

Tropical Asia harbours a quarter of Earth's species: knowledge gaps and priorities for protecting a global biodiversity hotspot

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Supplementary Text

Biomes and ecosystems

Terrestrial

The interplay of climatic, geological, hydrological, and edaphic factors have given rise to the tremendous diversity of biomes and ecosystems across tropical Asia¹. In perhumid Sundaland (Fig. 1) and areas of the Philippines, lowlands (<700–1,000 m) are covered by mixed dipterocarp forests, dominated by emblematic trees in the family Dipterocarpaceae^{1,2}. Lowland forests in the region are occasionally punctuated by unusual vegetation types, typically on extreme soils. On nutrient-poor soils derived from sandstone plateaus or raised Pleistocene beaches, kerangas – a type of short-statured (heath) forest may develop. Forests of such type are largely limited to Borneo, and they harbor a depauperate but distinctive flora and fauna^{3,4}. Similarly, serpentine or ultramafic substrates are renowned for their plant endemism, no doubt due to the adaptations necessary to survive in the nutrient-poor and metal-rich soils^{5–7}. Limestone or karst-associated ecosystems, which are patchy but extensive on the Asian tropical mainland, Borneo, the Philippines, Sulawesi, and New Guinea^{8,9}, may harbor highly specialized and micro-endemic species, some of which are restricted to single cave systems^{10,11}.

Tropical Asia also contains over 60% of the world's tropical peatlands (including peat swamp forests), most of which are concentrated in sub-coastal parts of the Sunda shelf and to a lesser extent in New Guinea^{12–14}. Tropical peatlands largely develop in perhumid, low-lying and poorly draining areas where woody plant debris accumulates to form peat. The rapid loss and degradation of these habitats with exceptionally dense soil organic carbon is of global conservation concern^{15,16}. Due to the unique hydrological and edaphic conditions, peat swamps host endemic freshwater fauna^{13,17}. Few plant and vertebrate species occur exclusively in peat swamps, but they are important habitats for a variety of organisms¹³.

Seasonal forests and savannas cover much of Indochina, India, Sri Lanka, Java, and the Lesser Sunda Islands, and are characterized by prolonged dry periods (2–8 months) of low monthly precipitation (<100 mm)¹. Such seasonal forests can host herbaceous layers rich in C4 grasses, which in turn support a diverse, mammalian megafauna, including some of Asia's largest and most threatened bovids such as the gaur (*Bos gaurus*) and banteng (*Bos javanicus*).

The tectonic dynamism of the region has also given rise to high mountains >4,000 m, both relatively young (e.g., Mount Kinabalu in Borneo, Sunda volcanic arc, New Guinea highlands) and ancient (e.g., Indochinese mountain ranges)¹⁸. Such highlands support a variety of montane ecosystems: lower montane forests (starting at about 1,000 m), upper montane forests, subalpine woodlands and grasslands or scrub above about 2,600 m¹⁸. The complex and changing topographical, climatic and edaphic environments of mountains promote the formation of endemic floras and faunas distinct from the lowlands¹⁹.

Freshwater

Mainland tropical Asia has numerous large rivers, of which the six largest (exceeding 2,300 km in length) — the Mekong, Brahmaputra, Indus, Salween, Ganga (Ganges) and Irrawaddy — originate in the Himalayas^{20,21}. Other large mainland rivers (between 1,000–2,200 km long) are mostly rainfed and include the Godavari, Krishna and Narmada of Peninsular India, the Red and Chao Phraya rivers of Indochina, and the Zhujiang (Pearl River) of Southern China^{20–22}. In contrast, the rivers of insular tropical Asia (e.g., Sri Lanka, Malay Peninsula, Sunda islands), are comparatively small; only a handful of moderately large rivers (~900–1,100 km) can be found on Borneo (e.g. the Kapuas, Mahakam, Barito) and New Guinea (e.g. Fly, Mamberamo, Sepik)^{21,23}.

The vast majority of the region's lentic (lake and swamp) habitats comprise shallow fluvial (floodplain) lakes and wetlands that are seasonally-influenced²¹. These include Tonlé Sap, the region's largest lake^{21,24}, as well as the Kapuas floodplain-lake system^{21,25}. Much less prominent are tectonic and volcanic lakes²⁶, which can be found scattered throughout insular Southeast Asia (e.g., Lake Toba in Sumatra)²⁴.

Tropical Asia's freshwater ecosystems are most strongly influenced by seasonal rainfall coinciding with the summer monsoons²⁷. The onset of the rainy season can result in dramatic physical changes to habitats, such as in Tonlé Sap, which expands from a dry-season extent of 2,500 km² to a wet-season extent of 10,000–15,000 km²^{21,24}. Seasonal wet-dry cycles tend to be more pronounced at higher latitudes, whereas most equatorial areas experience rainfall all year round^{20,21}. Peak rainfall timings are also highly heterogeneous, with northern areas experiencing the heaviest rainfall in the middle of the year, whereas areas in the south are wettest at the end of the year^{24,28}.

Marine and coastal

Tropical Asia has the most biodiverse shallow-marine and coastal ecosystems in the world^{29–32}. Southeast Asia is bound longitudinally by two large and continuous continental shelves (Sunda and Sahul) which harbor fairly homogeneous seafloor environments, but the intervening areas are highly complex in their geomorphology and bathymetry; and dominated by deep basins such as the Banda and Celebes Seas, which reach bathyal and abyssal depths (Fig. 1). Mangrove, seagrass and coral ecosystems are distributed along coastlines of continental shelves and at oceanic islands across the region^{33–36}. However, it is in the vicinity of the numerous islands between the Sunda and Sahul shelves, and the Philippines – an area known as the Coral Triangle – that the richest coral reef ecosystems in the world are found^{37,38}. Karstic areas of Indonesia and Vietnam also develop anchialine lakes, sometimes referred to as marine lakes, as they have varying degrees of subterranean connection to ocean waters, which host a unique but understudied biota^{39,40}.

Outside of Southeast Asia, coastal and marine ecosystems are no less extensive or spectacular (Fig. 1). Immense mangrove systems can be found at the mouth of large river systems such as the Ganges Delta (i.e., the Sundarbans)

and the Irrawaddy Delta (Myanmar Coast mangroves), and are vastly important for wildlife and human livelihoods. The coral reefs of the Maldives and Lakshadweep islands in the Indian Ocean are also among the most extensive reef systems in the world⁴¹.

Supplementary Methods

All data processing, analyses and plotting were carried out in R 4.4⁴² using the packages alphahull⁴³, arrow⁴⁴, Cairo⁴⁵, CoordinateCleaner⁴⁶, cowplot⁴⁷, dplyr⁴⁸, elevatr⁴⁹, ggnewscale⁵⁰, ggplot2⁵¹, ggtext⁵², httr2⁵³, iucnredlist⁵⁴, jsonlite⁵⁵, lubridate⁵⁶, parallel⁴², patchwork⁵⁷, pbmcapply⁵⁸, plyr⁵⁹, purrr⁶⁰, readr⁶¹, readxl⁶², reshape2⁶³, scales⁶⁴, scatterpie⁶⁵, sf^{66,67}, shadowtext⁶⁸, sp^{69,70}, stringi⁷¹, stringr⁷², terra⁷³, tidyr⁷⁴, tidyterra⁷⁵, units⁷⁶.

Taxonomic and distribution data

We selected 23 taxonomic groups for which there was relatively comprehensive distribution data available across tropical Asia. In particular, we included less well-studied invertebrate groups, even if data was likely to be less complete than vertebrate groups, as they are generally absent from such large-scale analyses. Taxonomic groups were organised into four organismal groups: vascular plants (ferns, flowering plants, gymnosperms, lycophytes); terrestrial and freshwater vertebrates (amphibians, birds, freshwater fish, mammals and reptiles); terrestrial and freshwater invertebrates (ants, bees, butterflies, caddisflies, centipedes, flies, freshwater crabs, millipedes, mirid bugs, spiders, stick and leaf insects); and marine groups (bony fish, reef corals, and sharks and rays).

Processing distribution data for the taxa in our analyses depended upon whether they had checklist (a list of species known to be present within geographical or political units) or range maps (spatial polygons defining the boundaries of a given species' distribution). Broadly, we followed a standardized process for each data type, however, due to the differing nature of the data sources used, each taxon required slight modifications, outlined below and in Extended Data Table 1. Where such information was available, we removed cases of non-native portions of ranges.

In all cases, the number of species recorded in Extended Data Tables 1–3, both globally and within tropical Asia, is the number of species provided by the data source of each taxon (after the removal of species that were not considered; for example, exclusively marine species were removed from terrestrial and freshwater groups). The numbers presented are therefore not meant to be interpreted as definitive values of richness and endemism as they are also dependent upon the completeness of taxonomic and distributional knowledge for that taxon⁷⁷ – for all taxonomic groups there will be undescribed species that are missing from the data source (the Linnaean shortfall), as well as areas where a given species occurs but where we have yet to observe it (the Wallacean shortfall). The levels of shortfall varies between taxa (e.g.⁷⁸), and even within-taxon there may be differences between different data sources if they have used different taxonomies⁷⁹. Therefore, the true number of species may be considerably higher than our current estimates for less

well-studied taxonomic groups. Furthermore, due to the different spatial resolutions of distribution data between taxonomic groups, exact delineations of tropical Asia and its subregions unavoidably differ as well (see ‘Geographic scope’ below). Therefore, numbers of richness and endemism are not always directly comparable between taxonomic groups, and should be viewed in relation to the geographic scopes outlined for each taxonomic group on Extended Data Table 1 and Extended Data Fig. 1. Nevertheless, the numbers reflect the current state of knowledge for each group, whilst allowing for data-poor invertebrate groups that are generally excluded.

For each taxon we extracted description years directly from the spatial data source, or if not available, from the taxonomic authority that the spatial data source was based upon. For plants, where available, we deferred to the year of basionym description. All steps for data processing and cleaning are available at <https://github.com/peeb-lab-nus/Biodiversity-of-tropical-Asia>, and are reproducible once the raw datasets have been downloaded from the respective data sources.

Geographic scope

The boundaries of tropical Asia and subregions depended upon the type of spatial data we had for each taxonomic group. For groups with range maps, we intersected range map polygons with the terrestrial and marine subregions shown in Fig. S1. This delineation excludes the northern, highest elevation portions of Nepal and Bhutan, the dry and high elevation portions of north-west India, and includes only the subtropical parts of Guangdong, Guangxi and Yunnan provinces in China, as well as the Ryukyu Islands from Okinawa Island southwards. For groups with checklist data, however, checklists were generally available only at the province-level, and so in these cases the delineation of tropical Asia includes all of India, Nepal, Bhutan, Guangdong, Guangxi, Yunnan and the Ryukyu Islands. Additionally, for taxonomic groups with range maps, the Taliabu Islands and Aru Islands were assigned to Sulawesi and New Guinea, respectively, based on well-known biogeographical affinities⁸⁰, whereas for groups with checklist data both were retained as part of Maluku as they are a part of that administrative province. The exact delineations of tropical Asia and subregions for each taxonomic group are outlined below, in Extended Data Table 1, and visualised as the background maps in Extended Data Fig. 1.

Groups with range map data

For terrestrial and freshwater taxa with range map data (amphibians, ants, birds, freshwater fish, mammals, reptiles), we removed exclusively marine species, and the marine portions of range maps for remaining species. Conversely, for marine taxa (bony fish, reef corals, sharks and rays), we excluded portions of ranges or occurrence points falling on land. For taxa using range maps provided by IUCN (amphibians, birds, freshwater fish, bony fish, reef corals, sharks and rays) we excluded ‘Extinct’, ‘Possibly extinct’, ‘Presence uncertain’, ‘Introduced’, ‘Vagrant’, ‘Assisted colonisation’,

181 ‘Non-breeding’ and ‘Passage’ portions of ranges. The global total number of species was then calculated as the number
182 of species with range maps remaining in that data source.

