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The database of the PREDICTS (Projecting Responses of Ecological Diversity In Changing Terrestrial Systems) project

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The database of the PREDICTS (Projecting Responses of Ecological Diversity In Changing Terrestrial Systems) project

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**Santiago L. Poggio[395] | Natalia Politi[396] | Pere Pons[397] | Katja Poveda[398] |
Eileen F. Power[399] | Steven J. Presley[400] | Vânia Proença[401] | Marino Quaranta[402] |
Carolina Quintero[370] | Romina Rader[403] | B. R. Ramesh[379] | Martha P. Ramirez-Pinilla[404] |
Jai Ranganathan[405] | Claus Rasmussen[406] | Nicola A. Redpath-Downing[407] |
J. Leighton Reid[408] | Yana T. Reis[409] | José M. Rey Benayas[410] | Juan Carlos Rey-Velasco[411] |
Chevonne Reynolds[412,413] | Danilo Bandini Ribeiro[414] | Miriam H. Richards[415] |
Barbara A. Richardson[416,417] | Michael J. Richardson[416,417] | Rodrigo Macip Ríos[418] |
Richard Robinson[419] | Carolina A. Robles[420] | Jörg Römbke[421,422] |
Luz Piedad Romero-Duque[423] | Matthias Rös[424] | Loreta Rosselli[425] |
Stephen J. Rossiter[11] | Dana S. Roth[426] | T'ai H. Roulston[427,428] | Laurent Rousseau[429] |
André V. Rubio[430] | Jean-Claude Ruel[9] | Jonathan P. Sadler[431] | Szabolcs Sáfián[432] |
Romeo A. Saldaña-Vázquez[433] | Katerina Sam[194,434,435] | Ulrika Samnegård[238,349] |
Joana Santana[60] | Xavier Santos[60] | Jade Savage[436] | Nancy A. Schellhorn[437] |
Menno Schilthuizen[438,439] | Ute Schmiedel[440] | Christine B. Schmitt[441,442] |
Nicole L. Schon[443] | Christof Schüepp[260] | Katharina Schumann[444] | Oliver Schweiger[183] |
Dawn M. Scott[445] | Kenneth A. Scott[446] | Jodi L. Sedlock[447] | Steven S. Seefeldt[448] |
Ghazala Shahabuddin[449] | Graeme Shannon[223,450] | Douglas Sheil[451] |
Frederick H. Sheldon[452,453] | Eyal Shochat[454,455] | Stefan J. Siebert[255] |
Fernando A. B. Silva[456] | Javier A. Simonetti[430] | Eleanor M. Slade[208] | Jo Smith[457] |
Allan H. Smith-Pardo[458,459] | Navjot S. Sodhi[460] | Eduardo J. Somarriba[112] |
Ramón A. Sosa[461] | Grimaldo Soto Quiroga[112,462] | Martin-Hugues St-Laurent[463] |
Brian M. Starzomski[464] | Constanti Stefanescu[211,392,465] | Ingolf Steffan-Dewenter[179] |
Philip C. Stouffer[466,467] | Jane C. Stout[399] | Ayron M. Strauch[468] | Matthew J. Struebig[66] |
Zhimin Su[469,470] | Marcela Suarez-Rubio[471] | Shinji Sugiura[298] | Keith S. Summerville[472] |
Yik-Hei Sung[473] | Hari Sutrisno[474] | Jens-Christian Svenning[475] | Tiit Teder[476] |
Caragh G. Threlfall[477] | Anu Tiitsaar[476] | Jacqui H. Todd[302] | Rebecca K. Tonietto[478] |
Ignasi Torre[465] | Béla Tóthmérész[479] | Teja Tscharntke[55] | Edgar C. Turner[480] |
Jason M. Tylianakis[4,481] | Marcio Uehara-Prado[482] | Nicolas Urbina-Cardona[483] |
Denis Vallan[484] | Adam J. Vanbergen[485] | Heraldo L. Vasconcelos[486] | Kiril Vassilev[487] |
Hans A. F. Verboven[488] | Maria João Verdasca[489] | José R. Verdú[320] |
Carlos H. Vergara[490] | Pablo M. Vergara[491] | Jort Verhulst[492] | Massimiliano Virgilio[493] |
Lien Van Vu[494] | Edward M. Waite[495] | Tony R. Walker[352,496] | Hua-Feng Wang[497] |
Yanping Wang[498] | James I. Watling[499] | Britta Weller[189] | Konstans Wells[500,501] |
Catrin Westphal[55] | Edward D. Wiafe[502] | Christopher D. Williams[503] |
Michael R. Willig[504,505] | John C. Z. Woinarski[446] | Jan H. D. Wolf[506] |
Volkmar Wolters[243] | Ben A. Woodcock[507] | Jihua Wu[508] | Joseph M. Wunderle, Jr[509] |
Yuichi Yamaura[341] | Satoko Yoshikura[510] | Douglas W. Yu[511,512] | Andrey S. Zaitsev[243,513] |
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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 metadata 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 metadata 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 (Hurtt 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”

