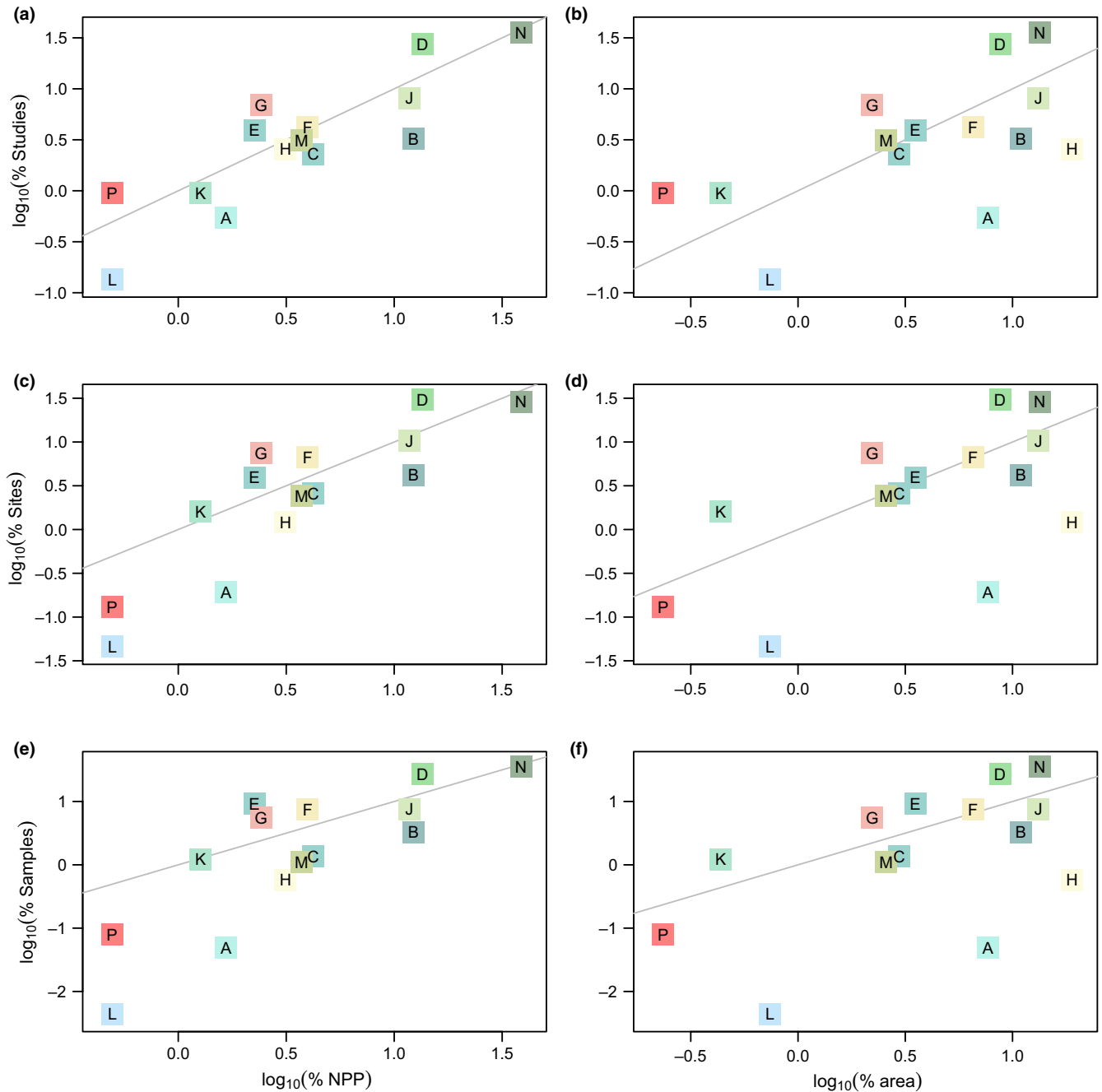


FIGURE 2 Coverage of biomes. The percentage of Studies (a and b), Sites (c and d), and samples (e and f) against percentages of terrestrial NPP (Net Primary Productivity, computed as in Hudson et al., 2014; a, c, and e) and terrestrial area (b, d, and f). Biome codes and colors are as in Figure 1

rank of the matching COL record was unexpected (e.g., a COL record for a true fly within a Study that examined birds). Many more validation checks were applied; a complete description is in Hudson et al. (2014).

3 | RESULTS

3.1 | Geographical coverage

This release of the PREDICTS database contains 3,250,404 records, from 26,114 sampled Sites (Figure 1), collated from 480 DataSources

and 666 Studies. The data represent all of the world's 14 terrestrial biomes, in approximate proportion to their contribution to global total primary productivity (Figure 2). The sampled Sites span 94 of the world's countries (including all 17 megadiverse countries; Mittermeier, Gil, & Mittermeier, 1997), 281 of the 814 terrestrial ecoregions (The Nature Conservancy 2009) and 32 of Conservation International's 35 biodiversity hotspots (Myers, Mittermeier, da Fonseca, & Kent, 2000; circles on Figure 3). Although the database focuses on land use, it also includes data from regions that have so far seen relatively little land-use change, such as some