183 All remaining range polygons were reprojected to the same equal-area cylindrical projection as the subregions. As
184 there were discrepancies between the coastlines used in some range map sources and those of our subregions, and for
185 some taxa single polygons covered both terrestrial and marine areas (e.g. shorebirds), we masked each polygon to land
186 for terrestrial and freshwater species, or to ocean for marine species, using GADM v4.1 (<https://gadm.org>), the same
187 source of coastlines used in generating the subregions. For each species we then calculated the area of intersection
188 between the range map polygons and each subregion, both as absolute area, and as a proportion of the global range size
189 of the species (the sum area of all polygons after the processing steps outlined above).

190 There are two potential sources of inaccuracy in using range map data. First, our delimitation of the extent of
191 tropical Asia is purposely coarse and generalised, and so will have inaccuracies in the exact locations of its borders.
192 Furthermore, the subregions that we designated were necessarily constrained by administrative boundaries to enable
193 the use of checklist data. Therefore, some areas may be inappropriately assigned to particular subregions, especially
194 in the case of small islands.

195 Second, a large potential source of error comes from the range maps themselves, which are accurate at only very
196 coarse scales ($> 200 \text{ km}^2$)⁸¹. In particular, the presence or absence of species on many of the smaller and more remote
197 islands may not be known with certainty, and this level of precision was unlikely to be applied when the range maps
198 were constructed. It is therefore inappropriate to assume species presence within an area simply by taking intersections
199 between range map polygons and subregion polygons, a process that implicitly assumes perfect precision⁸².

200 To account for these fine-scale inaccuracies, we defined a species as present within a subregion using two criteria:
201 1) if the species range occupied at least 5% of that subregion and/or 2) if at least 25% of the global species range fell
202 within that subregion. This minimises false presences on small islands or other regions (i.e., the range map wrongly
203 ascribes a presence to that island or region), or cases where that small island or region is not representative of the
204 subregion as a whole (i.e. our definition of the subregion is inaccurate with regards to that island or region). It also
205 removes temperate species where very small fractions of their estimated range fall within our specification of tropical
206 Asia. Finally, we defined a species as endemic to tropical Asia where $\geq 95\%$ of the global species range fell inside
207 tropical Asia.

208 The selected thresholds were chosen based on the expert opinion of the authors (FER) for birds, however, we also
209 applied more conservative (7.5% of the subregion occupied and/or 35% of the global species range occurs within the
210 subregion for presence within a subregion; 99% threshold to be considered endemic to tropical Asia) and more liberal
211 (2.5% and 15% for presence within a subregion; 90% threshold to be considered endemic to tropical Asia) thresholds
212 in order to provide lower and upper diversity estimates.

Groups with checklist data

For taxa with checklist data (bees, butterflies, caddisflies, centipedes, ferns, flies, flowering plants, freshwater crabs, gymnosperms, lycophytes, millipedes, mirid bugs, spiders and stick insects), where the majority of information was resolved to the province, state or island-level, or to botanical countries, we extracted individual geographic units from the text descriptions of geographic distributions, and matched them to subregions using look-up tables constructed for each dataset. All look-up tables are available as spreadsheets, along with R scripts outlining any other cleaning steps, in the code repository (<https://github.com/peeb-lab-nus/Biodiversity-of-tropical-Asia>).

If there was uncertainty in a given description, for example descriptions containing ‘possibly’ or ‘?’, the records were discarded. In some cases, geographic descriptions were too broad to assign a record to a single subregion. For example, where a checklist entry was ‘Indonesia’ or ‘Malaysia’, we assigned that species to all relevant subregions that encompass that description. However, if that species also had higher-resolution information within those subregions, then we deferred to the higher-resolution information. For example, a species with only one entry, ‘Malaysia’, would be assigned to both the Malay Peninsula and Borneo. However, if the species had two entries, ‘Malaysia’ and ‘Peninsular Malaysia’, we would only assign the species to the Malay peninsula, and not Borneo.

For a given taxonomic group, if a large proportion (>25%) of species records in China or Japan were labelled only as ‘China’ or ‘Japan’ respectively, with no province information, then we excluded all Chinese provinces (Guangdong, Guangxi, Hainan, Hong Kong, Macao and Yunnan), Taiwan and Japan (Okinawa) from our tropical area definition. This was necessary for millipedes ($n = 324$ out of 605 species with records for China and Japan in the database), spiders ($n = 6,639$ out of 7,115) and stick insects ($n = 451$ out of 470). For other taxa, the proportion of cases were much smaller (bees: $n = 3$ out of 485; caddisflies: $n = 425$ out of 1,712; flies: $n = 1,391$ out of 6,420; mirid bugs: $n = 68$ out of 836). In these cases, we retained the tropical provinces of China, Taiwan and Japan in the Indochina subregion, but we 1) did not assign those species to Indochina unless information from other countries inside Indochina was available, and 2) also assumed the species was present outside of tropical Asia.

Occasionally, a geographic description would specify a range rather than a specific location, i.e. that a species occurs from region X to region Y (flies = 179 entries; mirid bugs = 2; spiders = 171). In these cases, we assumed the species was present in subregions between these two locations. For a few species (flies = 188 species; millipedes = 7; mirid bugs = 12; spiders = 12) a given geographic description was too vague to assign the species to any subregion, but where we could confidently say that it did occur within our definition of tropical Asia (e.g. ‘South-east Asia’). If there was more specific information enabling us to assign the species to one or more subregions, we defaulted to that information, but otherwise, we included it in the overall counts of species native to tropical Asia, but excluded them from the subregion-level analyses.

Descriptions of taxonomic groups

Amphibians – All species from the class Amphibia with IUCN v2024-1 range maps⁸³. All range maps were masked to land using GADM v4.1⁸⁴. We excluded ‘Extinct’, ‘Possibly extinct’, ‘Presence uncertain’, ‘Introduced’, ‘Vagrant’, ‘Assisted colonisation’, ‘Non-breeding’ and ‘Passage’ portions of ranges.

Ants – All species in the family Formicidae. We broadly followed the methods described in Kass et al. 2022⁸⁵ to construct alpha hulls around occurrence points to generate range map polygons, using the cleaned occurrence data from the Global Ant Biodiversity Informatics database (GABI)⁸⁶ provided in that paper after removing spatial duplicates. The dataset contains data at the subspecies-level in some cases, in which case we aggregated points to the species-level.

For species with at least three remaining points we constructed alpha hulls ($\alpha = 15$). For a small subset of these species it was not possible to construct alpha hulls, and so following Kass et al. 2022 we constructed alpha shapes ($\alpha = 30$) instead. In both cases, we then buffered the resulting polygon by 30 km. For species with fewer than three points we buffered the points by 30 km and then merged the resulting polygons. We then removed marine areas (using GADM v4.1⁸⁴) and freshwater lakes (<https://naturalearthdata.com>; ne_10m_lakes v5.0.0) from each range polygon, and retained only those species that overlapped with the tropical Asia region.

Description year was extracted from the field ‘author_citation’ from the AntCat database⁸⁷ using the AntCat REST API (<https://antcat.org/v1/taxa/>). Three species, *Hypoconerops exoecata*, *Myrmoteras cuneonodus* and *Polyrhachis glabrinotum*, were represented in the Kass et al. 2022 dataset, but absent from AntCat. We manually added the description year for these species using information from AntWiki (www.antwiki.org).

Bees – Species from the families Andrenidae, Apidae, Colletidae, Halictidae, Megachilidae, Melittidae and Stenotritidae. The dataset, extensively documented in Orr et al. 2021⁸⁸, is derived from a global dataset citing full distributional information⁸⁹ – an authoritative list of species per administrative area generated at the country-level, and for most larger countries at state-, province- and/or island-level, as well as select well-known areas. This was based on original species descriptions, published literature records from reliable sources (key publications are given in⁸⁸), iNaturalist and other directly verified citizen science resources, and digitised but not yet publicly-shared specimens.

We relied upon expert-defined categorisation for endemism for tropical Asia as encoded in the dataset. The global number of species was taken from (63). Most ‘China’ or ‘Japan’ entries were coded to provinces or prefectures (and their islands) respectively allowing the relevant components of those faunas to be enumerated excepting a few doubtful cases which were excluded ($n = 3$).

Birds – Species from the class Aves with Birdlife International v2023-1 range maps⁹⁰. We excluded pelagic species, defined as all species from the following families: Alcidae, Diomedidae, Fregatidae, Hydrobatidae, Oceanitidae, Phaethontidae, Procellariidae, Spheniscidae, Stercorariidae and Sulidae. All marine portions of ranges were excluded by masking range maps to land using GADM v4.1⁸⁴. We excluded ‘Extinct’, ‘Possibly extinct’, ‘Presence uncertain’, ‘Introduced’, ‘Vagrant’, ‘Assisted colonisation’, ‘Non-breeding’ and ‘Passage’ portions of ranges. The range map area for *Rhyticeros narcondami* was added manually because the original range map had no overlap with land areas defined by the GADM 4.1⁸⁴. Note, species considered sensitive to exploitation, which are not included with the public versions of the range maps, were included in this analysis.

Bony fish – Range maps for marine species of class Actinopterygii fish according to IUCN v2024-2⁹¹. The range maps, however, are not complete for all marine fish, but include the following groups: blennies (families Blenniidae, Chaenopsidae, Clinidae, Dactyloscopidae, Grammatidae, Labrisomidae and Tripterygiidae); bonefish, tarpons and ladyfish (orders: Albuliformes and Elopiformes); butterflyfish, angelfish and allies (families: Acanthuridae, Caesionidae, Callanthiidae, Caproidae, Centrarchidae, Cepolidae, Chaetodontidae, Dinopercidae, Drepaneidae, Emmelichthyidae, Ephippidae, Gerreidae, Haemulidae, Haplogenyidae, Leiognathidae, Lethrinidae, Lobotidae, Lutjanidae, Luvaridae, Malacanthidae, Monodactylidae, Moronidae, Nemipteridae, Pomacanthidae, Priacanthidae, Scatophagidae, Sciaenidae, Siganidae, Sillaginidae, Sparidae, Zancidae); carangiform fishes (families: Achiridae, Achiropsettidae, Bothidae, Carangidae, Centropomidae, Citharidae, Coryphaenidae, Cynoglossidae, Echeneidae, Istiophoridae, Lactariidae, Latidae, Leptobramidae, Menidae, Nematistiidae, Oncopteridae, Paralichthodidae, Paralichthyidae, Pleuronectidae, Poecilopsettidae, Polynemidae, Psettodidae, Rachycentridae, Rhombosoleidae, Samaridae, Scopthalmidae, Soleidae, Sphyrnidae, Toxotidae, Xiphiidae); clupeiforms (order: Clupeiformes); eels (orders: Anguilliformes and Saccopharyngiformes); groupers (family: Epinephelidae); pufferfish and relatives (order: Tetraodontiformes); sturgeons and paddlefish (order: Acipenseriformes); seahorses and allies (families: Syngnathidae, Aulostomidae, Centriscidae, Fistulariidae and Solenostomidae); tuna, billfish and swordfish (families: Istiophoridae, Scombridae and Xiphiidae) and wrasse and parrotfish (family: Labridae).

All freshwater portions of ranges were excluded by masking range maps to the ocean using GADM v4.1⁸⁴. We excluded ‘Extinct’, ‘Possibly extinct’, ‘Presence uncertain’, ‘Introduced’, ‘Vagrant’, ‘Assisted colonisation’, ‘Non-breeding’ and ‘Passage’ portions of ranges. For species with point data, we buffered points by a 25 km radius, before merging with the range map if present.