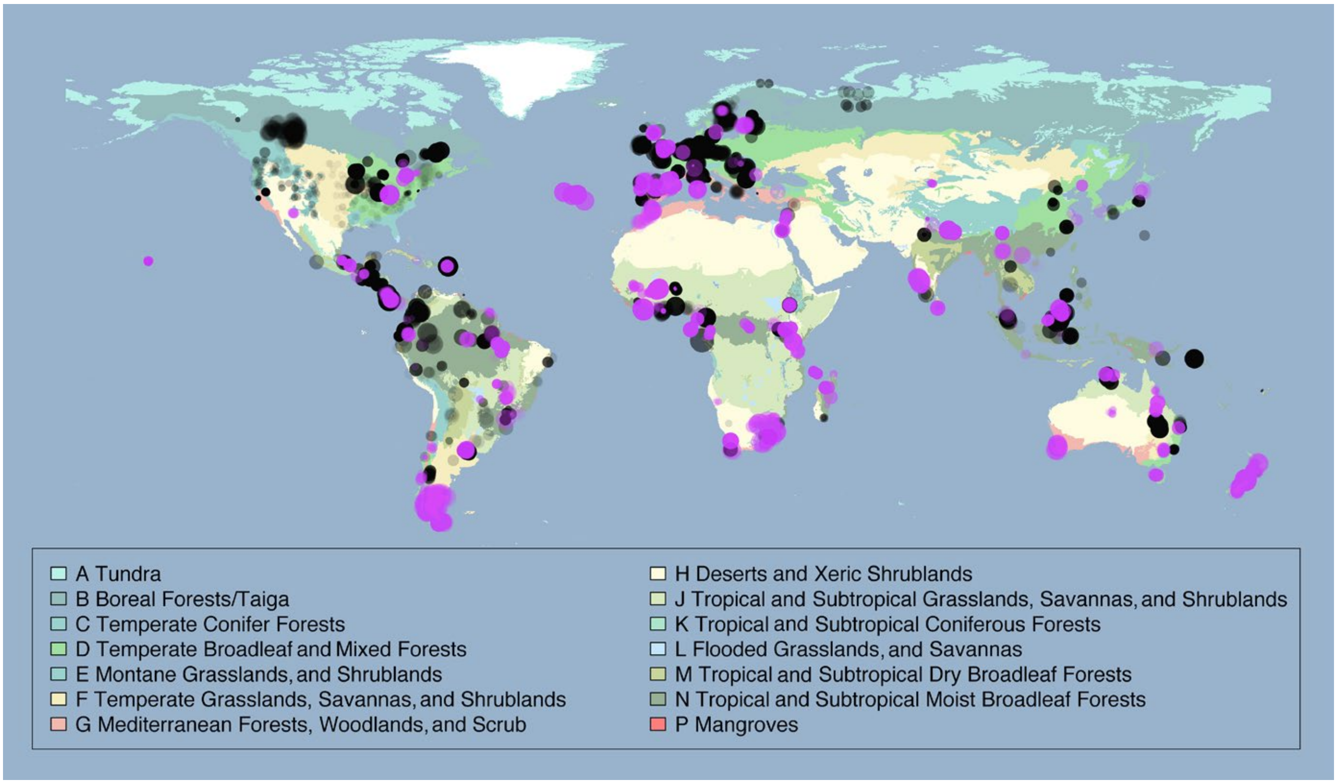

FIGURE 1 Sampling locations. Map colors indicate biomes, taken from the Terrestrial Ecoregions of the World dataset (The Nature Conservancy, 2009), shown in a geographic (WGS84) projection. Circle radii are proportional to $\log_{10}$ of the number of samples at that Site. All circles have the same degree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

