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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: global biodiversity modelling, data sharing, global change, habitat destruction, land use

Introduction

Many indicators are available for tracking the state of biodiversity through time, e.g., in order to assess progress towards 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 (McKinney 1997; Lawton et al. 1998; 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 et al. 2013). Fourth, most ecosystem services and their underpinning processes are mediated by local rather than global biodiversity (Grime 1998; Cardinale et al. 2012): 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 et al. 2003; Collen et al. 2009; Hull et al. 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; Vellend et al. 2013; Dornelas et al. 2014), 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 modelling efforts. However, it has been rare for such papers to publish data in full, even as supplementary 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, 2016a), 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.

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 sub-projects on particular regions, land uses or taxa. We also made general requests for data at conferences and through published articles (Newbold et al. 2012; Hudson et al. 2013b, 2014). 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 harmonised land-use scenarios for 1500-2100 (Hurtt et al. 2011) in order to facilitate spatial and temporal projections of modelled 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' 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 (MacKenzie et al. 2002; Hayward et al. 2015).

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 (Newbold et al. 2014, 2015; De Palma et al. 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 Supplementary File S1.

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 Supplementary File S1). 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 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).

Results

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 et al. 1997), 281 of the 814 terrestrial ecoregions (The Nature Conservancy 2009) and 32 of Conservation International's 35 biodiversity hotspots (Myers et al. 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 high biodiversity wilderness areas (Mittermeier et al. 2003; squares on Figure 3).

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 3 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 over-represented 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).

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 modelling. 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).

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 (10.5519/0066354) as comma-separated variable (CSV) files and as RDS files, the latter for use with the R statistical modelling 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 visualisation of the database schema, is given in Supplementary File S1. This paper makes all the data in this version of the database freely available to anyone wishing to use them for any purpose. The terms of the licence 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 10.5519/0066354 contains bibliographic information for all DataSources in both CSV and BibTeX formats.

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 done at each Site within a Study, was chosen to facilitate such modelling. Table 1 identifies a range of longstanding 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 done 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 towards 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 et al. 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, though they are increasingly used in modelling species distributions (e.g., Pineda & Lobo 2008) and habitat suitability (e.g., Ficetola et al. 2015). As of April 2016, GBIF holds over 560 million georeferenced occurrence records of around 1.5 million species, though coverage is taxonomically uneven (e.g., most records are of birds) and patchy even among the best-recorded groups (Meyer et al. 2015).

Databases of species traits continue to be collated and published, many of them are relevant to taxa in the PREDICTS 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 et al. 2013a) 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 specialisation 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, physiological and functional traits of bees (De Palma et al. 2015); see Table 1, Q. 3.

Although our targeting of data from under-represented 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 data sets 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 harmonised 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 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 metres (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 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/contribute.html. As with PREDICTS, the new project will seek to make its data freely available.

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Figure captions

Figure 1: Sampling locations. Map colours 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.

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 colours are as in Figure 1.

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 coloured 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.

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 grey, 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.

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). Colours 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 & Heilmann-Clausen (2009), 4 Domínguez et al. (2012), 5 López-Quintero et al. (2012), 6 Nöske et al. (2008), 7 Norton et al. (2006), 8 Peri et al. (2013), 9 Robinson & Williams (2011), 10 Barratt et al. (2005), 11 Bonham et al. (2002), 12 Boutin et al. (2009), 13 Carpenter et al. (2012), 14 Gaigher & Samways (2010), 15 Ge et al. (2012), 16 Hayward (2009), 17 Leighton-Goodall

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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 colours and letters are as in Figure 1.