Butterflies – Species from the families Hesperidae, Lycaenidae, Nymphalidae, Papilionidae, Pieridae and Riodinidae. Butterfly data came from curated checklists generated for the subregions used in the study. They included the tropical regions of China (Guangdong, Hainan, Hong Kong, Macau and Yunnan) and Taiwan, but excluded Guangxi

and the Okinawa province of Japan (southern Ryukyu Islands).

To generate an expert-curated checklist for tropical Asia, we compiled species checklists for individual geographic and political regions in tropical Asia using the following sources: Thailand⁹²; Laos^{93,94}; Vietnam⁹⁵; Sri Lanka⁹⁶; peninsular Malaysia⁹⁷; Bangladesh^{98,99}; Bhutan^{100,101}; Andamans and Nicobars^{102,103}, Indian mainland^{102,103}, Cambodia¹⁰⁴, Nepal^{105–107}, Hainan, China¹⁰⁸; Yunnan, China¹⁰⁹; Guangdong, China¹¹⁰; Taiwan¹¹¹; Philippines¹¹²; and Myanmar¹¹³. The checklist for South Asia was aggregated from checklists of India, Sri Lanka, Nepal, Bhutan, and Bangladesh. The checklist for continental Southeast Asia was aggregated from the checklists of Myanmar, Thailand, Laos, Cambodia, Vietnam, Hainan, Yunnan, Guangzhou, and Taiwan.

Comprehensive checklists of Indonesian butterflies have not previously been compiled, nor are there authoritative lists for the islands of Borneo and New Guinea, which include Indonesian provinces and at least one other country. Georeferenced specimen information was aggregated from GBIF.org (downloaded February–March 2021)^{114–130}, the specimen collection of David J. Lohman, and numerous literature sources^{131–191}. The checklist for Borneo included two checklists for Brunei^{192,193}, and the checklist for New Guinea included sources document species found in the Indonesian provinces of Papua and West Papua^{145,154,155,157,158,162,172,174,175,187} as well as the country of Papua New Guinea¹⁶¹.

Scientific names were recorded at the subspecies-level if available, or as binomials if no subspecific names were provided in the original source. We used Lamas 2015¹⁹⁴ as the master list of butterfly taxonomy, which includes all known junior synonyms together with their currently valid name at the lowest possible taxonomic resolution valid under the International Code of Zoological Nomenclature (i.e., no infrasubspecific taxa). Binomials provided in the source literature were first checked against the list of all valid species and exact matches were accepted as current names. When trinomials were provided, the genus and subspecies name were checked against the list of all valid binomials. All exact matches were reviewed to ensure that these names, representing subspecies recently raised to specific status, were valid. Then, the genus and species names of a trinomial were checked against valid binomials; exact matches were regarded as valid species. Of the names not matched in one of these ways, the genus name was checked against a list of valid genera to ensure that the genus name was current. The binomials of species placed in novel genera (different from the original source) were then evaluated as described above. All remaining unmatched names were evaluated individually. These non-matches resulted from: 1) misspellings in the source document; 2) lack of gender agreement between genus and specific names (as enforced in Lamas' 2015 list); and 3) species placed in genera that became valid after 2015. The following post-2015 publications were used to update names of the affected taxa to the most current taxonomy published^{188,195–200}.

As the checklists only covered tropical Asia, they contain no information about the distributions of tropical Asia species outside the region. We therefore determined endemism to tropical Asia through the global checklist of Pinkert et al. 2022²⁰¹. If this checklist contained any geographic distribution outside of tropical Asia for a given species, the

species was assumed to be non-endemic. For 1,008 tropical Asia species in Pinkert et al. 2022 the only distributional information potentially outside of tropical Asia was ‘China’ with no further information of province or other locality, and therefore we could not determine if the species was confined to the areas of China we define as tropical (Hainan, Hong Kong, Guangdong, Guangxi, Macao and Yunnan), or if the species’ ranges also extended into temperate regions. For these species we used either the distributions predicted by species distribution models (SDMs) in Yau et al. 2025²⁰² ($n = 445$), or a cleaned set of occurrence points in the same study ($n = 341$), applying a threshold of 95% of the predicted distribution to occur within the tropical Asia region to account for overprediction errors. There were 223 remaining species not present in the Yau et al. 2025 dataset, and a further 178 species were present in our dataset but absent from both the Pinkert et al. 2022 and Yau et al. 2025 datasets. In both these cases we assigned endemism based upon expert opinion (DJL).

Caddisflies – Species from the insect order Trichoptera. Raw distributional data for the Oriental and Australasian regions were downloaded from the Trichoptera World Checklist (available at <https://trichopt.app.clemson.edu>)²⁰³. All record types of ‘Species nomen dubium’, ‘species nomen nudum’ and ‘fossil*’ records were removed. Where no distribution information was specified then the type locality was used to specify if the species was present within tropical Asia.

Out of 1,712 species with records in China and/or Japan there were 425 species (24.8%) that had no further province information. In these cases we could not determine if the species was endemic to tropical Asia (i.e., only occurs within tropical China or Japan) or is also found in temperate regions of those countries. We therefore assumed these species were not native to the tropical Asia region. The remaining species were assigned as inside/outside of the Indochina subregion on the basis of the additional province information.

There was no description year for ten species. In these cases years were manually added based on information from <https://trichopt.app.clemson.edu/>: *Helicopsyche petri*, *Hydropsyche moselyi*, *Hydroptila spirula*, *Macrostemum pseudoneura*, *Macrostemum quinquepunctatum*, *Oecetis angustipennis*, *Oecetis caelum*, *Rhyacophila chayulpa*, *Triaenodes aureus*, *Triaenodes longispinus*. For five species, *Agapetus agtuuganonis*, *Chimarra bicolor*, *Hydropsyche ciosi*, *Hydropsyche kimminsi*, and *Hydropsyche tanung*, there were discrepancies between the description year in the global dataset, and the subset of species that were tagged as ‘Oriental’ in the dataset. In these cases, we deferred to the description year in the Oriental subset.

Centipedes – Species from the class Chilopoda. Data was extracted from ChiloBase 2.0 (<https://chilobase.biologia.unipd.it>)²⁰⁴. The taxonomic information for one species, *Orphnaeus aporus*, was manually entered based upon information from Encyclopedia of Life (<https://eol.org>).

Flies – Species from the insect order Diptera. Data was extracted from Systema Dipterorum (<http://diptera.org>)²⁰⁵. We aggregated subspecies to species-level data, and retained the earliest date as the description year. For 6,420 species found in China and/or Japan, 1,391 species (21.7%) had no further province information. In these cases we could not determine if the species was endemic to tropical Asia (i.e. only occurs within tropical China or Japan) or is also found in temperate regions of those countries. We therefore assumed these species were not native to the tropical Asia region. The remaining species were assigned as inside/outside of the Indochina subregion on the basis of the additional province information.

There were 160 geographic descriptions across 179 species that were variations of ‘region X to region Y’ (for example ‘Eastern Africa to India and Indonesia’). In these cases we assumed the species was present in subregions between these two locations. For 188 species, the descriptions were too vague to assign the species to specific subregions (e.g. variations on ‘subtropical asia’, ‘circumtropical’) and there was no alternative information with more specific geographic locations. These species were excluded from subregion-level analyses, but retained for the total number of species occurring in tropical Asia.

Freshwater crabs – We only considered primary freshwater crab species, where all members are independent of the sea for completion of the life cycle²⁰⁶. Within tropical Asia, two families of primary freshwater crabs occur; Gecarcinucidae and Potamidae. Primary freshwater crabs, in contrast to their secondary or marine counterparts, lack marine planktonic phases, instead opting for direct development where the eggs mature and hatch out into miniature crabs. The lack of a planktonic phase severely limits their dispersal capability and, in combination with their comparatively low fecundity and stenotopic habitat requirements, have led to very narrow distribution ranges with correspondingly high levels of endemism²⁰⁶. Most species of primary freshwater crabs from tropical Asia are restricted to their respective watersheds and for some species, specific streams or caves.

A rough species checklist was first curated from past published checklists and the online database DecaNet²⁰⁷ (www.decanet.info). We subsequently narrowed species to the tropical Asia region by cross referencing against primary sources (i.e. systematic revisions and/or taxonomic description papers)^{208–517}. Distribution data was also recorded from primary sources, predominantly as occurrence points. Where available, reliable checklists (usually subregional and local in scope) were used to update or resolve conflicts on the species distribution data from the older literature.

Freshwater fish – Freshwater fish distribution data from IUCN includes species from the classes Actinopterygii, Chondrichthyes, Myxini, Petromyzonti and Sarcopterygii found within freshwater systems. The distribution data comes as three distinct data types: range map polygons, information on hydrobasins, and point data. For species with range map polygons, all marine portions of ranges were excluded by masking range maps to land using GADM v4.1⁸⁴.

We excluded ‘Extinct’, ‘Possibly extinct’, ‘Presence uncertain’, ‘Introduced’, ‘Vagrant’, ‘Assisted colonisation’, ‘Non-breeding’ and ‘Passage’ portions of ranges, and polygons where ‘marine’ = true. For species with point data, we buffered points by a 25 km radius in an equal-area projection. For hydrobasins data, we matched up hydrobasins information to the level 8, level 10 and level 12 hydroBASIN shapefiles (<https://www.iucnredlist.org/resources/spatialtoolsanddata>, version Aug. 2023). Where a species had both range maps and hydrobasin data, we retained only the range maps. In the majority of cases the distributions were identical between the two, but where they differed the range maps were found to generally estimate a more restricted distribution. For each species, we then merged together the range maps or hydrobasins, with the buffered points if available, to generate a final distribution map. Range maps for subspecies and subpopulations were aggregated to species-level.

For five species, *Arothron manilensis*, *Callogobius hasseltii*, *Mugilogobius abei*, *Pastinachus sephen* and *Urogymnus acanthobothrium*, there was no taxonomic information in the IUCN taxonomic spreadsheet, and so family and description year were manually added based on the species page on the IUCN website (www.iucnredlist.org/species). One species that occurs outside of tropical Asia in northern Australia, *Melanotaenia* sp. nov. ‘*Malanda*’, is awaiting formal description at the time of publication of the IUCN range maps and so has no description year, but was included in the global number of species.

Mammals – Species from the class Mammalia following the taxonomy of Mammal Diversity Database v1.2^{518,519}. Exclusively marine species were excluded, but species present in both marine and freshwater realms were included. In all cases, however, marine portions of ranges were excluded by masking range maps⁵¹⁹ to land using GADM v4.1⁸⁴. When matching the range maps to the Mammal Diversity Database v1.2 taxonomy⁵¹⁸ there was one name discrepancy, *Paradoxurus philippensis* to *Paradoxurus philippinensis*, which was manually corrected.

Millipedes – Species from the class Diplopoda. Data are aggregated in the global taxonomic database MilliBase⁵²⁰ (www.millibase.org), which also includes the classes Symphyla (garden centipedes) and Pauropoda (dwarf myriapods), but these were excluded from this study. The millipede data in MilliBase on tropical Asia are based on the publication data from original descriptions, secondary literature and relevant taxonomic catalogues for the respective millipede families and orders^{521–529}. Additionally, the following millipede species checklists of geographic and political regions in tropical Asia were checked and used for data compilation in MilliBase: Bangladesh⁵³⁰, Cambodia⁵³¹, India⁵³², Myanmar⁵³³, Singapore⁵³⁴, Thailand⁵³⁵, and Vietnam⁵³⁶. At least 415 literature sources were used in MilliBase for the distribution data on tropical Asia. We excluded all fossil and uncertain (nomen dubium, taxon inquirendum) species.