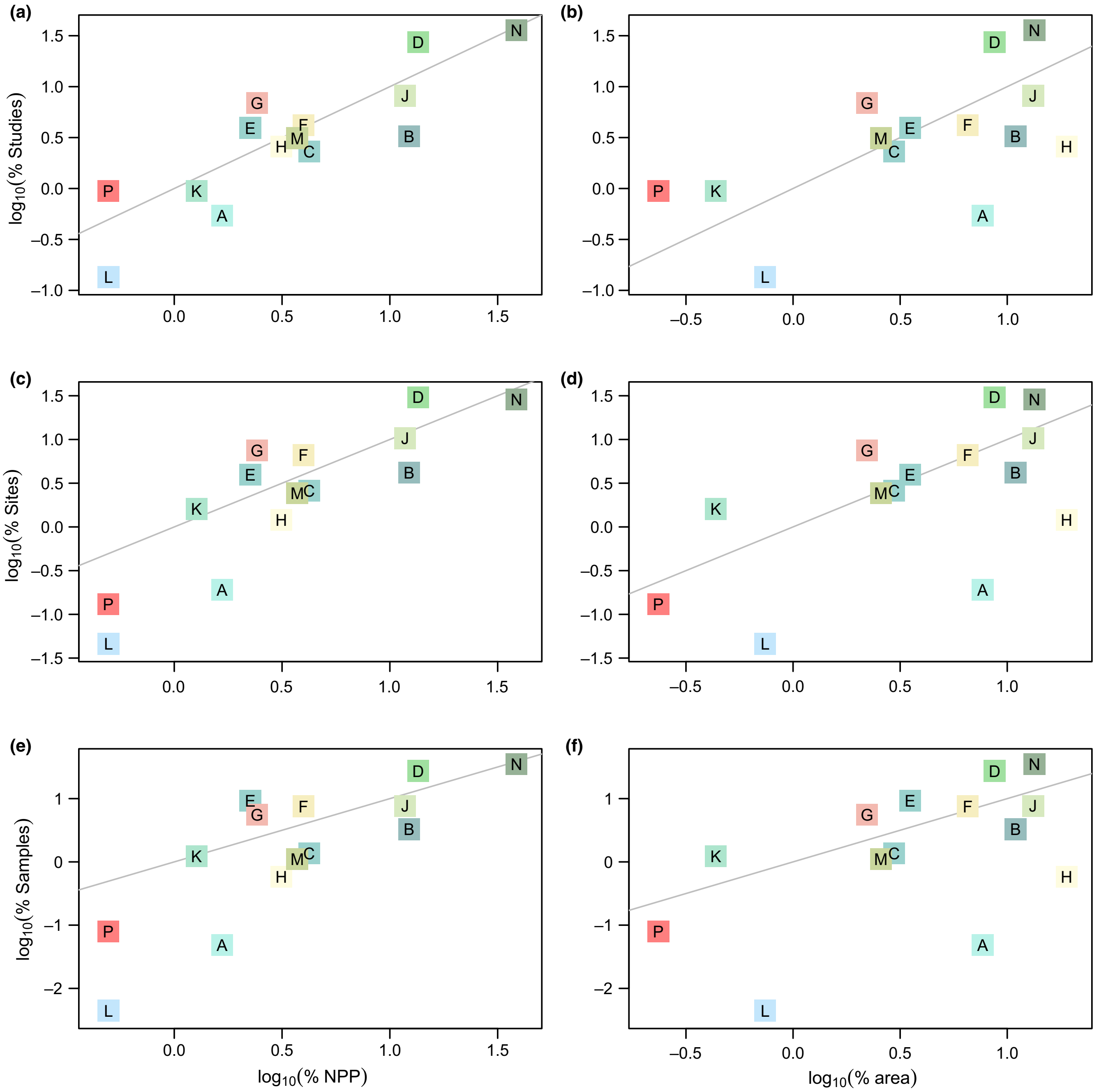

FIGURE 2 Coverage of biomes. The percentage of Studies (a and b), Sites (c and d), and samples (e and f) against percentages of terrestrial NPP (Net Primary Productivity, computed as in Hudson et al., 2014; a, c, and e) and terrestrial area (b, d, and f). Biome codes and colors are as in Figure 1

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, 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

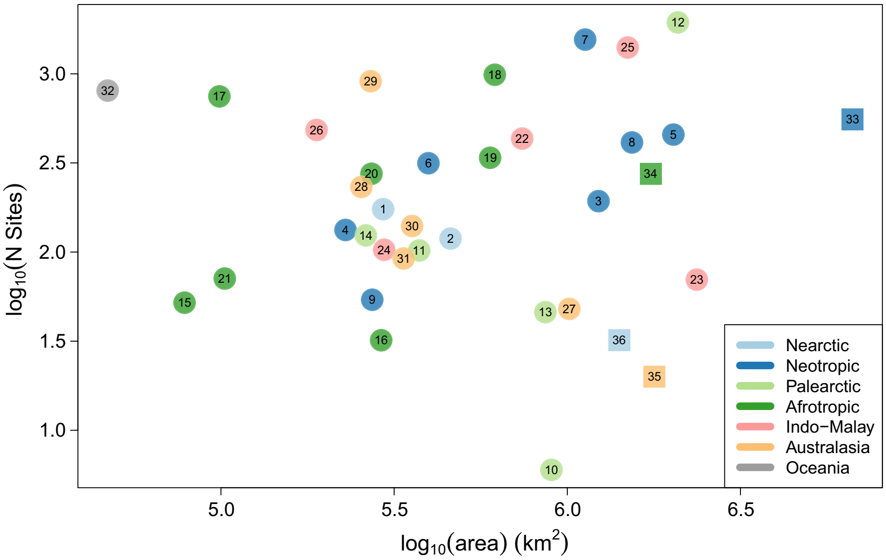

FIGURE 3 Numbers of Sites against the areas of biodiversity hotspots and of high biodiversity wilderness areas (HBWAs). Hotspots are shown by circles and HBWAs by squares; symbols are colored by the predominant biogeographic realm in which they fall. Hotspots are 1 California Floristic Province, 2 Madrean 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 Afromontane, 18 Guinean Forests of West Africa, 19 Madagascar and the Indian Ocean Islands, 20 Maputaland-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

