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BioTIME 2.0: Expanding and Improving a Database of Biodiversity Time Series

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ABSTRACT

Motivation: Here, we make available a second version of the BioTIME database, which compiles records of abundance estimates for species in sample events of ecological assemblages through time. The updated version expands version 1.0 of the database by doubling the number of studies and includes substantial additional curation to the taxonomic accuracy of the records, as well as the metadata. Moreover, we now provide an R package (BioTIMEr) to facilitate use of the database.

Main Types of Variables Included: The database is composed of one main data table containing the abundance records and 11 metadata tables. The data are organised in a hierarchy of scales where 11,989,233 records are nested in 1,603,067 sample events, from 553,253 sampling locations, which are nested in 708 studies. A study is defined as a sampling methodology applied to an assemblage for a minimum of 2 years.

Spatial Location and Grain: Sampling locations in BioTIME are distributed across the planet, including marine, terrestrial and freshwater realms. Spatial grain size and extent vary across studies depending on sampling methodology. We recommend gridding of sampling locations into areas of consistent size.

Time Period and Grain: The earliest time series in BioTIME start in 1874, and the most recent records are from 2023. Temporal grain and duration vary across studies. We recommend doing sample-level rarefaction to ensure consistent sampling effort through time before calculating any diversity metric.

Major Taxa and Level of Measurement: The database includes any eukaryotic taxa, with a combined total of 56,400 taxa.

Software Format: csv and. SQL.

1 | Background

The BioTIME database stores a curated collection of observations that can be used to estimate biodiversity metrics through time. Specifically, the database contains a collection of time series of observations of species abundances within biological assemblages that were sampled with consistent methods. With these data, it is possible to estimate temporal change in most metrics of taxonomic diversity (Magurran 2004), including, for example, species richness, evenness, and compositional change and population trends. We have assembled the database with the aim of facilitating synthesis studies and the re-use of these data by providing it in a standardised and curated format.

Since the publication of BioTIME version 1.0 (Dornelas et al. 2018), the database has been used for many different purposes. The first published analysis of the database revealed ubiquitous change in community composition, underpinned by roughly matched gains and losses of species through time (Dornelas et al. 2014). Other examples included the following: quantification of geographical variation in biodiversity change (Blowes et al. 2019; van Klink et al. 2020); estimation of the effects of temperature change (Antão et al. 2020), forest loss (Daskalova et al. 2020) and protected areas (Nowakowski et al. 2023) on biodiversity change; an estimation of the relationship between range shifts and population trends (Chaikin et al. 2024); and the quantification of change in organismal body size (Terry et al. 2021; Martins et al. 2023). Analysis of the BioTIME database also contributed one indicator to the first global assessment of biodiversity change produced by IPBES (2019).

In parallel with the proliferation of uses of BioTIME, the expansion and improvement of the database have continued. For BioTIME 2.0, additional dataset contributors were recruited, and updates were sourced for existing studies where data collection had continued. User feedback was also critical to flagging and resolving several inconsistencies not detected during the curation process of version 1.0. Moreover, metadata regarding methodology was updated and curation protocols were enhanced. In addition, the accuracy of taxonomic classification was checked and corrected where necessary. Finally, we developed a package in R (R Core Team 2023) to facilitate the usage of the database BioTIMEr (Sagouis 2024). We note that other databases have also been published with more focused criteria for inclusion (e.g., RivFishTIME focused on freshwater fish; Comte et al. 2020; InsectChange focused on insects; van Klink et al. 2021) or broader scopes (e.g., BioDeepTime which combines paleo and modern biodiversity time series; Smith et al. 2023). It is worth noting that there is only partial overlap between these databases and BioTIME because inclusion criteria differ across databases. For example, BioDeepTime includes

only BioTIME time series longer than 10 years and combines these with multiple fossil databases. In addition, many studies in InsectChange did not meet BioTIME criteria for taxonomic resolution and/or lack of information on sampling methodology, which needed to be sourced independently. In summary, overlap among databases is nuanced, and care should be taken if combining BioTIME with other databases to avoid duplicate datasets.

Here, we release the updated version of BioTIME version 2.0. Given the twofold increase of studies in the database, the membership of the BioTIME consortium is also appropriately updated, as one of the goals of the database is to give credit to the data collectors.