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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 et al. (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., by using mixed-effects models).	-
Q 2.	Do changes in land-use facilitate success of invasive species?	Dukes & Mooney (1999); Theoharides & 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 et al. (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., by 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 & 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 & Blackburn (1997); Purvis et al. (2000)	Analyse 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 et al. (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 modelling options are then possible depending on the precise question: e.g., fit land use interacting with suitability when modelling abundance in order to test whether any correlation depends on land use.	-

Question		Early example references	Approach	Example using PREDICTS database
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., by using mixed effects models).	Fig 1b, 1c in Newbold et al. (2015)
Q 9.	How do land use and other pressures reduce compositional intactness?	Scholes & Biggs (2005)	Because net changes are affected by gains of non-native species as well as losses of those originally present, modelling 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 et al. (2016a)
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 modelled 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 et al. (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 e.g., 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)

Question		Early example references	Approach	Example using PREDICTS database
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 e.g., characteristics from remote sensing or Dynamic Global Ecosystem Models if required), accounting for among-Study differences (e.g., using mixed effects models).	Newbold et al. (2016b)
Q 15.	Are land-sparing or land-sharing strategies optimal for local biodiversity?	Green et al. (2005)	Analyse 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.	-
Other questions				
Q 16.	How accurate are current extent of occurrence/range maps e.g., 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?	-

Table 1: Questions that could be answered using the PREDICTS database.

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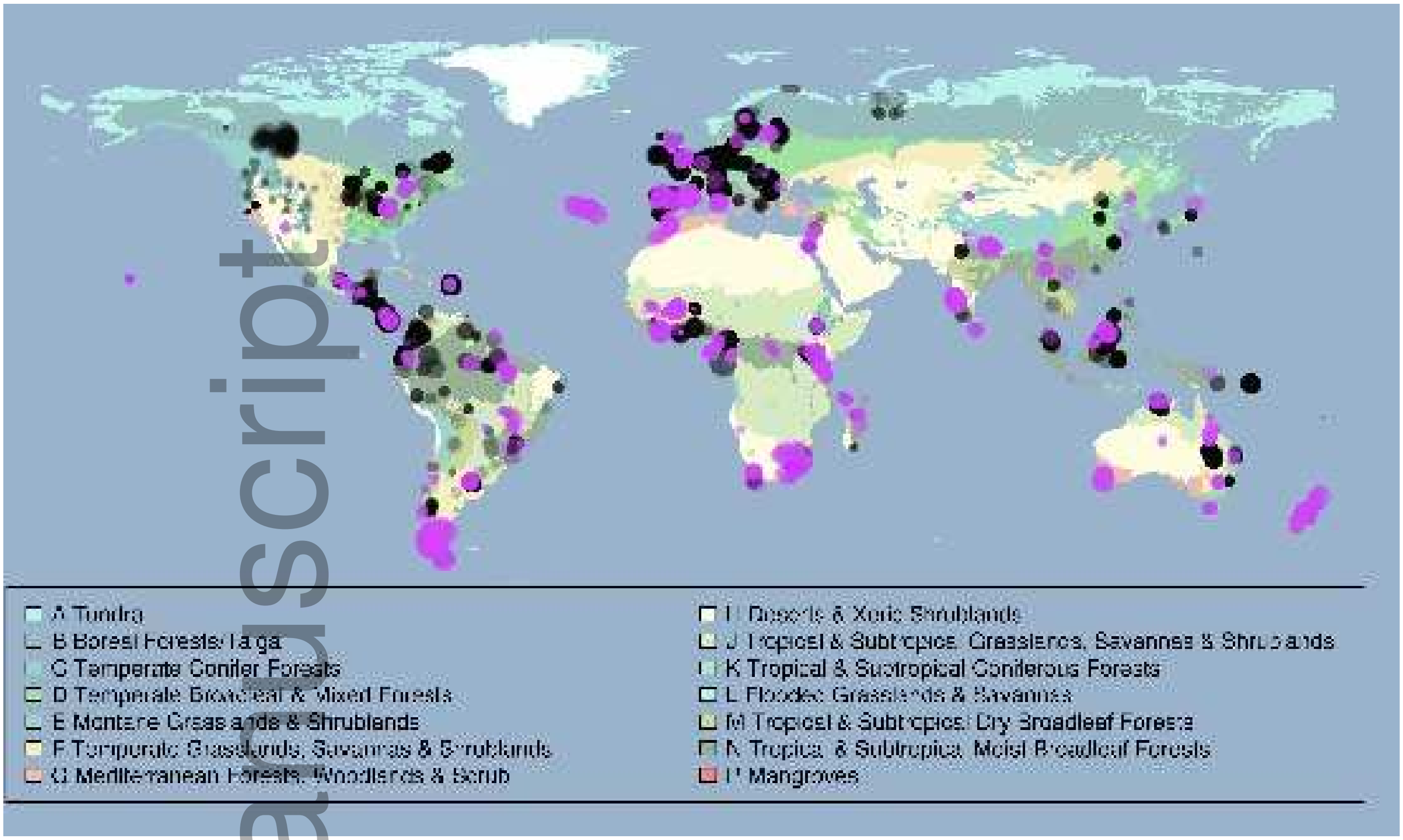
Supporting Information