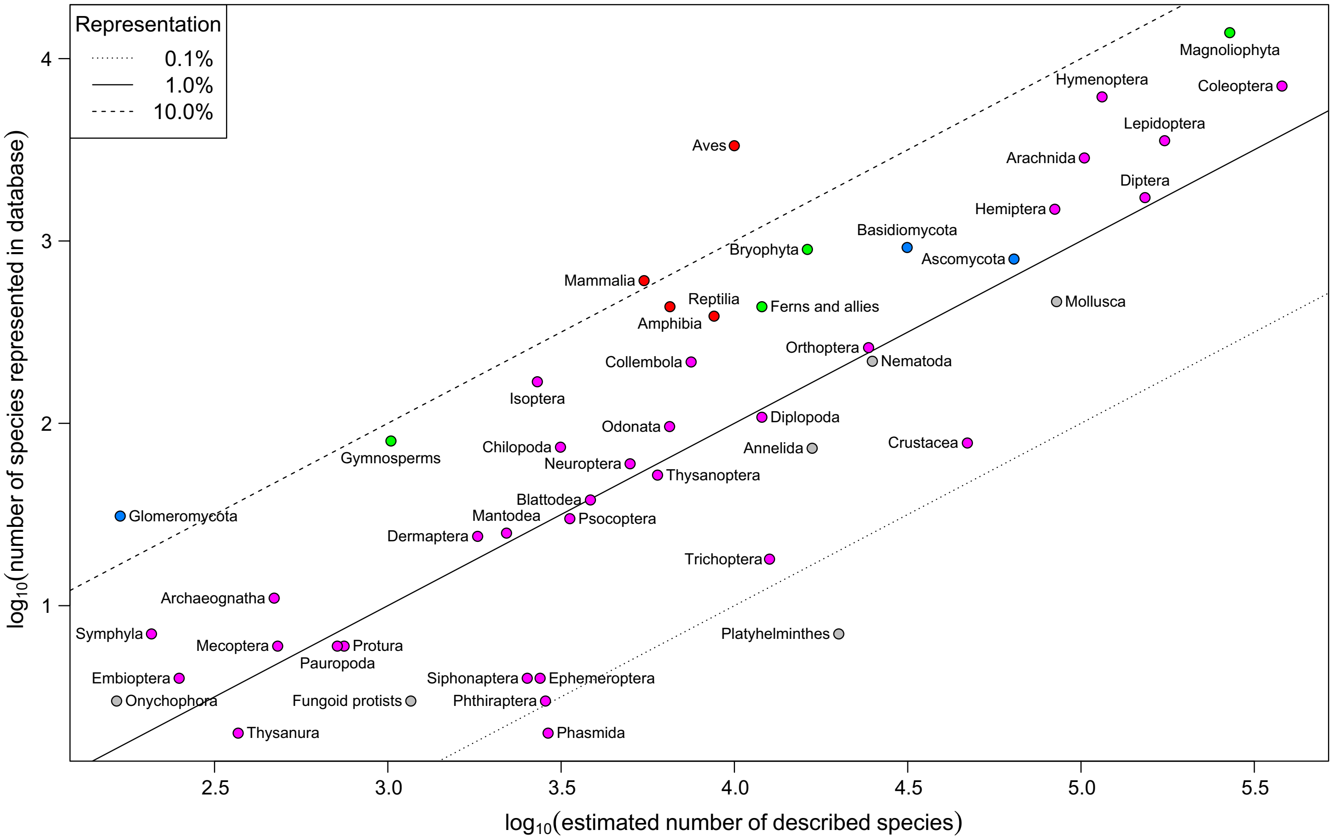

FIGURE 4 Taxonomic coverage. The numbers of species in our database against the numbers of described species within each of 59 higher taxa, as estimated by Chapman (2009), on logarithmic axes. Vertebrates are shown in red, arthropods in pink, other animals in gray, plants in green, and fungi in blue. 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