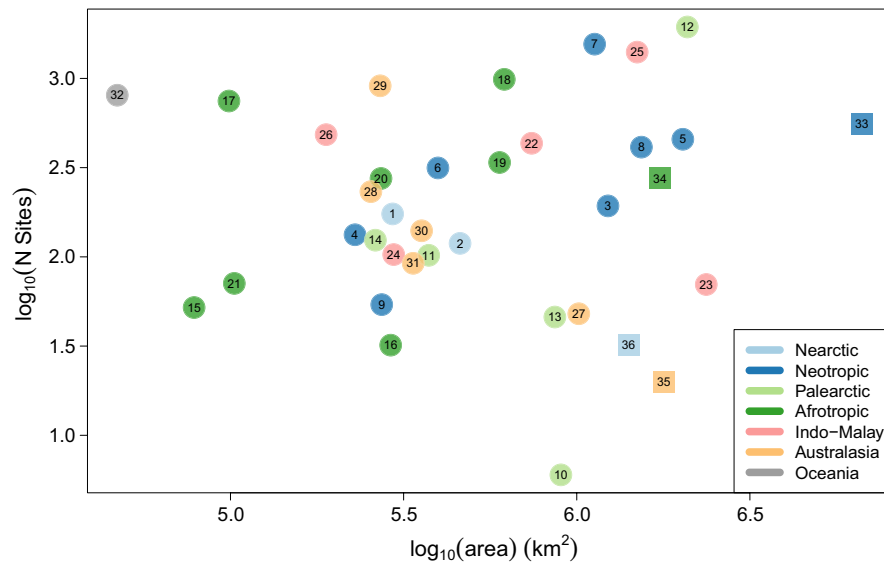


FIGURE 3 Numbers of Sites against the areas of biodiversity hotspots and of high biodiversity wilderness areas (HBWAs). Hotspots are shown by circles and HBWAs by squares; symbols are colored by the predominant biogeographic realm in which they fall. Hotspots are 1 California Floristic Province, 2 Madrean Pine-Oak Woodlands, 3 Atlantic Forest, 4 Caribbean Islands, 5 Cerrado, 6 Chilean Winter Rainfall and Valdivian Forests, 7 Mesoamerica, 8 Tropical Andes, 9 Tumbes-Choco-Magdalena, 10 Irano-Anatolian, 11 Japan, 12 Mediterranean Basin, 13 Mountains of Central Asia, 14 Mountains of Southwest China, 15 Cape Floristic Region, 16 Coastal Forests of Eastern Africa, 17 Eastern Afrotropical, 18 Guinean Forests of West Africa, 19 Madagascar and the Indian Ocean Islands, 20 Moputaland-Pondoland-Albany, 21 Succulent Karoo, 22 Himalaya, 23 Indo-Burma, 24 Philippines, 25 Sundaland, 26 Western Ghats and Sri Lanka, 27 East Melanesian Islands, 28 Forests of East Australia, 29 New Zealand, 30 Southwest Australia, 31 Wallacea, 32 Polynesia-Micronesia and HBWAs are 33 Amazonia, 34 Congo Forests, 35 New Guinea, 36 North American Deserts. Unrepresented are the hotspots Caucasus, Horn of Africa, New Caledonia and the HBWA Miombo-Mopane Woodlands and Savannas

high biodiversity wilderness areas (Mittermeier et al., 2003; squares on Figure 3).

3.2 | Taxonomic coverage

Records in the PREDICTS database represent 47,044 species (see Hudson et al., 2014 for how species numbers are estimated in the face of imprecise taxon names), which is over 2% of the number thought to have been formally described (Chapman, 2009)—29,737 animals, 15,545 plants, 1,759 fungi, and three protists. The taxonomic distribution of taxa in the database is in rough proportion to the numbers of described species in major taxonomic groups of animals and plants (Figure 4), and the data represent more than 1% as many species as have been described in the following groups: Amphibia, Arachnida, Archaeognatha, Ascomycota, Aves, Basidiomycota, Bryophyta, Chilopoda, Coleoptera, Collembola, Dermaptera, Diptera, Embioptera, Ferns and allies, Glomeromycota, Gymnosperms, Hemiptera, Hymenoptera, Isoptera, Lepidoptera, Magnoliophyta, Mammalia, Mantodea, Mecoptera, Neuroptera, Odonata, Onychophora, Orthoptera, Reptilia, Symphyla and Zoraptera (Figure 4). Vertebrates—and especially birds—are overrepresented owing to biases in the published literature (Figure 4), but less so than in many other data compilations (e.g., over half of the records currently in the Global Biodiversity Information Facility [GBIF] are of birds; www.gbif.org, accessed in April 2016). Most Studies in the PREDICTS database sampled at least multiple families, if not multiple orders, classes, phyla,

or even kingdoms (Figure 5). However, some Studies sampled only a single family, genus, or even species (Figure 5).

3.3 | Temporal coverage

We focused primarily on data sampled since 2000 because most global layers describing human pressure are collected after this year and, in particular, to facilitate use of contemporaneous Moderate-resolution Imaging Spectroradiometer (MODIS) remotely sensed data (Justice et al., 1998; Tuck et al., 2014) in modeling. However, in filling certain taxonomic and geographic gaps, we also collated some data that were sampled before 2000 (Figure 6). Data are sparse after 2012 because of the natural time lags between data collection in the field, publication and then assimilation into the PREDICTS database (Figure 6).