File S1. Database schema and description of data extract columns.



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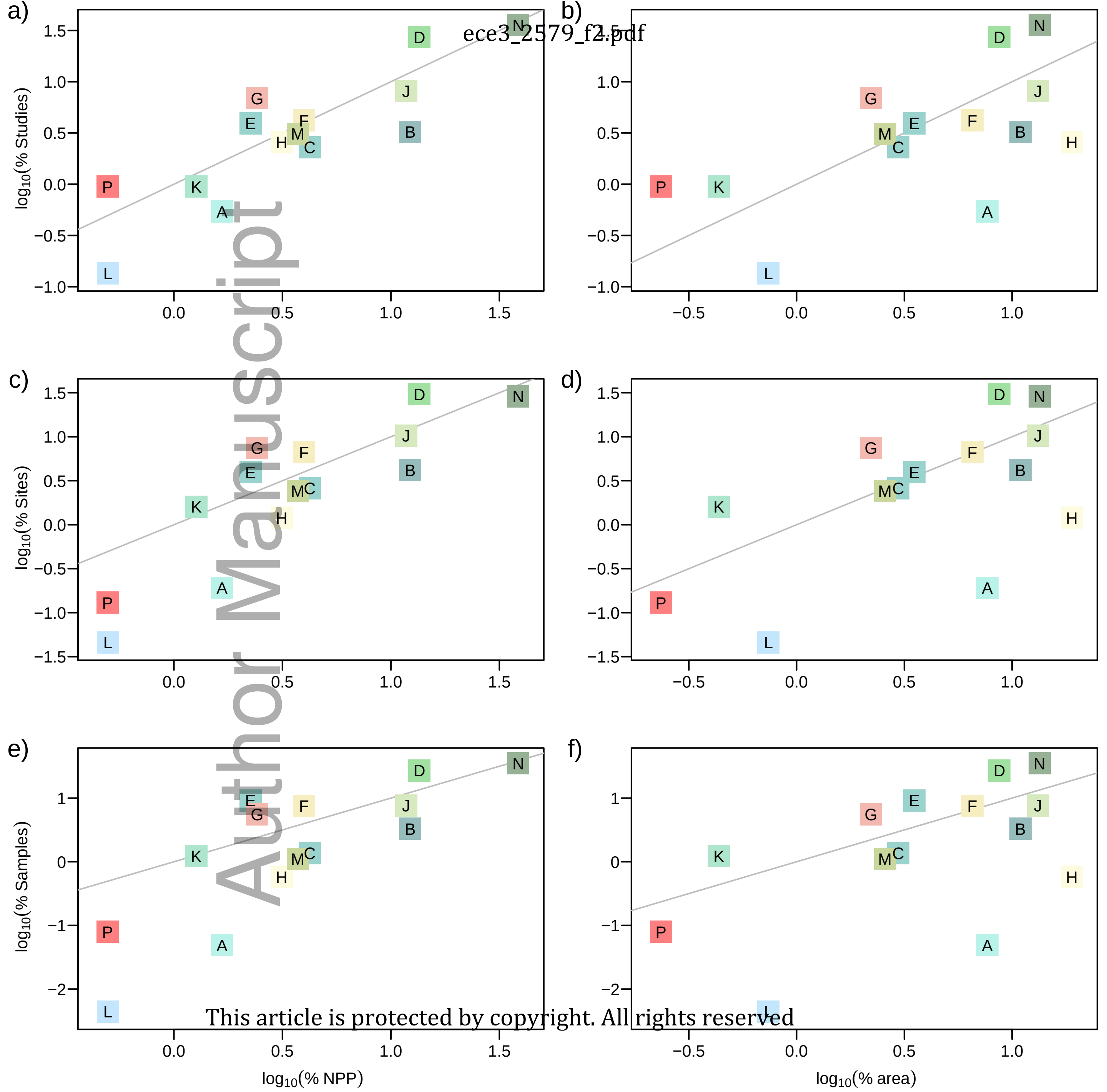
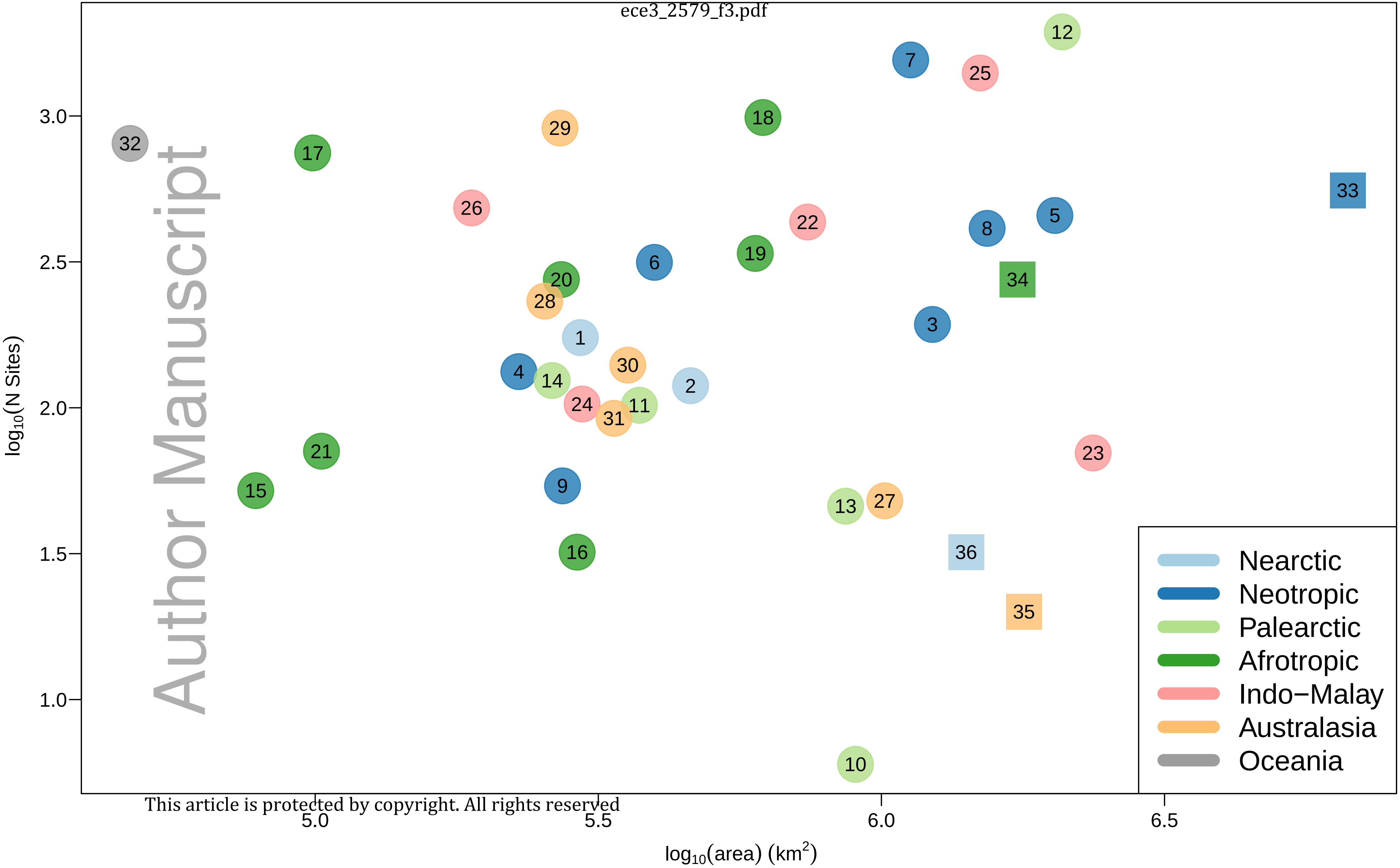