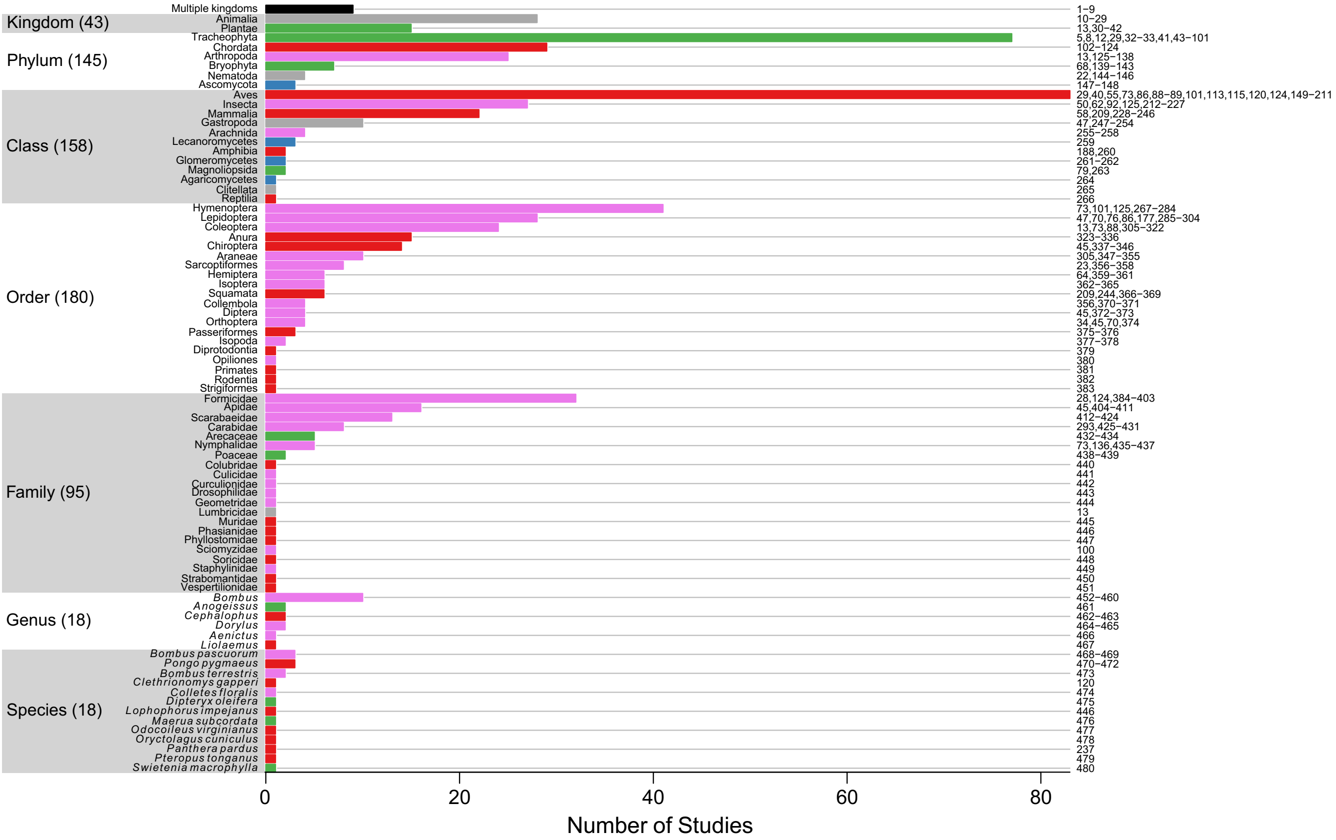

FIGURE 5 Number of Studies by lowest common taxonomic group. Bars show the number of Studies within each lowest common taxon (so, one Study examined the species *Swietenia macrophylla*, three Studies examined the species *Bombus pascuorum*, ten Studies examined multiple species within the genus *Bombus*, 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 Domínguez, 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 Deconchat (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 Tscharntke (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 Alcala, Alcala, 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),

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FIGURE 5 (Continued)