Subspecies were aggregated to species-level. Where a species had more than one description year, we deferred to the earliest date. Taxonomic and description year details were added manually for *Cystogonopus bicornis*, *Julus*

celebensis, *Platyrrhacus loriae*, *Polydesmopeltis xanthotrichus*, *Trachyjulus nordquisti* based on information from <https://millibase.org>. One species, *Orthomorpha bisculcata*, has no description year in the database, and so was retained for distributional analyses but excluded from analyses of temporal patterns of description rates.

For 605 species found in China and/or Japan, 324 species (53.6%) had no further province information. In these cases, we could not determine if the species was endemic to tropical Asia (i.e. only occurs within tropical China or Japan) or is also found in temperate regions of those countries. We therefore excluded provinces of China (Guangdong, Guangxi, Hainan, Hong Kong, Macao and Yunnan) and Japan (Okinawa) that fall within our tropical Asia definition, as well as Taiwan.

Mirid bugs – Species from the family Miridae. Data was extracted from the Planetary Biodiversity Inventory (PBI) for mirid bugs version March 2013 (<https://research.amnh.org/pbi/index.html>)⁵³⁷. Out of 836 species with records in China and/or Japan there were 68 species (8.14%) that had no further province information. In these cases we could not determine if the species was endemic to tropical Asia (i.e. only occurs within tropical China or Japan) or is also found in temperate regions of those countries. We therefore assumed these species were not native to the tropical Asia region. The remaining species were assigned as inside/outside of the Indochina subregion on the basis of the additional province information.

There were two cases where the distributional information was ‘region X to region Y’ (‘India east to Solomon Is.’ and ‘Sri Lanka east to Samoa’). In these cases we assumed the species was present in subregions between these two locations. For one species, the description was too vague to assign the species to a specific subregion (‘Ostindien’) and there was no alternative information with more specific geographic locations. The species were excluded from subregion-level analyses, but retained for the total number of species occurring in tropical Asia.

Reef corals – Reef corals were defined by IUCN v2024-2⁹¹ as all warm water reef-building corals species of the families Acroporidae, Agariciidae, Astrangiidae, Astrocoeniidae, Cladocoridae, Coscinaraeidae, Diploastraeidae, Euphylliidae, Faviidae, Fungiidae, Helioporidae, Leptastreidae, Lobophylliidae, Meandrinidae, Merulinidae, Milleporidae, Montastraeidae, Oculinidae, Oulastreidae, Plerogyridae, Plesiastreidae, Pocilloporidae, Poritidae, Psammocoridae, Rhizangiidae, Tubiporidae, Turbinoliidae, and the genera *Balanophyllia*, *Duncanopsammia*, *Heterocyathus*, *Heteropsammia*, *Pachyseris*, *Solenastrea*, and *Turbinaria*.

All freshwater portions of ranges were excluded by masking range maps to ocean using GADM v4.1⁸⁴. We excluded ‘Extinct’, ‘Possibly extinct’, ‘Presence uncertain’, ‘Introduced’, ‘Vagrant’, ‘Assisted colonisation’, ‘Non-breeding’ and ‘Passage’ portions of ranges. One species, *Pseudocyathoceras avis*, had no range map and so was excluded from the analyses, but was included in the overall global diversity numbers.

Reptiles – Species from the classes Crocodylia, Squamata, Rhynchocephalia and Testudines. Exclusively marine species (marine turtles and sea snakes) are excluded from GARD v1.7 range maps^{538–540}. For all other species, any existing marine portions of ranges were excluded by masking range maps to land using GADM v4.1⁸⁴.

We extracted the description year for each species from www.reptile-database.org⁵⁴¹. The majority of species were matched using versions 03/2015 and 05/2021 of the reptile checklist that matched those used when generating the GARD v1.7 range maps, where the latter checklist took precedence between the two in cases of overlap. There were 22 tropical Asian species in the GARD v1.7 range maps dataset not represented in either version of the reptile checklist, which were matched to current valid names using the 04/2023 synonym list also available from www.reptile-database.org. Of these, four GARD v1.7 names were not represented in the synonym list. We manually added the synonyms of these species to the synonym list based on information from www.reptile-database.org: *Ctenophorus macropus* to *Ctenophorus slateri*; *Diploderma fasciata* to *Diploderma fasciatum*; *Diploderma ngoclinensis* to *Diploderma ngoclinense*; *Rhabdophis rudis* to *Pseudagkistrodon rudis*.

Spiders – Species from the order Araneae. Data was extracted from the World Spider Catalog v25.0⁵⁴². The majority of species occurring in China and/or Japan (6,639 species out of 7,115 species found in China or Japan) did not have further province information. In these cases we could not determine if the species was endemic to tropical Asia (i.e. only occurs within tropical China or Japan) or is also found in temperate regions of those countries. We therefore excluded provinces of China (Guangdong, Guangxi, Hainan, Hong Kong, Macao and Yunnan) and Japan (Okinawa) that fall within our definition of tropical Asia, as well as Taiwan.

There were 104 geographic descriptions across 171 species that were variations of ‘region X to region Y’ (for example ‘Sri Lanka to Indonesia Java’ or ‘Eastern Africa to India and Indonesia’). In these cases, we assumed the species was present in subregions between these two locations.

For 12 species, the descriptions were too vague to assign the species to specific subregions (e.g. variations on southeast, tropical and subtropical asia, ‘Indonesia Moluccas or New Guinea’, ‘Malaysia or Indonesia Java’) and there was no alternative information with more specific geographic locations. These species were excluded from subregion-level analyses, but retained for the total number of species occurring in tropical Asia.

Stick and leaf insects – Species from the order Phasmida. Data was extracted from Phasmida Species File (<https://phasmida.speciesfile.org/>)⁵⁴³. The majority of species occurring in China and/or Japan (451 species out of 470 species found in China or Japan) did not have further province information. In these cases we could not determine if the species was endemic to tropical Asia (i.e. only occurs within tropical China or Japan) or is also found in temperate regions of those countries. We therefore excluded provinces of China (Guangdong, Guangxi, Hainan, Hong Kong, Macao and Yunnan) and Japan (Okinawa) that fall within our tropical Asia definition, as well as Taiwan.

The description year for *Pylaemenes scrupeus*, and higher taxonomic information for *Phanclloidea baculus*, were added manually based on information from <https://phasmida.speciesfile.org>.

Sharks and rays – Species from the class Chondrichthyes (sharks, rays and chimaeras) according to IUCN v2024-2⁹¹. All freshwater portions of ranges were excluded by masking range maps to ocean using GADM v4.1⁸⁴. We excluded ‘Extinct’, ‘Possibly extinct’, ‘Presence uncertain’, ‘Introduced’, ‘Vagrant’, ‘Assisted colonisation’, ‘Non-breeding’ and ‘Passage’ portions of ranges. Three species, *Bythaelurus alcockii*, *Carcharhinus obsoletus* and *Raja pita*, have no valid range maps and so were excluded from the analyses, but included in the calculation of total global diversity.

Vascular plants (ferns, flowering plants, gymnosperms, lycophytes) – We used taxonomic and distribution data from the World Checklist of Vascular Plants v13 (WCVP)^{544,545}, available at <https://powo.science.kew.org>. Species were separated into groups according to families - ferns: Aspleniaceae, Cystodiaceae, Cyatheaceae, Dennstaedtiaceae, Dipteridaceae, Equisetaceae, Gleicheniaceae, Hymenophyllaceae, Marattiaceae, Marsileaceae, Matoniaceae, Ophioglossaceae, Osmundaceae, Polypodiaceae, Psilotaceae, Pteridaceae, Salviniaceae, Saccolomataceae and Schizaceae; lycophytes: Isoetaceae, Lycopodiaceae, Selaginellaceae; gymnosperms: Araucariaceae, Cephalotaxaceae, Cupressaceae, Cycadaceae, Ephedraceae, Gnetaceae, Pinaceae, Podocarpaceae, Taxaceae. All remaining families were assigned to angiosperms (flowering plants).

Distribution data is organised into ‘botanical country’ geographic units, as defined by the International Working Group on Taxonomic Databases (TDWG; <https://www.tdwg.org>)⁵⁴⁶. Botanical countries generally correspond to countries, but may subdivide larger countries into states or provinces (usually delimited by the geographic granularity of its constituent data), or may aggregate territories from multiple areas or countries into a single coherent biogeographic unit (e.g., Borneo, New Guinea). We identified vascular plant species from tropical Asia and each subregion using the following botanical countries (3-letter code): South Asia (‘WHM’, ‘NEP’, ‘IND’, ‘EHM’, ‘ASS’, ‘BAN’, ‘SRL’), Indochina (‘MYA’, ‘LAO’, ‘VIE’, ‘THA’, ‘CBD’, ‘SCS’, ‘CHC’, ‘CHS’, ‘NNS’, ‘CHH’, ‘TAI’), Malay Peninsula (‘MLY’), Sumatra (‘SUM’), Philippines (‘PHI’), Java (‘JAW’), Sulawesi (‘SUL’), Borneo (‘BOR’), Lesser Sundas (‘LSI’), Andamans (‘AND’, ‘NCD’), Maluku (‘MOL’) and New Guinea (‘NWG’, ‘BIS’). As many of the botanical countries at the northern limits of tropical Asia (‘CHC’, ‘CHS’, ‘NNS’, ‘CHH’, ‘TAI’) may also contain non-tropical elements, we only included vascular plant species that were tagged as ‘tropical’ (‘climate_description’ column in WCVP) or found in other botanical countries that we considered part of tropical Asia. Though not included in any of the subregions we defined, we also included data from the following botanical countries in our definition of tropical Asia: ‘LDV’ and ‘MDV’. There are slight differences in geographic limitation of subregions associated with the use of WCVP. The island of Bali was considered part of the Lesser Sunda Islands botanical country (‘LSI’), instead of with Java (‘JAW’).

Coverage of occurrence records

We explored the spatio-temporal coverage of biodiversity sampling through time in the same taxonomic groups explored in our diversity analyses. We used the Global Biodiversity Information Facility (GBIF) database (archived on 01/10/2024)⁵⁴⁷ for terrestrial and freshwater groups, and the Ocean Biodiversity Information System (OBIS) database (archived on 23/07/2024)⁵⁴⁸ for marine groups. Although not exhaustive, these two databases are the most comprehensive repositories of open-access biodiversity data, and additionally aggregate information from many other biodiversity projects (e.g. iNaturalist.org). Our taxonomic groups globally composed over 2.6 billion occurrence records out of around 3 billion records in total in GBIF, and 41 million out of 128 million records within OBIS.

Both databases use taxonomies that may differ from the specific taxonomic authorities used for our distributional databases described above, the GBIF taxonomic backbone⁵⁴⁹, and the World Register for Marine Species (WoRMS)⁵⁵⁰ in the case of OBIS. Where authorities are not identical, this means that exact numbers of species, as well as species identities, will differ slightly from the diversity analyses. Therefore, we focus on the spatial and temporal distribution of occurrence records within groups, but do not explore species-level patterns.

There were two main differences from the diversity analyses. First, we did not *a priori* remove marine species, or marine portions of ranges for terrestrial and freshwater groups (or terrestrial and freshwater species and terrestrial or freshwater portions of ranges for marine groups), but only removed points that fell within oceanic areas (or outside for marine groups), as defined by GADM v4.1⁸⁴. Second, we also did not remove records representing vagrant or introduced portions of ranges, as this information is not available from the occurrence records data.