a)
b)
c)
d)
e)
f)
log10(% Studies)
log10(% Sites)
log10(% Samples)
log10(% NPP)
log10(% area)
−1.0
−0.5
0.0
0.5
1.0
1.5
−1.5
−2
−1
0
1
−0.5
0.0
0.5
1.0
1.5
A
B
C
D
E
F
G
H
J
K
L
M
N
P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2.0
1.5
1.0
log$_{10}$(area) (km^2)
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5.5
6.0
6.5
12
7
25
18
29
32
17
33
26
22
5
8
6
19
20
34
28
3
1
30
4
14
2
24
11
31
23
21
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13
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35
10
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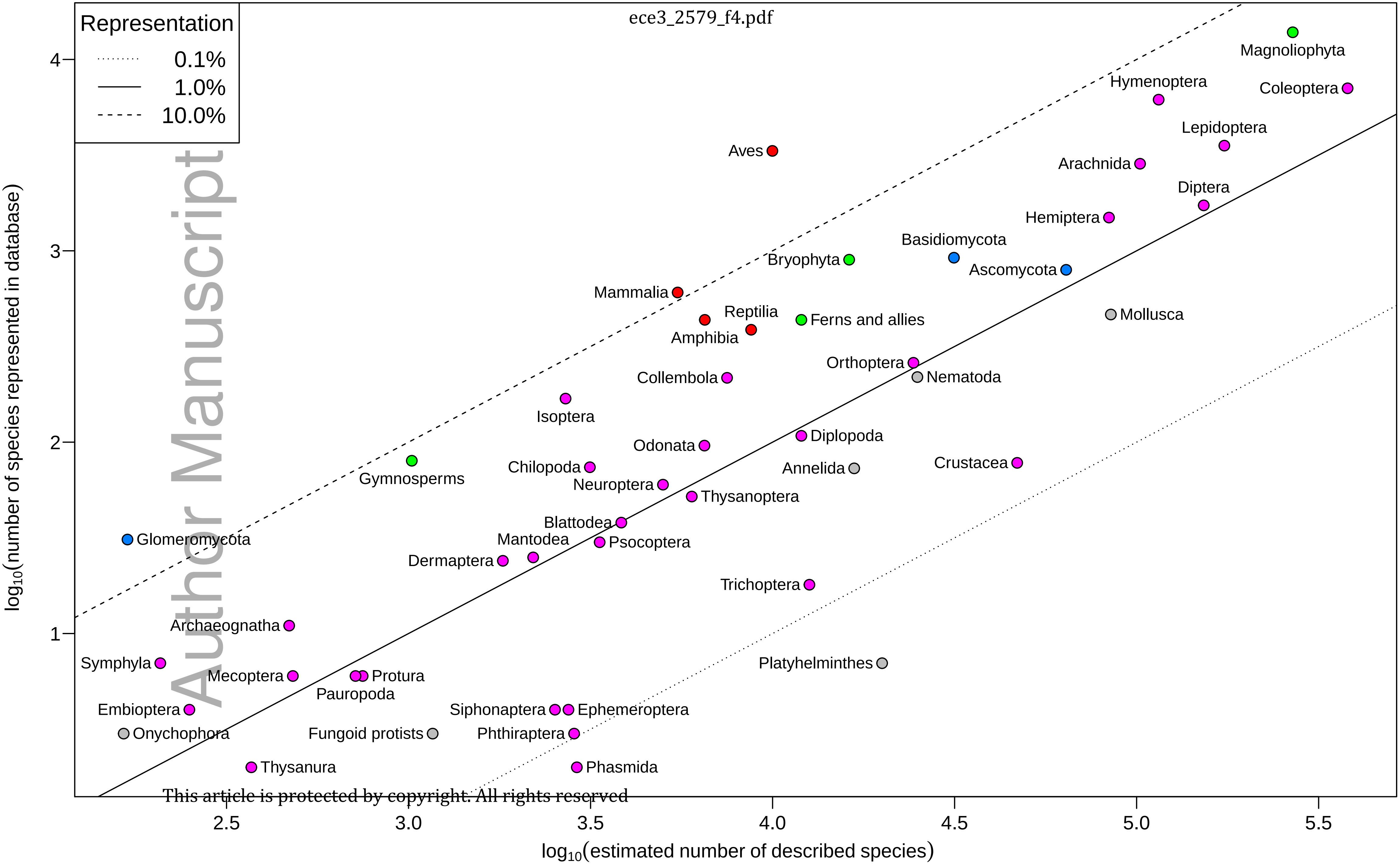
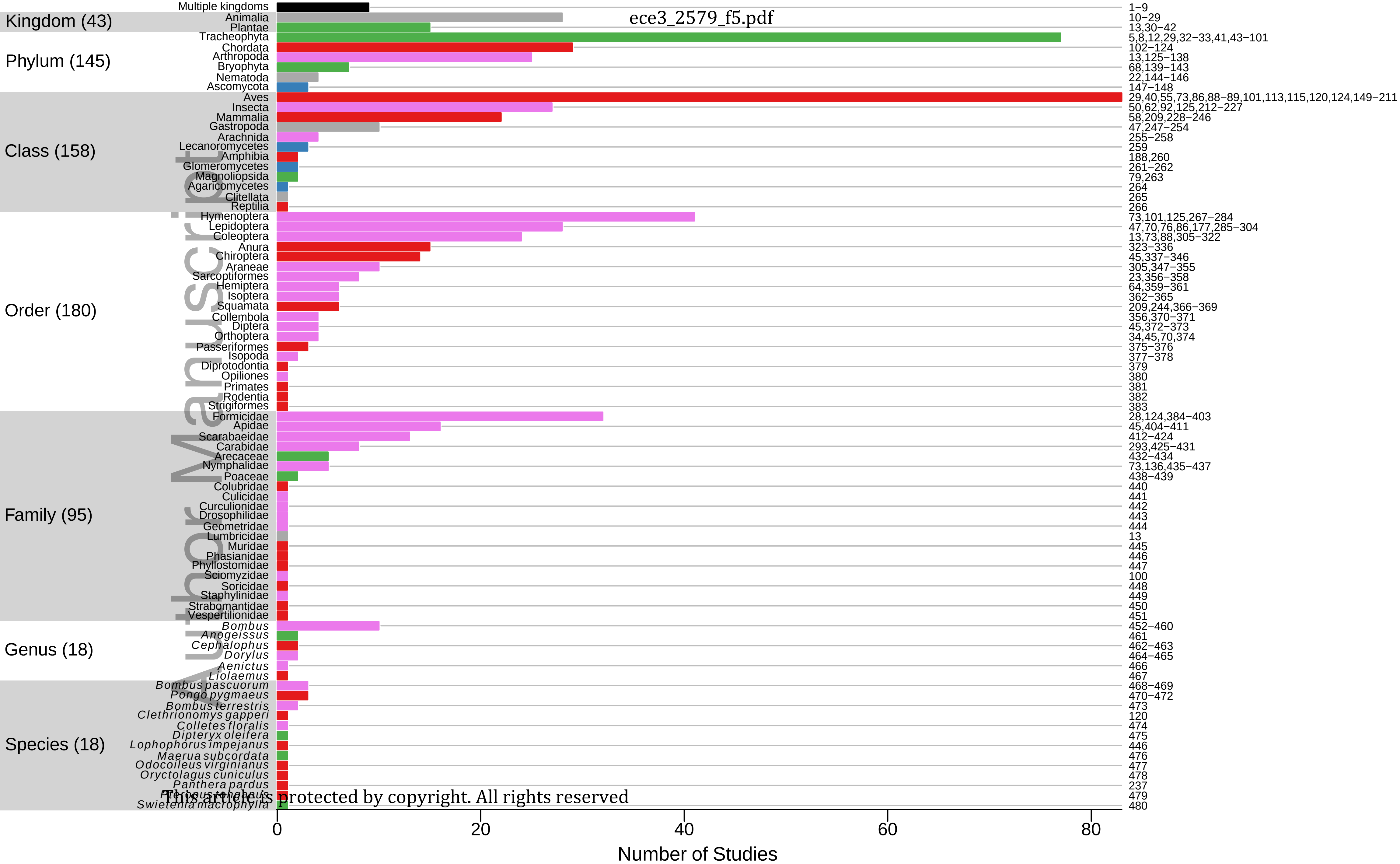
Neotropic
Palearctic
Afrotropic
Indo−Malay
Australasia
Oceania