106 Craig et al. (2012), 107 Craig, Grigg, Hobbs, and Hardy (2014), 108 Craig, Stokes, StJ. Hardy, and Hobbs (2015), 109 de Thoisy et al. (2010), 110 Endo et al. (2010), 111 Garden, McAlpine, and Possingham (2010), 112 Kurz, Nowakowski, Tingley, Donnelly, and Wilcove (2014), 113 Kutt and Woinarski (2007), 114 Kutt, Vanderduys, and O'Reagain (2012), 115 Lehouck et al. (2009), 116 Macip-Ríos and Muñoz-Alonso (2008), 117 McCarthy, McCarthy, Fuller, and McCarthy (2010), 118 Parry, Barlow, and Peres (2009), 119 Peres and Nascimento (2006), 120 St-Laurent, Ferron, Hins, and Gagnon (2007), 121 Sung, Karraker, and Hau (2012), 122 Urbina-Cardona, Olivares-Perez, and Reynoso (2006), 123 Woinarski and Ash (2002), 124 Woinarski et al. (2009), 125 Billeter et al. (2008); Le Féon et al. (2010), 126 Borges et al. (2006), 127 Cabra-García, Bermúdez-Rivas, Osorio, and Chacón (2012), 128 Hanley (2011), 129 Lachat et al. (2006), 130 Cardoso et al. (2009); Meijer, Whittaker, and Borges (2011), 131 Nakamura, Proctor, and Catterall (2003), 132 Norfolk, Abdel-Dayem, and Gilbert (2012), 133 Poveda, Martinez, Kersch-Becker, Bonilla, and Tscharntke (2012), 134 Rousseau, Fonte, Tellez, van der Hoek, and Lavelle (2013), 135 Turner and Foster (2009), 136 Uehara-Prado et al. (2009), 137 Waite (2012); Waite, Closs, Van Heezik, Berry, and Dickinson (2012), 138 Woodcock et al. (2007), 139 Albertos, Lara, Garilleti, and Mazimpaka (2005), 140 Draper, Lara, Albertos, Garilleti, and Mazimpaka (2006), 141 Giordano et al. (2004), 142 Hylander and Weibull (2012), 143 Medina et al. (2010), 144 Hu and Cao (2008), 145 Wu, Fu, Chen, and Chen (2002), 146 Zhang, Li, and Liang (2010), 147 Giordani et al. (2010), 148 Giordani (2012), 149 Aben, Dorenbosch, Herzog, Smolders, and Van Der Velde (2008), 150 Arbeláez-Cortés, Rodríguez-Correa, and Restrepo-Chica (2011), 151 Aumann (2001), 152 Azhar et al. (2013), 153 Azman et al. 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(2011), 180 Munyekenye, Mwangi, and Gichuki (2008), 181 Naidoo (2004), 182 Naithani and Bhatt (2012), 183 Naoe, Sakai, and Masaki (2012), 184 Ndang'ang'a, Njoroge, and Githiru (2013), 185 Neuschulz, Botzat, and Farwig (2011), 186 O'Dea and Whittaker (2007), 187 Owiunji and Plumptre (1998), 188 Pearman (2002), 189 Politi, Hunter Jr. and Rivera (2012), 190 Pons and Wendenburg (2005), 191 Ranganathan, Chan, and Daily (2007), 192 Ranganathan, Daniels, Chandran, Ehrlich, and Daily (2008), 193 Reid, Harris, and Zahawi (2012), 194 Rey-Benayas, Galvan, and Carrascal (2010), 195 Reynolds and Symes (2013), 196 Rosselli (2011), 197 Sam, Koane, Jeppy, and Novotny (2014), 198 Santana, Porto, Gordinho, Reino, and Beja (2012), 199 Shahabuddin and Kumar (2006, 2007), 200 Sheldon, Styring, and Hosner (2010), 201 Sodhi et al. (2010), 202 Soh, Sodhi, and Lim (2006), 203 Sosa, Benz, Galea, and Poggio Herrero (2010), 204 Stouffer, Johnson, Bierregaard, Richard, and Lovejoy (2011), 205 Suarez-Rubio and Thomlinson (2009), 206 Vergara and Simonetti (2004), 207 Verhulst, Báldi, and Kleijn (2004), 208 Waite, Closs, van Heezik, and Dickinson (2013), 209 Wang, Bao, Yu, Xu, and Ding (2010), 210 Wunderle, Henriques, and Willig (2006), 211 Li, Zou, Zhang, and Sheldon (2013), 212 Bates et al. (2011), 213 Blake, Westbury, Woodcock, Sutton, and Potts (2011), 214 Blanche, Ludwig, and Cunningham (2006), 215 Cleary et al. (2004), 216 Farwig et al. (2009), 217 Franzén and Nilsson (2008), 218 Kohler, Verhulst, van Klink, and Kleijn (2008), 219 Litchwark (2013), 220 Meyer, Gaebele, and Steffan-Dewenter (2007), 221 Jauker, Krauss, Jauker, and Steffan-Dewenter (2013); Meyer, Jauker, and Steffan-Dewenter (2009), 222 Mudri-Stojnic, Andric, Jozan, and Vujic (2012), 223 Quintero, Morales, and Aizen (2010), 224 Rader, Bartomeus, Tylianakis, and Laliberte (2014), 225 Schüepp, Herrmann, Herzog, and Schmidt-Entling (2011), 226 Summerville (2011), 227 Vergara and Badano (2009), 228 Bernard, Fjeldsa, and Mohamed (2009), 229 Cáceres, Nápoli, Casella, and Hannibal (2010), 230 Cassano, Barlow, and Pardini (2014), 231 Danquah, Oppong, and Nutsuakor (2012), 232 Garmendia, Arroyo-Rodriguez, Estrada, Naranjo, and Stoner (2013), 233 Gheler-Costa, Vettorazzi, Pardini, and Verdade (2012), 234 Granjon and Duplantier (2011), 235 Henschel (2008), 236 Hoffmann and Zeller (2005), 237 Kittle, Watson, Chanaka Kumara, and Nimalka Sanjeewani (2012), 238 Lantschner, Rusch, and Hayes (2012), 239 Martin, Gheler-Costa, Lopes, Rosalino, and Verdade (2012), 240 McShea et al. 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(2014), 255 Freire and Motta (2011), 256 Lo-Man-Hung, Gardner, Ribeiro-Júnior, Barlow, and Bonaldo (2008), 257 Shochat, Stefanov, Whitehouse, and Faeth (2004), 258 Zaitsev, Chauvat, Pug, and Wolters (2002), 259 Walker, Crittenden, Young, and Prystina (2006), 260 Malonza and Veith (2012), 261 Alguacil, Torrecillas, Hernandez, and Roldan (2012), 262 Brito, Goss, de Carvalho, Chatagnier, and van Tuinen (2012), 263 Baral and Katzensteiner (2009), 264 Robles, Carmaran, and Lopez (2011), 265 Römbke, Schmidt, and Höfer (2009), 266 Luja, Herrando-Perez, Gonzalez-Solis, and Luiselli (2008), 267 Cameron et al. (2011), 268 Cunningham, Schellhorn, Marcora, and Batley (2013), 269 Fowler (2014), 270 Gould et al. (2013), 271 Lentini, Martin, Gibbons, Fischer, and Cunningham (2012), 272 Malone et al. (2010), 273 Marshall, West, and Kleijn (2006), 274 Oertli, Muller, and Dorn (2005), 275 Osgathorpe, Park, and Goulson (2012), 276 Quaranta et al. (2004), 277 Richards et al. 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(2009), 293 Ishitani, Kotze, and Niemela (2003), 294 Krauss, Steffan-Dewenter, and Tscharntke (2003), 295 Littlewood (2008), 296 Pe'er, Maanen, Turbe, Matsinos, and Kark (2011), 297 Safian, Csontos, and Winkler (2011), 298 Summerville and Crist (2002), 299 Summerville, Conoan, and Steichen (2006), 300 Sutrisno (2010), 301 Uehara-Prado, Brown, Spalding, and Lucci Freitas (2007), 302 Verdasca et al. (2012), 303 Vu (2005), 304 Vu (2009), 305 Banks, Sandvik, and Keesecker (2007), 306 Barratt et al. (2012), 307 Blanche and Cunningham (2005), 308 Buse, Levanony, Timm, Dayan, and Assmann (2008), 309 Elek and Lovei (2007), 310 Ewers, Thorpe, and Didham (2007), 311 Gaublomme, Hendrickx, Dhuyvetter, and Desender (2008), 312 Gray, Slade, Mann, and Lewis (2014), 313 Jonsell (2012), 314 Légaré, Hébert, and Ruel (2011), 315 Mico,