3.4 | Data access and structure

This 2016 release of the database—the complete dataset and also site-level summaries—is available on the data portal of the Natural History Museum, London (doi: 10.5519/0066354) as comma-separated variable (CSV) files and as RDS files, the latter for use with the R statistical modeling language (R Core Team 2015; RDS files were generated using R 3.3.1). A complete description of the columns in the extracts, along with a visualization of the database schema, is given in Supporting Information. This paper makes all the data in this version of the database freely available to anyone wishing to use

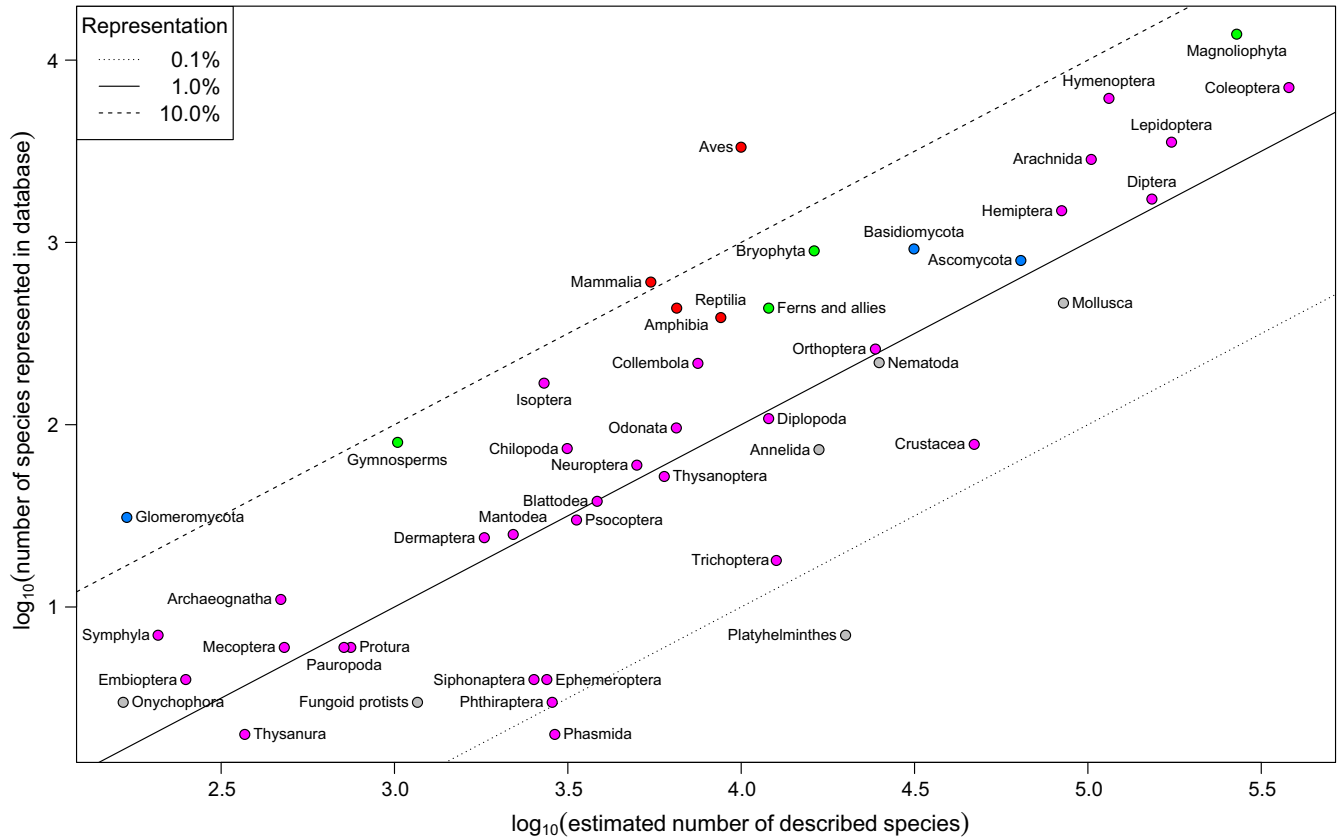


FIGURE 4 Taxonomic coverage. The numbers of species in our database against the numbers of described species within each of 59 higher taxa, as estimated by Chapman (2009), on logarithmic axes. Vertebrates are shown in red, arthropods in pink, other animals in gray, plants in green, and fungi in blue. The dashed, solid, and dotted lines indicate 10, 1, and 0.1% representation, respectively. Groups with just a single species represented (Diplura and Zoraptera) are not shown

them for any purpose. The terms of the license require that anyone publishing research based on these data should cite this paper and/or the original sources of the data used, as appropriate. The dataset at doi: 10.5519/0066354 contains bibliographic information for all DataSources in both CSV and BibTeX formats.

4 | DISCUSSION

The PREDICTS database is designed to be able to address a range of questions about how land use and related pressures have influenced the occurrence and abundance of species and the diversity of ecological assemblages. The highly structured nature of the data, with comparable surveys having been carried out at each Site within a Study, was chosen to facilitate such modeling. Table 1 identifies a range of long-standing general questions for which the PREDICTS data may be useful, referencing early papers addressing questions of each type. It also outlines the steps required to tackle each kind of question, in conjunction with other information about the Sites and species where necessary, and refers to papers that have performed so.