For some groups, higher taxonomic classifications in GBIF and OBIS differ significantly from the distributional databases used for the diversity analyses. We separated vascular plants into taxonomic groups according to classes: Polypodiopsida (ferns); Magnoliopsida and Liliopsida (flowering plants); Pinopsida, Gnetopsida, Cycadopsida and Ginkgoopsida (gymnosperms); and Lycopodiopsida (lycophytes). For birds, we did not exclude marine groups, but filtered occurrence records only for terrestrial areas. For freshwater crabs we considered the families Deckeniidae, Gecarcinucidae, Potamidae, Potamonautidae, Pseudothelphusidae, Trichodactylidae. In the GBIF taxonomic backbone there is no single grouping corresponding to freshwater fish, so we included all possible fish groups, before filtering out any records occurring in ocean areas. We included the orders Acipenseriformes, Albuliformes, Amiiformes, Anguilliformes, Ateleopodiformes, Atheriniformes, Aulopiformes, Batrachoidiformes, Beloniformes, Beryciformes, Cetomimiformes, Characiformes, Clupeiformes, Cypriniformes, Cyprinodontiformes, Elopiformes, Esociformes, Gadiformes, Gasterosteiformes, Gobiesociformes, Gonorynchiformes, Gymnotiformes, Lampriformes, Lepisosteiformes, Lophiiformes, Mugiliformes, Myctophiformes, Notacanthiformes, Ophidiiformes, Osmeriformes, Osteoglossiformes, Perciformes, Percopsiformes, Pleuronectiformes, Polymixiiformes, Polypteriformes, Saccopharyngiformes, Salmoniformes, Scorpaeniformes, Siluriformes, Stephanoberyciformes, Stomiiformes, Synbranchiformes, Syngnathiformes,

Tetraodontiformes, Zeiformes, as well as the classes Coelacanthi, Dipneusti, Elasmobranchii, Holocephali, Myxini and Petromyzonti. For reptiles, we included the classes Crocodylia, Squamata, Sphenodontia and Testudines.

For the marine groups using OBIS data, we extracted the classes Chondrostei, Holostei and Teleostei for bony fish, and the classes Elasmobranchii and Holocephali for sharks and rays. For all other groups, we followed the same taxonomic criteria as outlined in the descriptions for distribution data.

Cleaning workflow

There are four issues with occurrence data that limit its applicability for our analyses, and so it is critical to thoroughly clean occurrence records to ensure high data quality⁵⁵¹. First, there are extensive and well-known inaccuracies in occurrence records^{552–555}, ranging from temporal (e.g. invalid dates), taxonomic (e.g. misidentifications or difficulties in tracking nomenclature changes over time) and spatial (e.g. wrong coordinates) issues, often arising from incorrect data entry⁵⁵⁵. Second, records may not have the full complement of information necessary for our analyses (i.e. taxonomic identification at species-level, complete coordinates and a record date to at least year resolution). Third, records may be recorded at spatial, temporal or taxonomic resolutions too coarse for our uses (e.g. high coordinate uncertainty, or only identified to the level of family or order). Finally, we also removed spatiotemporal duplicates, defined as records for a given species with the same coordinates and year, month and day (where we could interpret a valid date). Such duplicate records provide no additional information. Furthermore, there are inconsistencies in data entries in GBIF, whereby some collections add the observation of multiple individuals of a species at a given point in time and space as a single entry, adding information on the number of individuals in a separate column, and others adding a new entry for each individual.

Therefore, to ensure standardisation across groups, we applied an identical cleaning workflow to all groups in order to filter out potentially erroneous or low-quality data (see Table S1 for details on all steps and parameters used). We do not attempt to curate a perfect dataset, but rather to allow us to compare the quantities of data collected on different groups across space and time (Table S2). On average 2.19% of the original global occurrence records were retained after cleaning, ranging from 0.15% for mirid bugs to 10.84% for freshwater crabs. The thresholds used were already relatively lenient, only requiring complete name, coordinates and year, and a threshold of 100 km for coordinate uncertainty (the grain size at which we were aggregating) Applying less stringent thresholds would potentially increase data quantity but at the expense of higher spatial, temporal and taxonomic uncertainty.

Details of facets of spatio-temporal coverage explored

To explore our ability to accurately recover patterns of diversity in space, and to observe changes to these patterns over time, we investigated three facets of the spatio-temporal information coverage of occurrence records. To aid

interpretability, the measures are relatively simple and intuitive, and we standardised across taxa so that groups with large quantities of data were weighted equally as data-poor groups. In all cases we summarised the properties of the cleaned occurrence records within 100×100 km equal-area grid cells. For each taxonomic group we explored three facets of spatio-temporal coverage:

1) The standardised number of occurrence records was summarised as the proportion of the log number of records compared to the cell with the highest number of records, independent of species identity. Therefore, values range from 0 (cells with a single occurrence record) to 1 (the cell with the most records). This reflects the degree of sampling effort that has been carried out in each cell.

2) We summarised temporal coverage as the proportion of species within each cell that were recorded during only a single year ('temporal singletons'). This is a simple indication of our ability to determine changes in the status of a species in a given location.

3) Record age was summarised as the median year of occurrence records after removing species-year duplicates within a cell. This is an indicator of whether the majority of sampling effort for a given location was long ago (in which case it may not accurately reflect the current status of a species) or more recently.

We calculated each metric within each taxon separately, and then standardised across taxa within each organismal group (vascular plants, terrestrial and freshwater vertebrates, terrestrial and freshwater invertebrates, marine groups) by taking the median values for each cell. We therefore weighted all taxa equally, regardless of the overall quantity of data for each taxon.

We also explored the effect of citizen science data by repeating the analyses with data only from eBird (ebird.org; institution code = 'EBIRD') and iNaturalist (www.inaturalist.org; institution code = 'iNaturalist'). Data from eBird and iNaturalist represent 63.2% and 3.5% of occurrence records in the region, respectively, so although there may be other sources of citizen science data they are likely to represent a very small percentage of the overall data, and are therefore unlikely to alter the patterns observed when considering these two main sources only. There are a small number of museum specimen records uploaded to iNaturalist, some over a century old (e.g. www.inaturalist.org/observations/151937268). As these don't reflect citizen science data, we excluded records from before 2008 and 2002 for iNaturalist and eBird records respectively, as the years at which each platform was launched, although we expect that this may also remove a small number of genuine citizen science records from photos taken before this date, but subsequently uploaded to the platform.

Summarising threats

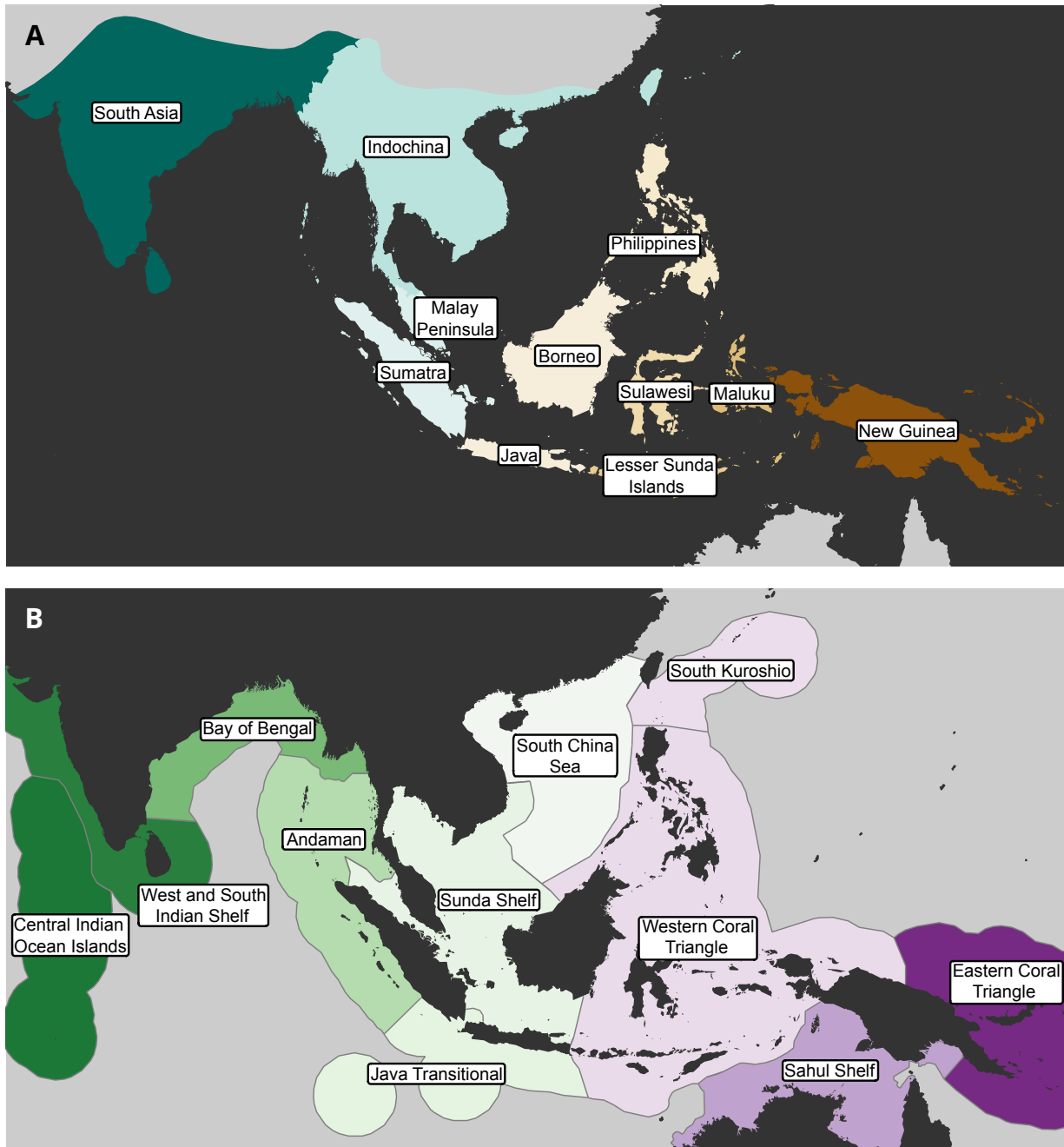
We investigated the proportion of species threatened with extinction according to the International Union for Conservation of Nature and Natural Resources (IUCN) Red List assessments (RL)⁵⁵⁶ for the same taxonomic groups as for

the diversity analyses. As the taxonomies used for the diversity analyses described above may not align with those of IUCN, where possible, we used distribution data as range maps provided from IUCN v2025-2⁵⁵⁶ and BirdLife International⁵⁵⁷ (amphibians, birds, bony fish, freshwater crabs, freshwater fish, mammals, reef corals, reptiles, sharks and rays). We followed the same methods as described above for diversity analyses for generating species lists for each subregion – we only considered extant, breeding portions of ranges and a species was assigned as present within a given subregion if the species range occupied at least 5% of that subregion and/or at least 25% of the species range occurs within that subregion. For other groups, distribution data came from the same checklists (bees, butterflies, caddisflies, centipedes, ferns, flies, flowering plants, gymnosperms, lycophytes, millipedes, mirid bugs, spiders, stick and leaf insects) and range maps from non-IUCN sources (ants) (see descriptions above for full details).