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Garcia-Lopez, Brustel, Padilla, and Galante (2013), 316 Noreika (2009), 317 Numa, Verdu, Rueda, and Galante (2012), 318 Nyeko (2009), 319 Otavo, Parrado-Rosselli, and Noriega (2013), 320 Rodrigues, Uchoa, and Ide (2013), 321 Sugiura, Tsuru, Yamaura, and Makihara (2009), 322 Verdú et al. (2007), 323 Adum, Eichhorn, Oduro, Ofori-Boateng, and Rodel (2013), 324 de Souza, de Souza, and Morato (2008), 325 Eigenbrod, Hecnar, and Fahrig (2008), 326 Faruk, Belabut, Ahmad, Knell, and Garner (2013), 327 Furlani, Ficetola, Colombo, Ugurlucan, and De Bernardi (2009), 328 Gutierrez-Lamus (2004), 329 Hilje and Aide (2012), 330 Isaacs-Cubides and Urbina-Cardona (2011), 331 Ofori-Boateng et al. 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(2011), 409 Parra-H and Nates-Parra (2007), 410 Rasmussen (2009), 411 Winfree, Griswold, and Kremen (2007), 412 da Silva (2011), 413 Davis and Philips (2005), 414 Filgueiras, Iannuzzi, and Leal (2011), 415 Gardner, Hernandez, Barlow, and Peres (2008), 416 Horgan (2009), 417 Jacobs, Scholtz, Escobar, and Davis (2010), 418 Navarrete and Halffter (2008), 419 Navarro, Roman, Gomez, and Perez (2011), 420 Noriega, Realpe, and Fagua (2007), 421 Noriega, Palacio, Monroy-G, and Valencia (2012), 422 Rös, Escobar, and Halffter (2012), 423 Silva, Costa, Moura, and Farias (2010), 424 Slade, Mann, and Lewis (2011), 425 Gu, Zhen-Rong, and Dun-Xiao (2004), 426 Koivula, Hyyrylainen, and Soininen (2004), 427 Liu, Axmacher, Wang, Li, and Yu (2012), 428 Noreika and Kotze (2012), 429 Rey-Velasco and Miranda-Esquivel (2012), 430 Vanbergen, Woodcock, Watt, and Niemela (2005), 431 Weller and Ganzhorn (2004), 432 Aguilar-Barquero and Jiménez-Hernández (2009), 433 Carvalho, Ferreira, Lima, and de Carvalho (2010), 434 Svenning (1998), 435 Benedick et al. (2006), 436 Fermon, Waltert, Vane-Wright, and Muhlenberg (2005), 437 Ribeiro and Freitas (2012), 438 Breedt, Dreber, and Kellner (2013), 439 Scott, Setterfield, Douglas, and Andersen (2010), 440 Cagle (2008), 441 Johnson, Gómez, and Pinedo-Vasquez (2008), 442 Su, Zhang, and Qiu (2011), 443 Gottschalk, De Toni, Valente, and Hofmann (2007), 444 Axmacher et al. (2009), 445 García, Ortiz Zapata, Aguayo, and D'Elia (2013), 446 Jolli and Pandit (2011), 447 Saldaña-Vázquez, Sosa, Hernández-Montero, and López-Barrera (2010), 448 Nicolas, Barriere, Tapiero, and Colyn (2009), 449 Sakchoowong, Nomura, Ogata, and Chanpaisaeng (2008), 450 García-R, Cárdenas-H, and Castro-H (2007), 451 Yoshikura, Yasui, and Kamijo (2011), 452 Connop, Hill, Steer, and Shaw (2011), 453 Darvill, Knight, and Goulson (2004), 454 Diekötter, Walther-Hellwig, Conradi, Suter, and Frankl (2006), 455 Goulson, Lye, and Darvill (2008), 456 Goulson et al. (2010), 457 Hanley et al. (2011), 458 Hatfield and LeBuhn (2007), 459 McFrederick and LeBuhn (2006), 460 Redpath, Osgathorpe, Park, and Goulson (2010), 461 Schumann, Wittig, Thiombiano, Becker, and Hahn (2011), 462 Nakashima, Inoue, and Akomo-Okoue (2013), 463 Wiafe and Amfo-Otu (2012), 464 Peters, Fischer, Schaab, and Kraemer (2009), 465 Peters, Lung, Schaab, and Waegele (2011), 466 Matsumoto, Itioka, Yamane, and Momose (2009), 467 Rubio and Simonetti (2011), 468 Herrmann, Westphal, Moritz, and Steffan-Dewenter (2007), 469 Knight et al. (2009), 470 Ancrenaz, Goossens, Gimenez, Sawang, and Lackman-Ancrenaz (2004), 471 Felton, Engstrom, Felton, and Knott (2003), 472 Knop, Ward, and Wich (2004), 473 Ewers, Bartlam, and Didham (2013), 474 Davis, Murray, Fitzpatrick, Brown, and Paxton (2010), 475 Hanson, Brunsfeld, Finegan, and Waits (2008), 476 Strauch and Eby (2012), 477 Ramos-Robles, Gallina, and Mandujano (2013), 478 Ferreira and Alves (2005, 2009), 479 Luskin (2010), 480 Grogan et al. (2008)