Changes in attitudes to—and the increasing ease of—data sharing have contributed to rapid growth in open compilations of structured biodiversity data and related pressure data targeted toward particular

kinds of research question. Examples of data types featured in such compilations include population time series (e.g., Inchausti & Halley, 2001), assemblage time series (e.g., Dornelas et al., 2014), assemblage inventories (e.g., Thibault, Supp, Giffin, White, & Ernest, 2011), and species traits (e.g., Madin et al., 2016). Other projects have collated or are collating large compilations of structured biodiversity data, such as BIOFRAG (Pfeifer et al., 2014; habitat fragmentation), BIOTIME (The BioTIME Research Group, 2016; detailed time-series data, still being compiled) and GLOBIO3 (Alkemade et al., 2009; pristine versus disturbed habitats, not publicly available).

The largest open compilation of biodiversity data is the Global Biodiversity Information Facility (GBIF; www.gbif.org), which aggregates mostly unstructured species occurrence data. The unstructured nature of most GBIF data limits the range of questions to which they can easily be put, although they are increasingly used in modeling species distributions (e.g., Pineda & Lobo, 2008) and habitat suitability (e.g., Ficetola, Rondinini, Bonardi, Baisero, & Padoa-Schioppa, 2015). As of April 2016, GBIF holds over 560 million georeferenced occurrence records of around 1.5 million species, although coverage is taxonomically uneven (e.g., most records are of birds) and patchy even among the best-recorded groups (Meyer, Kreft, Guralnick, & Jetz, 2015).

Databases of species traits continue to be collated and published, and many of them are relevant to taxa in the PREDICTS