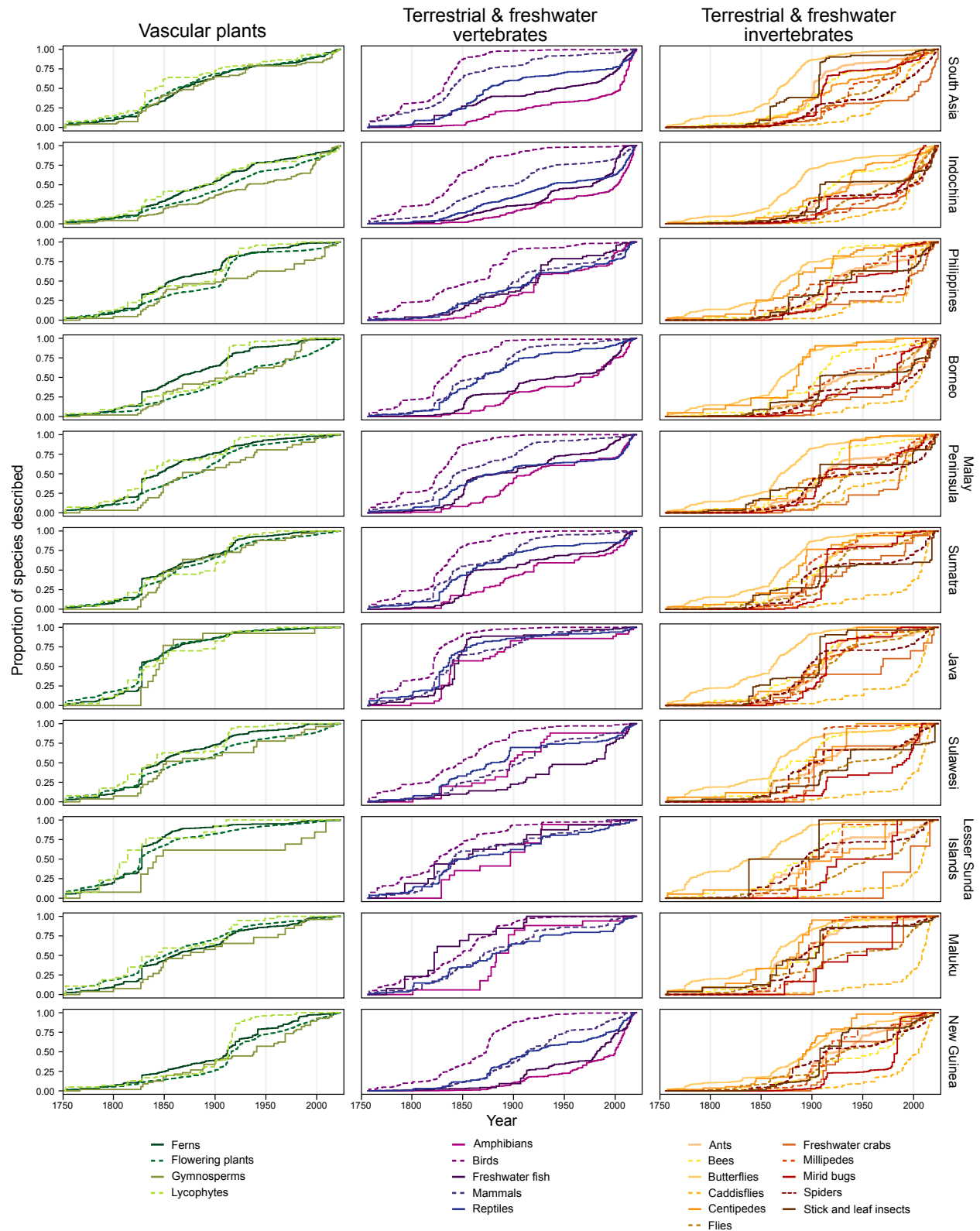
We retrieved assessments for all species through the IUCN Red List API v4 (<https://api.iucnredlist.org/>) using the iucnredlist package⁵⁴ (retrieved 02/06/2026–21/07/2026), filtering for the latest global assessments. Species in the distribution data sources without name matches to IUCN assessments were assumed to be non-assessed, although there may be cases where those species have been assessed but there are name differences between the two taxonomies. Species were assigned as Critically Endangered (CR), Endangered (EN), Vulnerable (VU), non-threatened (NT; both Near-Threatened (NT) and Least Concern (LC)), Data-Deficient (DD), or not evaluated (if no assessment could be found for that species). Some assessments used older Red List categories that are no longer in use ('LR/cd', 'LR/lc', 'LR/nt') and these were reassigned as non-threatened. Species in the distribution data assessed by IUCN as Extinct (EX) or Extinct in the Wild (EW) were removed.

We contrasted the temporal pattern of assessments with changes in human pressure from 2000-2024, measured as Human Footprint from Mu et al (2022)⁵⁵⁸, which summarises eight variables across equal-area 1 km × 1 km grid cells describing different aspects of human pressures: amount of built environment, population density, night-time light, proportion of croplands, proportion of pasture, distance to roads, distance to railways, and distance to navigable waterways. We calculated the median, 25th percentile, and 75th percentile Human Footprint across cells falling within each subregion for 2000–2024. Data for 2019–2024 was kindly provided directly from the authors.

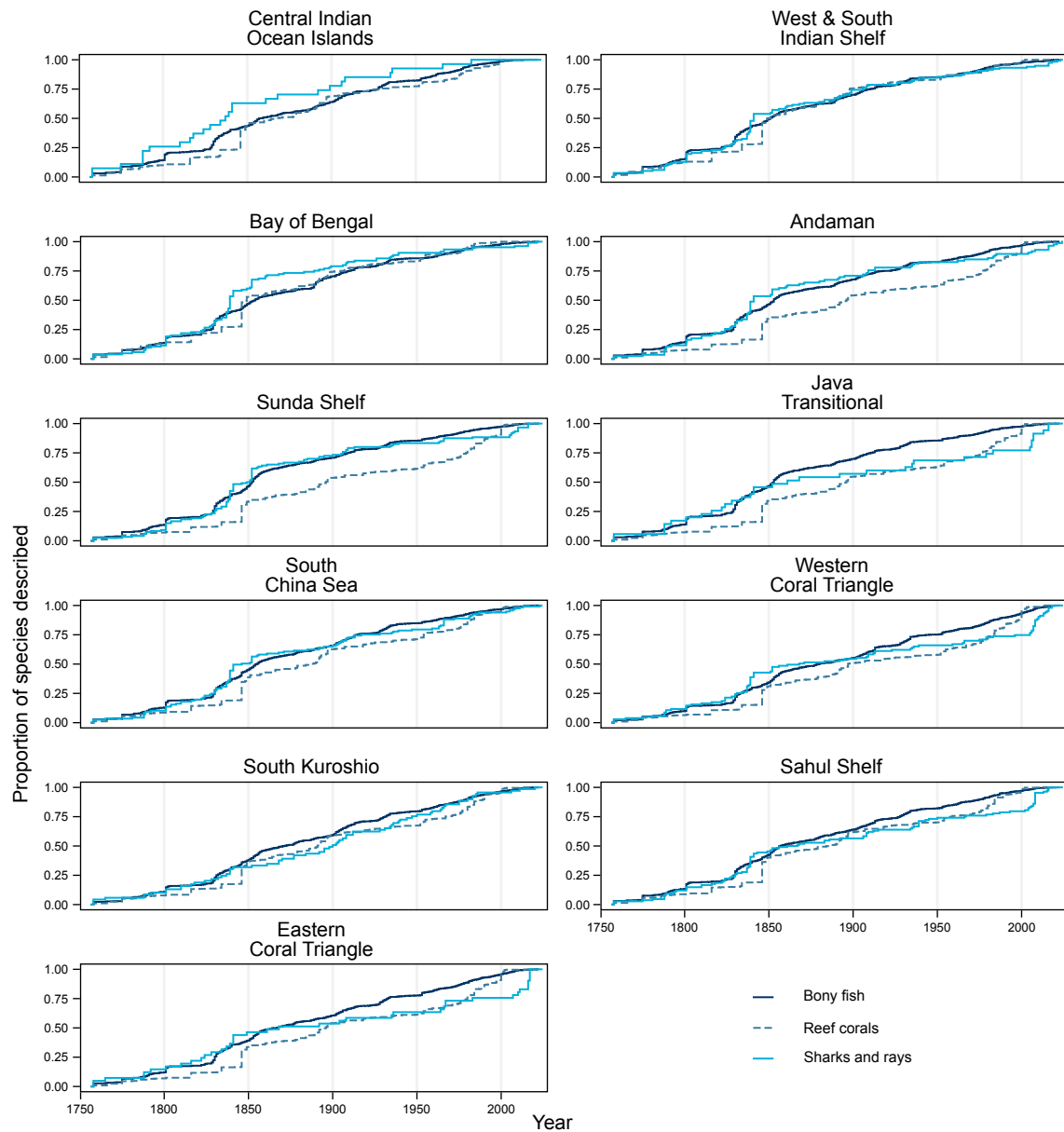
Supplementary Figures



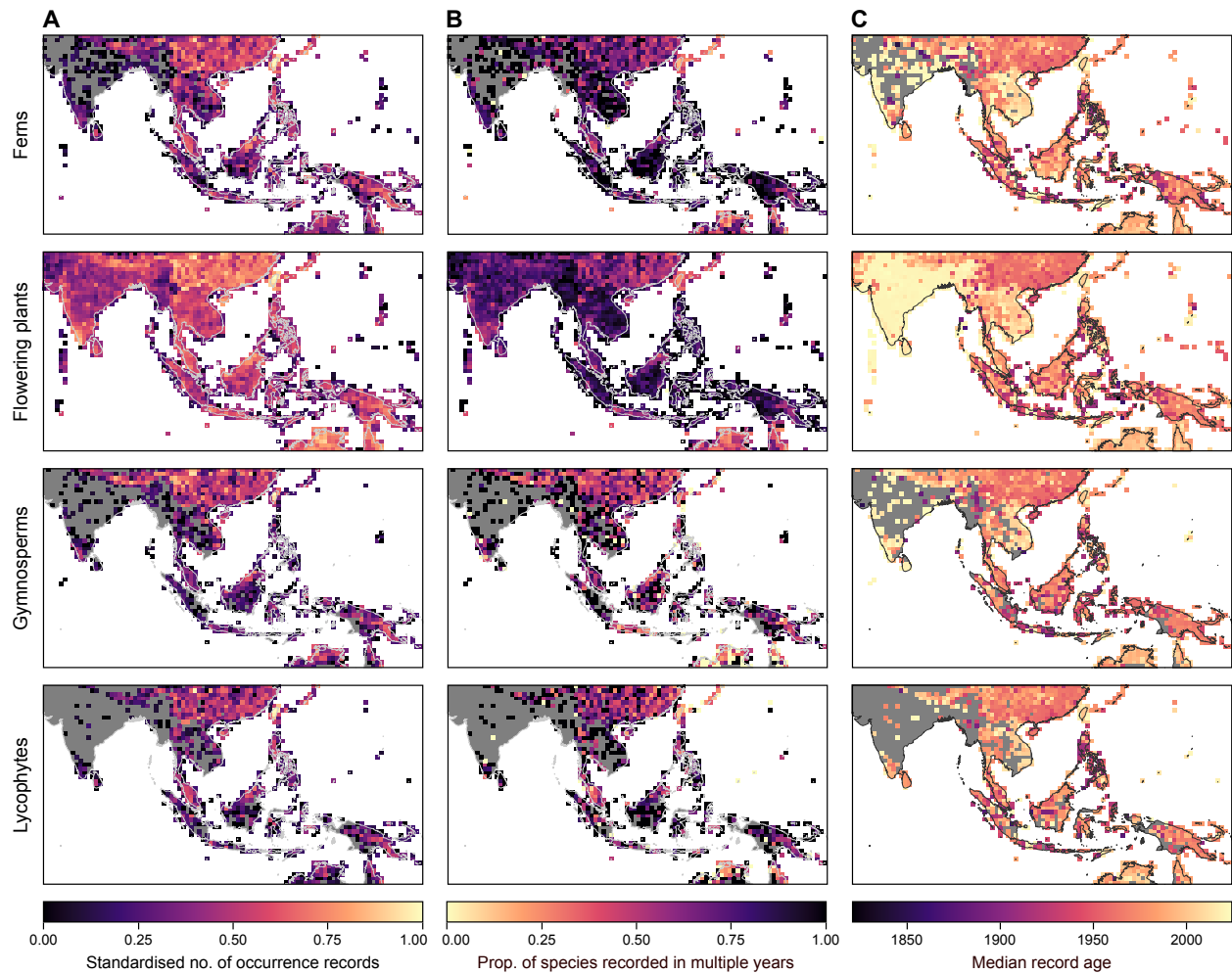
Supplementary Figure S1 | Subregions of tropical Asia defined in this study. (A) Terrestrial and freshwater subregions, roughly based on recognized areas of endemism^{559,560}. (B) Marine subregions, based on a bioregionalization analysis of marine diversity on coastal and shelf areas (Marine Ecoregions of the World)⁵⁶¹. Colours solely for clarity.