Representation
0.1%
1.0%
10.0%
log₁₀(number of species represented in database)
log₁₀(estimated number of described species)
1
2
3
4
2.5
3.0
3.5
4.0
4.5
5.0
5.5
Magnoliophyta
Hymenoptera
Coleoptera
Lepidoptera
Aves
Arachnida
Diptera
Hemiptera
Basidiomycota
Bryophyta
Ascomycota
Mammalia
Reptilia
Ferns and allies
Mollusca
Amphibia
Orthoptera
Collembola
Nematoda
Isoptera
Diplopoda
Odonata
Crustacea
Chilopoda
Annelida
Gymnosperms
Neuroptera
Thysanoptera
Blattodea
Glomeromycota
Mantodea
Psocoptera
Dermaptera
Trichoptera
Archaeognatha
Symphyla
Platyhelminthes
Mecoptera
Protura
Pauropoda
Embioptera
Siphonaptera
Ephemeroptera
Onychophora
Fungoid protists
Phthiraptera
Thysanura
Phasmida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Genus (18)
Species (18)
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Plantae
13,30–42
Tracheophyta
5,8,12,29,32–33,41,43–101
Chordata
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Arthropoda
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Bryophyta
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Nematoda
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Ascomycota
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Agaricomycetes
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Reptilia
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Opiliones
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Rodentia
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Strigiformes
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Carabidae
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Arecaceae
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Nymphalidae
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Poaceae
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Colubridae
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Culicidae
441
Curculionidae
442
Drosophilidae
443
Geometridae
444
Lumbricidae
13
Muridae
445
Phasianidae
446
Phyllostomidae
447
Sciomyzidae
100
Soricidae
448
Staphylinidae
449
Strabomantidae
450
Vespertilionidae
451
Bombus
452–460
Anogeissus
461
Cephalophus
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Dorylus
464–465
Aenictus
466
Liolaemus
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Bombus pascuorum
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Pongo pygmaeus
470–472
Bombus terrestris
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Clethrionomys gapperi
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Colletes floralis
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Dipteryx oleifera
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Lophophorus impejanus
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Maerua subcordata
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Odocoileus virginianus
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Oryctolagus cuniculus
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Panthera pardus
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Pteropus tonganus
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Swietenia macrophylla
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20
40
60
80
Number of Studies

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