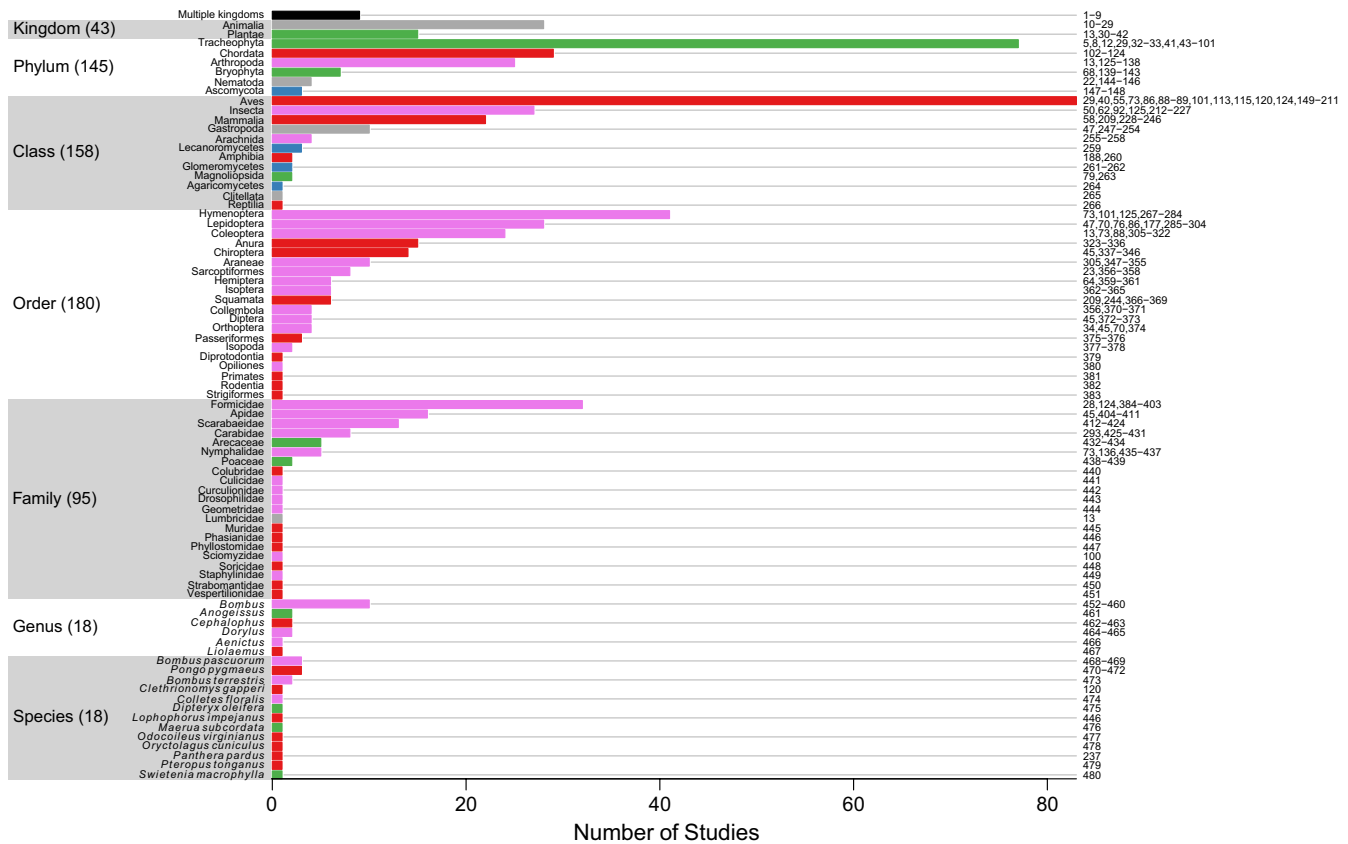


FIGURE 5 Number of Studies by lowest common taxonomic group. Bars show the number of Studies within each lowest common taxon (so, one Study examined the species *Swietenia macrophylla*, three Studies examined the species *Bombus pascuorum*, ten Studies examined multiple species within the genus *Bombus*, and so on). Colors are as in Figure 4. Numbers on the right are the primary references from which data were taken: 1 Basset et al. (2008), 2 Buscardo et al. (2008), 3 Christensen and Heilmann-Clausen (2009), 4 Dominguez, Bahamonde, and Muñoz-Escobar (2012), 5 López-Quintero, Straatsma, Franco-Molano, and Boekhout (2012), 6 Nöske et al. (2008), 7 Norton, Espie, Murray, and Murray (2006), 8 Peri, Lencinas, Martínez Pastur, Wardell-Johnson, and Lasagno (2013), 9 Robinson and Williams (2011), 10 Barratt et al. (2005), 11 Bonham, Mesibov, and Bashford (2002), 12 Boutin, Martin, and Baril (2009), 13 Carpenter et al. (2012), 14 Gaigher and Samways (2010), 15 Ge et al. (2012), 16 Hayward (2009), 17 Leighton-Goodall, Brown, Hammond, and Eggleton (2012), 18 Muchane et al. (2012), 19 Ngai et al. (2008), 20 Richardson, Richardson, and Soto-Adames (2005), 21 Schon, Mackay, Minor, Yeates, and Hedley (2008), 22 Schon, Mackay, Yeates, and Minor (2010), 23 Schon, Mackay, and Minor (2011), 24 Smith (2006), 25 Smith, Potts, Woodcock, and Eggleton (2008), 26 Smith, Potts, and Eggleton (2008), 27 Todd et al. (2011), 28 Vasconcelos et al. (2009), 29 Walker, Wilson, Norbury, Monks, and Tanentzap (2014), 30 Baeten, Velghe, et al. (2010), 31 Bakayoko, Martin, Chatelain, Traore, and Gautier (2011), 32 Center for International Forestry Research (CIFOR) (2013a), 33 Center for International Forestry Research (CIFOR) (2013b), 34 Dumont et al. (2009), 35 Firincioglu, Seefeldt, Sahin, and Vural (2009), 36 Haarmeyer, Schmiedel, Dengler, and Bosing (2010), 37 Joubert, Esler, and Privett (2009), 38 Norfolk, Eichhorn, and Gilbert (2013), 39 Page, Qureshi, Rawat, and Kushalappa (2010), 40 Proença, Pereira, Guilherme, and Vicente (2010), 41 Sheil et al. (2002), 42 Wang, Lencinas, Ross Friedman, Wang, and Qiu (2011), 43 Alignier and Deconhat (2013), 44 Baeten, Hermy, Van Daele, and Verheyen (2010), 45 Barlow, Gardner, et al. (2007), 46 Barrico et al. (2012), 47 Baur et al. (2006), 48 Berry et al. (2010), 49 Boutin, Baril, and Martin (2008), 50 Bouyer et al. (2007), 51 Brearley (2011), 52 Brunet et al. (2011), 53 Calviño-Cancela, Rubido-Bará, and van Etten (2012), 54 Castro, Lehsten, Lavorel, and Freitas (2010), 55 de Lima, Dallimer, Atkinson, and Barlow (2013), 56 Devineau, Fournier, and Nignan (2009), 57 Fensham, Dwyer, Eyre, Fairfax, and Wang (2012), 58 Fernandez and Simonetti (2013), 59 Fredriksson, Danielsen, and Swenson (2007), 60 Gendreau-Berthiaume, Kneeshaw, and Harvey (2012), 61 Golodets, Kigel, and Sternberg (2010), 62 Grass, Berens, Peter, and Farwig (2013), 63 Gutierrez et al. (2009), 64 Helden and Leather (2004), 65 Hernández, Delgado, Meier, and Duran (2012), 66 Hietz (2005), 67 Higuera and Wolf (2010), 68 Hylander and Nemomissa (2009), 69 Ishida, Hattori, and Takeda (2005), 70 Kati, Zografou, Tzirkalli, Chitos, and Willemse (2012), 71 Katovai, Burley, and Mayfield (2012), 72 Kessler et al. (2005), 73 Kessler et al. (2009), 74 Kolb and Diekmann (2004), 75 Krauss, Klein, Steffan-Dewenter, and Tschardtke (2004), 76 Krauss et al. (2010), 77 Kumar and Shahabuddin (2005), 78 Letcher and Chazdon (2009), 79 Louhaichi, Salkini, and Petersen (2009), 80 Lucas-Borja et al. (2011), 81 Måren (2011), 82 Måren, Bhattarai, and Chaudhary (2013), 83 Marin-Spiotta, Ostertag, and Silver (2007), 84 Mayfield, Ackerly, and Daily (2006), 85 McNamara, Erskine, Lamb, Chantalangsy, and Boyle (2012), 86 Milder et al. (2010), 87 O'Connor (2005), 88 Paritsis and Aizen (2008), 89 Phalan, Onial, Balmford, and Green (2011), 90 Pincheira-Ulbrich, Rau, and Smith-Ramirez (2012), 91 Poggio, Chaneton, and Ghersa (2013), 92 Power and Stout (2011), 93 Power, Kelly, and Stout (2012), 94 Ramesh et al. (2010), 95 Romero-Duque, Jaramillo, and Perez-Jimenez (2007), 96 Schmitt, Senbeta, Denich, Preisinger, and Boehmer (2010), 97 Shannon et al. (2008), 98 Siebert (2011), 99 Vassilev, Pedashenko, Nikolov, Apostolova, and Dengler (2011), 100 Williams, Sheahan, and Gormally (2009), 101 Yamaura et al. (2012), 102 Alcalá, Alcalá, and Dolino (2004), 103 Bicknell and Peres (2010), 104 Centro Agronómico Tropical de Investigación y Enseñanza (CATIE) (2010); Deheuvels, Avelino, Somarriba, and Malézieux (2012), Deheuvels et al. (2014); Rousseau, Deheuvels, Rodriguez Arias, and Somarriba (2012), 105 Craig et al. (2009), (Continues)