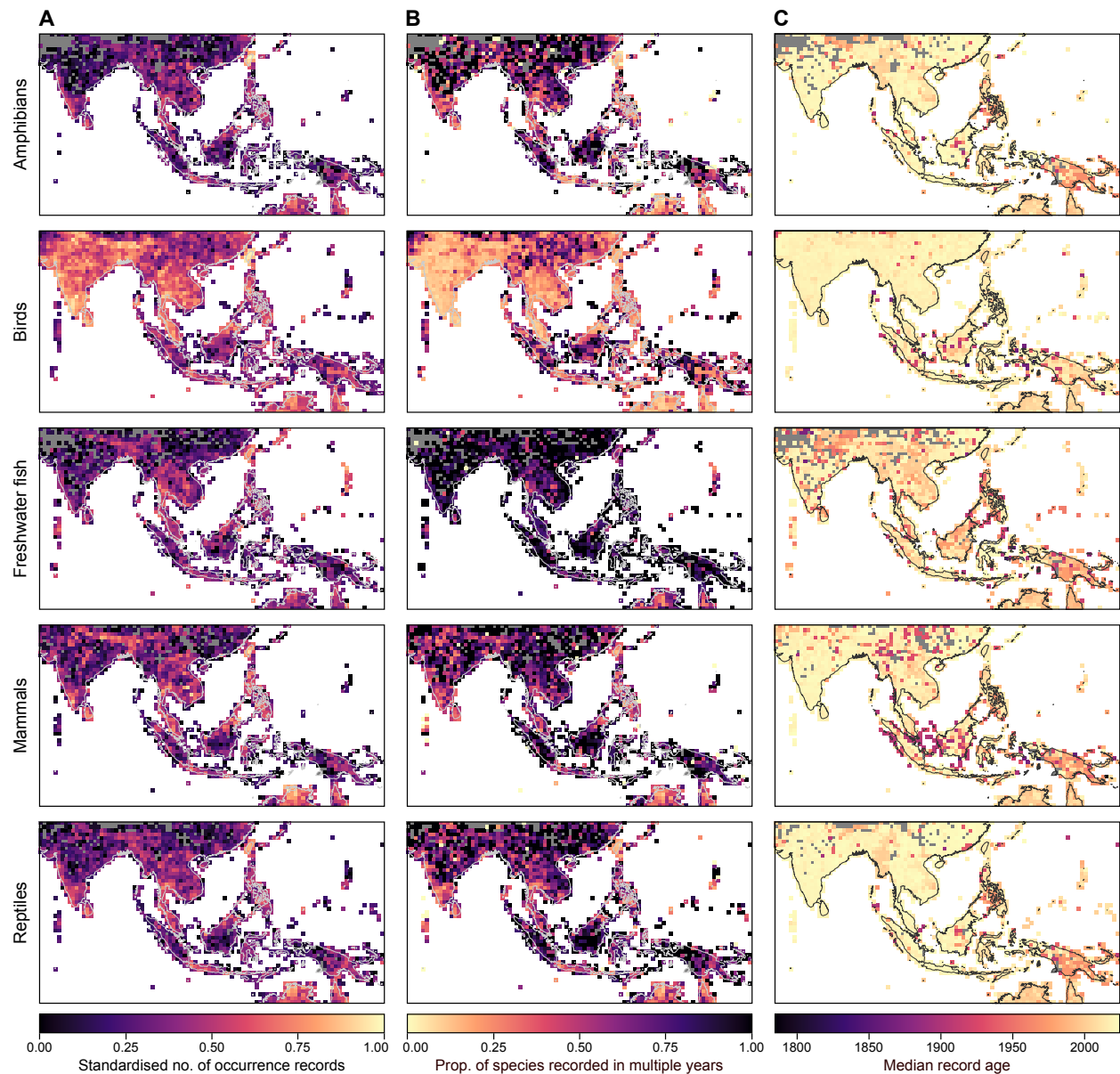
Supplementary Figure S2 | Species description accumulation curves for terrestrial and freshwater organisms for each subregion in tropical Asia. The year of description of a currently accepted species is defined as the publication year of its valid species epithet. After description, a species is assumed to be distributed in all subregions where it currently occurs. Values are scaled across organismal groups to their respective present-day species richness values.



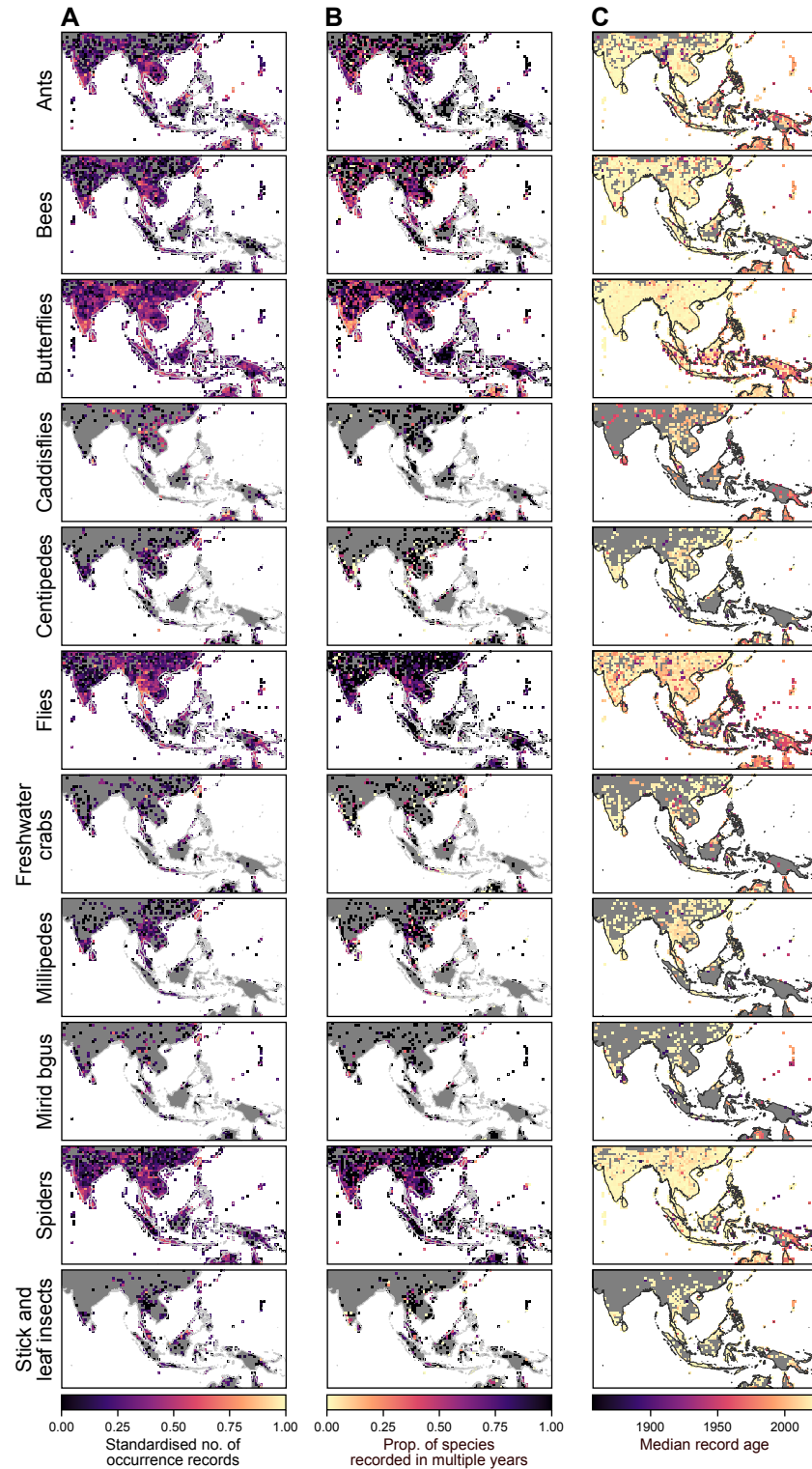
Supplementary Figure S3 | Species description accumulation curves for marine organisms for each subregion in tropical Asia. The year of description of a currently accepted species is defined as the publication year of its valid species epithet. After description, a species is assumed to be distributed in all subregions where it currently occurs. Values are scaled across organism groups to their respective present-day species richness values.



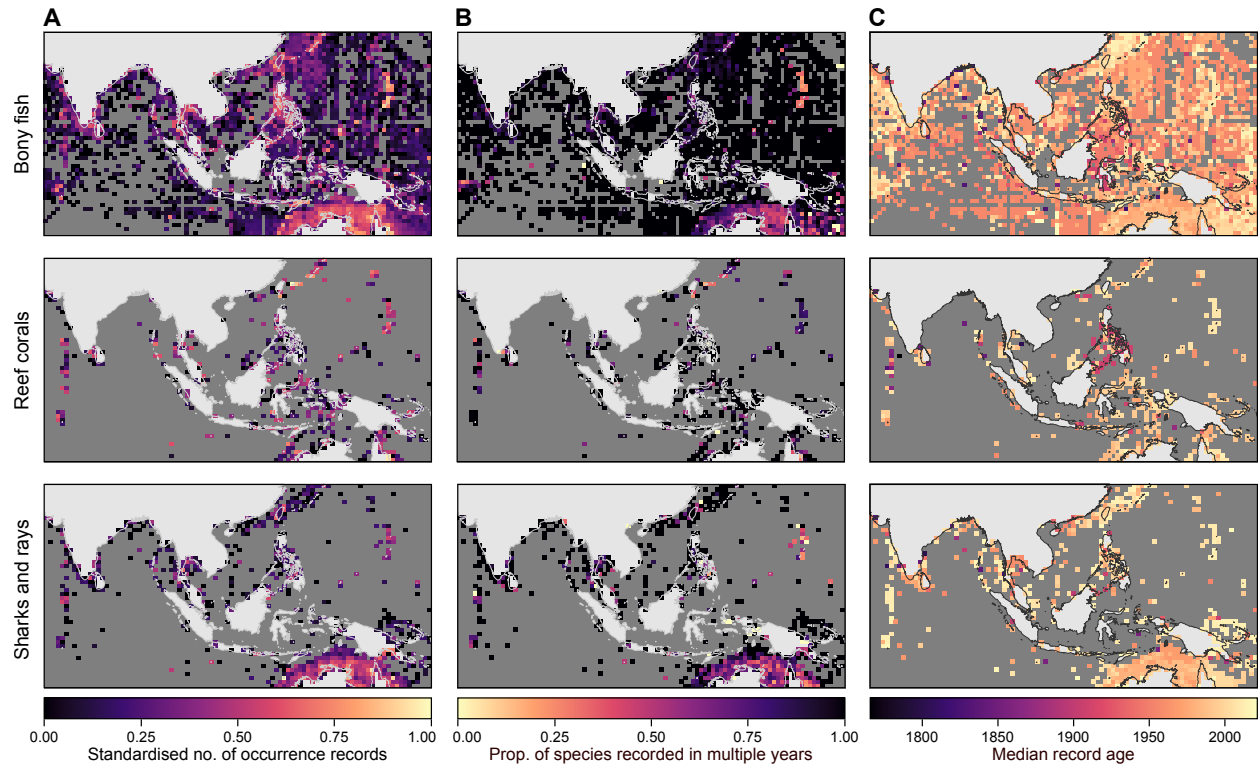
Supplementary Figure S4 | Spatiotemporal patterns in species occurrence data for vascular plant groups. Spatiotemporal coverage was calculated in 100×100 km grid cells for three facets of coverage: (A) Number of occurrence records standardized as the log number of records for all species in the group relative to the cell in that map with the most records (0 = cells with a single record; 1 = cell with the most records); (B) Proportion of species recorded in multiple years (0 = no species recorded in the cell were recorded in more than one year; 1 = all species recorded in the cell were recorded in multiple years); and (C) Median record age (median year for all unique species-year combinations). Dark grey cells have no occurrence records.