database. Recent examples include mammalian generation time (Pacifici 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,

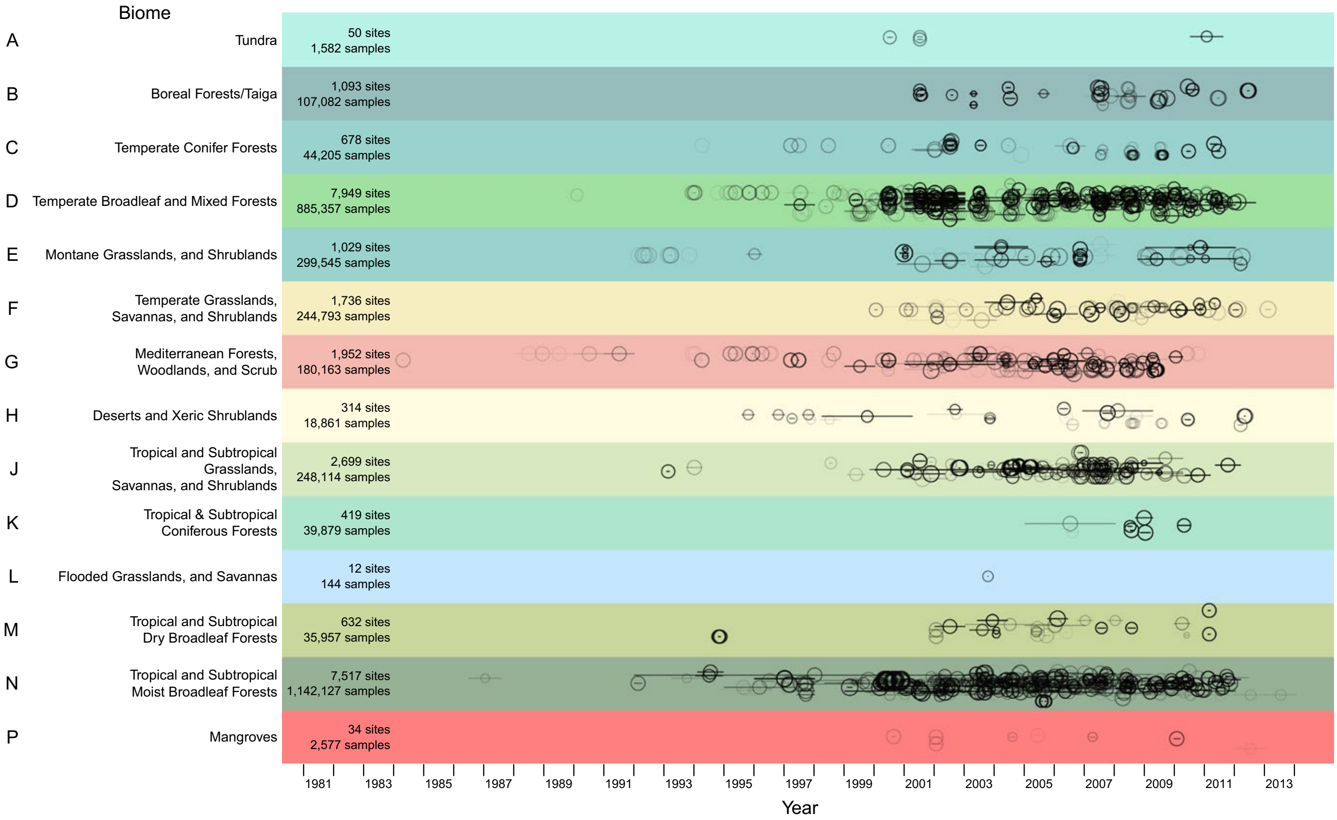

FIGURE 6 Spatiotemporal sampling coverage. Site sampling dates are shown by biome. Each Site is represented by a circle and line. Circle radii are proportional to $\log_{10}$ of the number of samples at that Site. Circle centers are at the midpoints of Site sampling dates; lines indicate the start and 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
Questions about taxa				
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.	–
Questions about sites				
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)
Questions above the site level				
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
Other questions				
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 • 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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