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database. Recent examples include mammalian generation time (Pacifci et al., 2013), a variety of mammalian traits (Jones et al., 2009), foraging attributes of birds and mammals (Wilman et al., 2014), field metabolic rates of birds and mammals (Hudson, Isaac, & Reuman, 2013) and functional traits of vascular plants (Kattge et al., 2011). Additional databases provide more abstract concepts such as species' threat status (International Union for Conservation of Nature, 2016) and estimates of the degrees of protection required

(Convention on International Trade in Endangered Species of Wild Fauna and Flora, 2016). Relating such data with measurements in the PREDICTS database makes possible investigation into how traits mediate species' responses to changes in land use and land-use intensity. Examples of published analyses have examined habitat specialization and geographical range size of birds and mammals (Newbold et al., 2014), functional traits of vascular plants (Bernhardt-Römermann et al., 2011) and a range of morphometric,

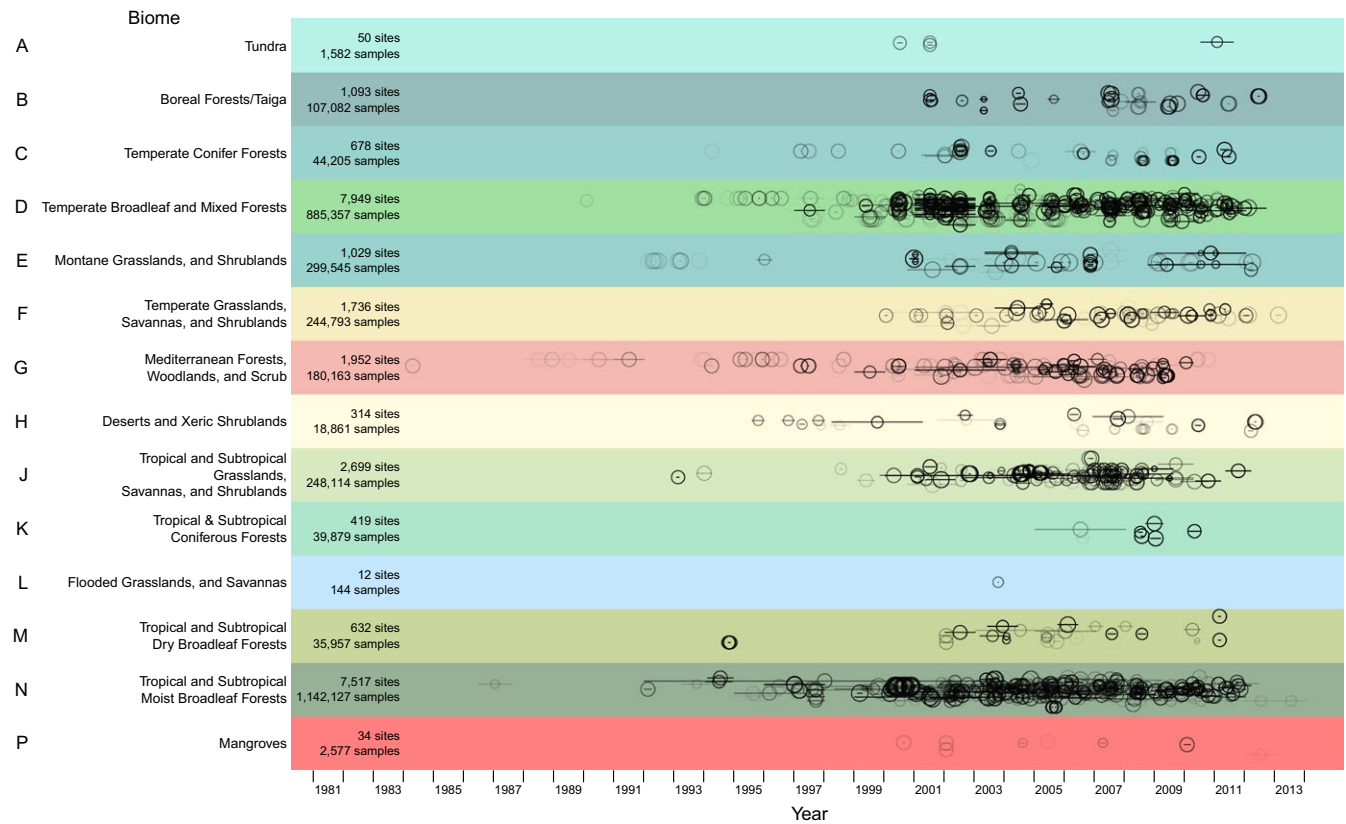


FIGURE 6 Spatiotemporal sampling coverage. Site sampling dates are shown by biome. Each Site is represented by a circle and line. Circle radii are proportional to \log_{10} of the number of samples at that Site. Circle centers are at the midpoints of Site sampling dates; lines indicate the start and end dates of sampling. Y-values have been jittered at the Study level. Circles and lines have the same degree of partial transparency. Biome colors and letters are as in Figure 1

physiological, and functional traits of bees (De Palma et al., 2015); see Table 1, Q. 3.