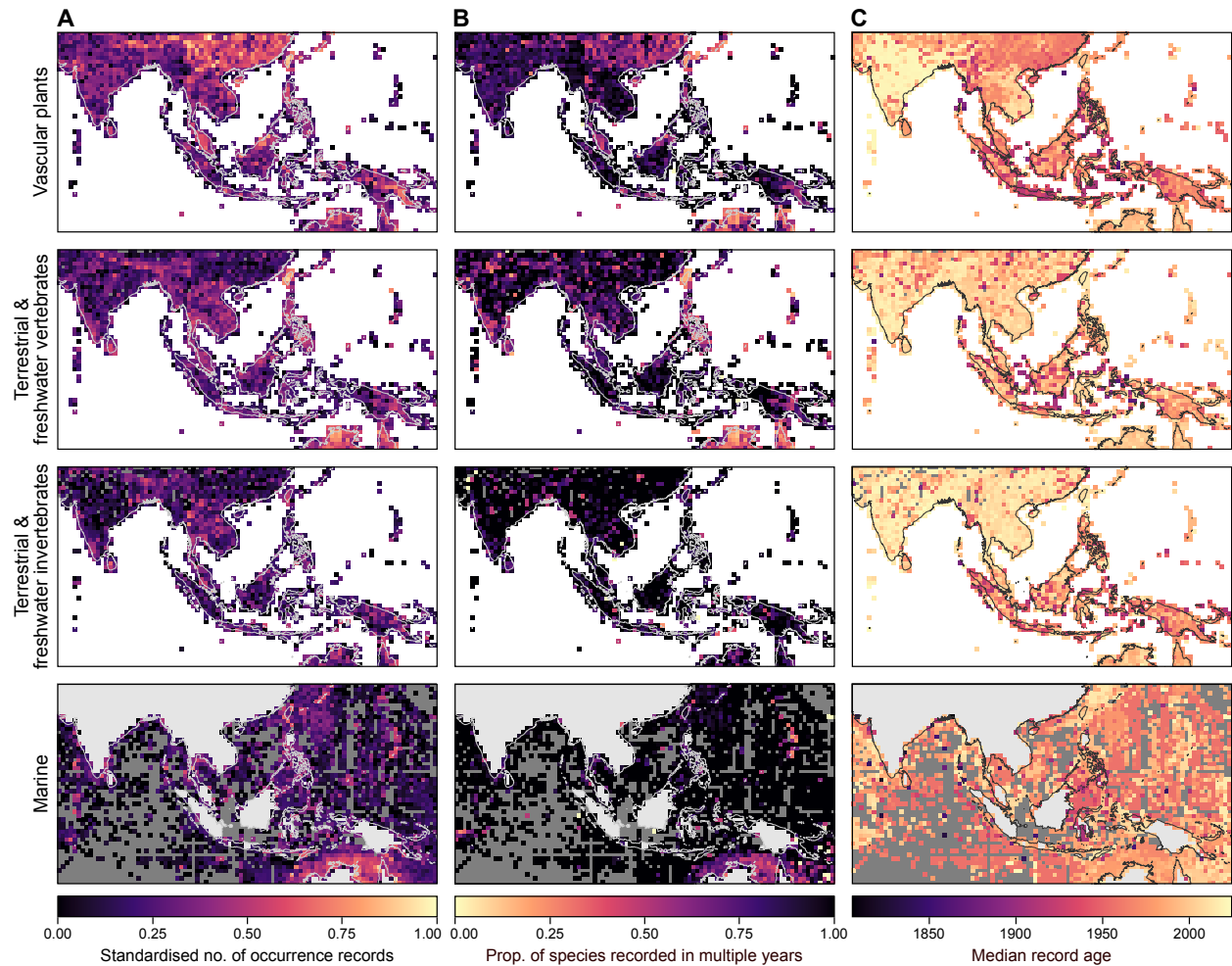
Supplementary Figure S5 | Spatiotemporal patterns in species occurrence data for terrestrial and freshwater vertebrate groups. Spatiotemporal coverage was calculated in 100×100 km grid cells for three facets of coverage: (A) Number of occurrence records standardized as the log number of records for all species in the group relative to the cell in that map with the most records (0 = cells with a single record; 1 = cell with the most records); (B) Proportion of species recorded in multiple years (0 = no species recorded in the cell were recorded in more than one year; 1 = all species recorded in the cell were recorded in multiple years); and (C) Median record age (median year for all unique species-year combinations). Dark grey cells have no occurrence records.



Supplementary Figure S6 | Spatiotemporal patterns in species occurrence data for terrestrial and freshwater invertebrate groups. Spatiotemporal coverage was calculated in 100×100 km grid cells for three facets of coverage: (A) Number of occurrence records standardized as the log number of records for all species in the group relative to the cell in that map with the most records (0 = cells with a single record; 1 = cell with the most records); (B) Proportion of species recorded in multiple years (0 = no species recorded in the cell were recorded in more than one year; 1 = all species recorded in the cell were recorded in multiple years); and (C) Median record age (median year for all unique species-year combinations). Dark grey cells have no occurrence records.



Supplementary Figure S7 | Spatiotemporal patterns in species occurrence data for marine groups. Spatiotemporal coverage was calculated in 100×100 km grid cells for three facets of coverage: (A) Number of occurrence records standardized as the log number of records for all species in the group relative to the cell in that map with the most records (0 = cells with a single record; 1 = cell with the most records); (B) Proportion of species recorded in multiple years (0 = no species recorded in the cell were recorded in more than one year; 1 = all species recorded in the cell were recorded in multiple years); and (C) Median record age (median year for all unique species-year combinations). Dark grey cells have no occurrence records.



Supplementary Figure S8 | Spatiotemporal patterns in species occurrence data excluding the citizen science platforms eBird and iNaturalist. Spatiotemporal coverage was calculated separately for each taxon in 100×100 km grid cells, and then standardised within each organismal group by taking the median values across taxa for each cell for three facets of coverage: (A) Number of occurrence records standardized as the log number of records for all species in the group relative to the cell in that map with the most records (0 = cells with a single record; 1 = cell with the most records); (B) Proportion of species recorded in multiple years (0 = no species recorded in the cell were recorded in more than one year; 1 = all species recorded in the cell were recorded in multiple years); and (C) Median record age (median year for all unique species-year combinations). Dark grey cells have no occurrence records.

Supplementary Tables

Supplementary Table S1 | Cleaning steps and parameterisation for removing dubious occurrence records and records outside of tropical Asia in GBIF and OBIS data.

Step	Filter	Description (GBIF/OBIS flags filtered, or column values)
1	Incomplete or missing coordinates	Remove records without both latitude and longitude coordinates. (Flag = COORDINATE_INVALID or COORDINATE_OUT_OF_RANGE)
2	Record type	Remove fossil records and captive individuals (zoos and botanic gardens). (basisOfRecord = FOSSIL_SPECIMEN, LIVING_SPECIMEN or LivingSpecimen)
3	Occurrence status	Remove records for non-presence of a species. (occurrenceStatus = ABSENT or 0)
4	Incomplete species name	Remove records with missing species name, or where name is not resolved to at least species-level. (Flag = TAXON_MATCH_NONE; taxonRank = KINGDOM, PHYLUM, CLASS, Class, ORDER, Order, FAMILY, Family, Subfamily, GENUS, Genus, or Subgenus)
5	Coordinates are 0, 0	Removes records where coordinates are exactly 0 longitude and 0 latitude. (Flag = ZERO_COORDINATE)
6	No date	Removes records with no entry for both eventDate and Year.
7	High coordinate uncertainty	Removes records where coordinate uncertainty is above 100 km.
8	Spatiotemporal duplicates	Removes records (retains first record) with exact same coordinates and date (day, month or year) for a given species. If no day and/or month are given, but year or month and year are identical then records are retained.
9	Points outside region	Remove records outside the bounding box of the BTAS grid region.
10	Points at country centroids	Remove records which are within 0.5 km of country centroids using coordinateCleaner v3.0.1 ⁴⁶ .
11	Points near institutions	Remove records which are within 0.5 km of research institutions using coordinateCleaner v3.0.1 ⁴⁶ .
12	Marine or terrestrial location	For terrestrial and freshwater groups, removes records that fall outside of land areas defined by GADM v4.1 ⁸⁴ , or vice-versa for marine groups.

Supplementary Table S2 | The number of cleaned occurrence records for each taxonomic group in GBIF and OBIS.

Taxonomic group	No. cleaned records	Perc. of all cleaned records for all studied taxa	Perc. records for taxon from citizen science sources*
<i>Vascular plants</i>			
Ferns	384,271	0.579 %	23.25 %
Flowering plants	5,791,341	8.723 %	17.21 %
Gymnosperms	55,968	0.084 %	10.76 %
Lycophytes	33,928	0.051 %	19.86 %
	$\Sigma = 6,265,508$	$\Sigma = 9.438 \%$	$\bar{x} = 17.77 \%$
<i>Terrestrial and freshwater vertebrates</i>			
Amphibians	328,648	0.495 %	25.67 %
Birds	57,238,482	86.209 %	89.60 %
Freshwater fish	276,955	0.417 %	19.82 %
Mammals	356,775	0.537 %	24.06 %
Reptiles	390,754	0.589 %	40.01 %
	$\Sigma = 58,591,614$	$\Sigma = 88.261 \%$	$\bar{x} = 39.83 \%$
<i>Terrestrial and freshwater invertebrates</i>			
Ants	49,016	0.074 %	56.78 %
Bees	36,413	0.055 %	69.47 %
Butterflies	656,279	0.988 %	71.32 %
Caddisflies	5,840	0.009 %	3.29 %
Centipedes	2,358	0.004 %	78.88 %
Flies	116,155	0.175 %	11.35 %
Freshwater crabs	3,434	0.005 %	67.27 %
Millipedes	6,044	0.009 %	87.52 %
Mirid bugs	1,682	0.003 %	70.87 %
Spiders	100,169	0.151 %	85.09 %
Stick and leaf insects	4,635	0.007 %	85.91 %
	$\Sigma = 982,025$	$\Sigma = 1.479 \%$	$\bar{x} = 62.52 \%$
<i>Marine</i>			
Bony fish	468,353	0.705 %	-
Reef corals	55,061	0.083 %	-
Sharks and rays	21,839	0.033 %	-
	$\Sigma = 545,253$	$\Sigma = 0.821 \%$	-

* Defined as all occurrence records from eBird and iNaturalist. GBIF records before 2002 and 2008 from eBird and iNaturalist, respectively, were not included as they predate the launch of respective platforms.

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