Although our targeting of data from underrepresented biomes and taxa (Hudson et al., 2014) reduces the effects of geographic and taxonomic biases in available data, the PREDICTS database nonetheless has many limitations, of which four are particularly important to note. First, our individual datasets seldom take a whole-ecosystem perspective, being instead taxonomically or ecologically restricted; consequently, our data shed little light on how trophic webs or other interactions are affected by human pressures. Second, even within the groups sampled, our data do not provide complete inventories of the species that would be found with comprehensive sampling; thus, failure to record a species from a Site does not provide strong evidence of absence. Third, Latin binomials were not available for a sizeable fraction of the species in our DataSources, limiting the prospects for linking the observations of occurrence and abundance to other information about the species (e.g., functional traits; Kattge et al., 2011). Last, because our database was designed to test hypotheses about local-scale variation in biodiversity, it is not particularly informative about large-scale biodiversity patterns such as the latitudinal gradient in species richness or how pressures with a coarse spatial grain (e.g., atmospheric nitrogen deposition; Simkin et al., 2016) influence Site-level diversity.

When using the PREDICTS database, or indeed any database, to model biodiversity responses, it is important to be aware of potential

mismatches in scale between Site-level data and pressure data such as MODIS remotely sensed data (Justice et al., 1998) and the harmonized land-use scenarios (Hurtt et al., 2011) and also between Site-level response variables and the scales of interest. The PREDICTS database contains some structural features that help with these issues. First, we assigned the Site-level land use and land-use intensity classifications based on the authors' descriptions of the habitats so these classifications do not suffer from the problem of scale mismatch. Second, Sites are represented as precisely as possible: Sites often represent individual quadrats, traps, or other points within a broader sampling regime (such as a transect), and we recorded (as latitude and longitude) the coordinates of each Site rather than aggregating them into coarser summaries across the broader sampling regime. Third, where the relevant information was available, we also recorded the maximum extent of sampling as a linear value in meters (for 22,199 Sites, see Hudson et al. (2014) for details). Users of the database therefore have flexibility in deciding how measurements in the PREDICTS database are related to available pressure data. Possible solutions to scale mismatches between biodiversity data and pressure data would be (1) to exclude from analyses any Sites where the extent of sampling is substantially greater than the grain size of the pressure data or (2) to conduct some sort of spatial averaging of the pressure data. Novel methods have been published both for downscaling pressure data (e.g., Hoskins et al., 2016) and for upscaling local biodiversity

TABLE 1 Questions that could be answered using the PREDICTS database

Question	Early example references	Approach	Example using PREDICTS database	
<i>Questions about taxa</i>				
Q 1.	What factors influence the occurrence and/or abundance of a particular focal species?	Austin, Nicholls, and Margules (1990)	Filter to remove species not of interest. Merge PREDICTS data with data on any additional site-level characteristics of interest. One possible analytical approach is to model effects of site characteristics on presence-absence and log (abundance when present) separately, the first with binomial errors and the second with Gaussian errors, while accounting for among-Study differences (e.g., using mixed-effects models).	-
Q 2.	Do changes in land-use facilitate success of invasive species?	Dukes and Mooney (1999), Theoharides and Dukes (2007)	Obtain lists of invasive species for the regions of interest and model presence-absence and/or abundance of invasives as above.	-
Q 3.	Which ecological attributes of species make them more or less sensitive to human pressures?	McKinney (1997), Davies, Margules, and Lawrence (2000), Cardillo et al. (2005)	Merge PREDICTS data with species-level data on traits of interest. Model how site and species characteristics affect presence-absence and log (abundance when present) separately as above, accounting for Study-level and taxon-level differences (e.g., using mixed-effects models).	Newbold et al. (2014), De Palma et al. (2015)
Q 4.	Which taxa have species that are more sensitive to human pressures, and which have less sensitive species?	Lawton et al. (1998), Mace and Balmford (2000), Gibson et al. (2011)	Add taxonomic group into models above as a fixed effect interacting with other fixed effects.	-
Q 5.	Are phylogenetically distinct species particularly sensitive?	Gaston and Blackburn (1997), Purvis, Agapow, Gittleman, and Mace (2000)	Analyze phylogenetic distinctiveness or unique evolutionary history in the same way as ecological attributes.	-
Q 6.	What are the relationships between geographic range size or occupancy and abundance?	Brown (1984)	Merge PREDICTS data with species-level data on range sizes or occupancy. Filter to the land uses of interest (e.g., primary vegetation if the focus is on natural systems), and examine within-Study relationship between abundance and relative range size or occupancy.	-
Q 7.	Do suitability estimates from environmental niche models predict abundance?	VanDerWal, Shoo, Johnson, and Williams (2009)	Use other data on occurrences of species to fit niche models for all species in within selected Studies and thereby estimate suitability of each Site. Various modeling options are then possible depending on the precise question: for example, fit land use interacting with suitability when modeling abundance in order to test whether any correlation depends on land use.	-
<i>Questions about sites</i>				
Q 8.	Which land uses and other Site-level pressures have the strongest net impact on levels of local biodiversity?	Lawton et al. (1998), Gibson et al. (2011)	Aggregate biodiversity data within a site to estimate relevant diversity metric (e.g., within-sample species richness, total abundance, rarefaction-based richness, species evenness). Merge Site-level biodiversity data with any additional data on Site-level characteristics of interest (e.g., from remotely sensed data) if required. Model Site-level diversity as a function of Site characteristics while accounting for among-Study differences (e.g., using mixed-effects models).	fig 1b,c in Newbold et al. (2015)

(Continues)

TABLE 1 (Continued)

Question	Early example references	Approach	Example using PREDICTS database
Q 9. How do land use and other pressures reduce compositional intactness?	Scholes and Biggs (2005)	Because net changes are affected by gains of non-native species as well as losses of those originally present, modeling compositional intactness gives a more sensitive indication of human impacts. Model Site-level abundance as a function of pressures as above, and how compositional similarity to assemblages in primary vegetation differs among land uses. Combine these models to estimate the Biodiversity Intactness Index (Scholes & Biggs, 2005)—the average abundance of a diverse set of species, relative to their abundance in an unimpacted assemblage.	Newbold, Hudson, Arnell, et al. (2016)
Q 10. Do land use and related pressures influence community trait values?	Garnier et al. (2007)	Combine data on species' occurrences or abundance with trait data to obtain average or community-weighted mean trait values, which can then be modeled like the Site-level response variables above.	fig 1d in Newbold et al. (2015)
Q 11. Does the biotic response to a given pressure vary regionally?	Gibson et al. (2011)	Add region as a fixed effect and test for interaction with other fixed effects.	–
Q 12. Which characteristics of Sites (e.g., duration of human impact and rate of climate change) mean that given land-use changes have particularly severe effects on biodiversity?	Balmford (1996), Travis (2003)	Merge Site-level diversity data with Site-level data on characteristics to be tested and assess the interaction of these variables with land use.	Gray et al. (2016)
Q 13. How accurate are global land-use data?	Giri, Zhu, and Reed (2005)	Use Site-level land-use data to calculate the receiver operating characteristic curve (i.e., sensitivity versus false-positive rate), using the area under the curve to quantify agreement. An extension of this could be to use the PREDICTS Site-level land use data as input into land use/land cover classification procedures, for example, by the remote sensing community, or at least use PREDICTS data to cross-check and validate land use and land cover maps with independent PREDICTS data.	Hoskins et al. (2016)
<i>Questions above the site level</i>			
Q 14. Is beta diversity lower in human-dominated than more natural land uses?	Tylianakis et al. (2005)	Estimate desired measures of similarity among Sites within studies. Model how biotic similarity among Sites depends on similarity of other attributes (including characteristics from remote sensing or Dynamic Global Ecosystem Models if required), accounting for among-Study differences (e.g., using mixed-effects models).	Newbold, Hudson, Hill, et al. (2016)
Q 15. Are land-sparing or land-sharing strategies optimal for local biodiversity?	Green, Cornell, Scharlemann, and Balmford (2005)	Analyze species by Sites and by Study and relate back to Q. 1. The overarching question about sparing versus sharing can be addressed by looking at the individual responses of species to land-use intensity, as measured by yield suggested by Green et al. (2005); this requires data on agricultural yields at relevant Sites in the PREDICTS database.	–

(Continues)

TABLE 1 (Continued)

Question	Early example references	Approach	Example using PREDICTS database	
<i>Other questions</i>				
Q 16.	How accurate are current extent of occurrence/range maps, for example, those produced by International Union for Conservation of Nature (2016)?	–	Cross-check existing extents of occurrence and ranges with PREDICTS data.	–
Q 17.	How representative are species catalogues?	–	Query clade-level (e.g., The Plant List, World List of Mammalian Species, Platnick's Spider Catalogue) and aggregated (e.g., Encyclopedia of Life and Catalogue of Life) lists with the Latin binomials and trinomials that were provided to PREDICTS by the data collectors. Subquestions include <ul style="list-style-type: none"> • How does coverage vary among taxonomic groups? • How does coverage depend on region? • Are there substantial differences among the aggregated services? • How well are synonyms and homonyms represented and resolved? 	–

measurements to estimate changes in gamma diversity over broader areas (e.g., Azaele et al., 2015); both approaches offer potential solutions to mismatches in scale.

The PREDICTS database continues to increase in size and currently contains a further 22 Studies with embargo dates that prevent their inclusion in this release. We intend to publish occasional updates to make these data freely available. We have also received a number of further offers of datasets that we hope to incorporate into the database and include in future releases. There are three priority categories of data that we are still seeking actively: bees from outside Western Europe; soil invertebrates and fungi; and geographic islands. The current database focuses entirely on spatial “control–impact” comparisons. A follow-on project that has recently begun focuses instead on temporal comparisons, collating data from “before–after” and (especially) “before–after–control–impact” studies of the effects of land-use change on terrestrial assemblages. We are therefore seeking datasets, linked to peer-reviewed publications, of comparable species-level surveys conducted at each sampling location, with temporal changes in land use and/or land-use intensity. If corresponding authors of such papers wish to offer their data, please complete our online form, available at www.predicts.org.uk/pages/contribute.html. As with PREDICTS, the new project will seek to make its data freely available.

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CONFLICT OF INTEREST

None declared.

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