2 | Database Description

Similar to version 1.0, version 2.0 of the BioTIME database is a relational database composed of one main data table and 11 metadata tables. The data contained in the main table have a hierarchical structure (Figure 1): at which the finest scale is a record showing the observed abundance of a species; records are nested into sampling events, that is, a discrete moment in time and space when an assemblage is observed; a site is a location in space where one or more samples occur; multiple sampling events taken over time at the same site make up a time series; and time series are grouped into studies, which are defined by the sampling methodology, for example a specific type of transect with set length and width, or the trawl of a net of specified mesh size over a certain distance or length of time. Depending on the spatial study extent and the user definition of the grain size required for site, a study can have only one or multiple time series (see below in usage notes about the gridding process to define site).

Metadata are stored in tables for: taxonomy (one table with taxonomy as provided and one table with standardised taxonomy), abundance type, biomass type, sample, study, methods, citation, contacts and curation. Only minor updates were done to the structure of the database relative to version 1.0, to accommodate additional taxonomic information (see below under Data curation and quality control and File S1 for a database schema which includes a description of the tables' fields).

3 | Data Acquisition and Curation

New dataset acquisition for BioTIME 2.0 followed multiple approaches: active recruitment of data contributors in seminars, conferences and social media, searches for papers and within databases (e.g., OBIS [2024], GBIF [2024]), contributor volunteering, and through the collaboration networks of current data contributors. Once a candidate study was identified, it underwent checks against inclusion criteria and a curation process. For inclusion in BioTIME, studies must meet four criteria: (1) sampling methods are constant over time; (2) sampled for a minimum of two years, not necessarily consecutive; (3) samples take place at the assemblage scale rather than population; and (4) taxonomic resolution is mostly at the species level. We define a study as a single set of sampling or surveying methodology. If there are changes in methodology over time, candidate studies are split into multiple studies to reflect these changes, and split studies must independently fulfil BioTIME study criteria.

Once a candidate study was identified, available metadata and methodology information were used to build the metadata records (see protocol in File S2). Metadata records consist of information relating to temporal, spatial and taxonomic scope, habitat, methodology, protected area status, data originators and data sources. Where manipulation treatments were applied to some of the data, these were assessed as to whether the treatments were purely experimental manipulations (e.g., the artificial warming of a section), in which case only control samples were retained. If treatments were part of normal phenomena for the ecosystem (e.g., grazing), all samples were retained. Differences in ecological management practices were also recorded in the site metadata table to account for any differences in human activity/interactions.

Prior to inclusion in the database, data were standardised in our curation process. Quality control checks included checking for appropriate data types (e.g., numeric for abundance, string for species), realistic maximum and minimum values for fields, such

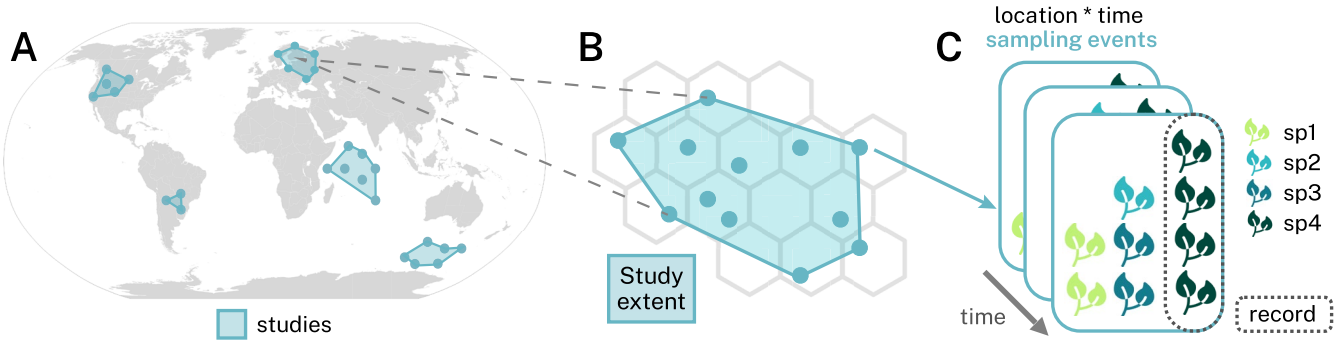

FIGURE 1 | Hierarchical structure of the BioTIME database. (A) Studies are defined by a sampling methodology which is constant over time, and have a minimum of one site and two sampling events in different years, with at least one sampling location each. (B) Study spatial extent was determined by the convex hull of the coordinates of all samples in the study. To facilitate comparisons across studies, we recommend standardising extent of the time series by gridding the data into constant area polygons. (C) Records are nested within sampling events, which are nested within locations. A sampling event is a time when sampling took place. The number of samples may change through time, and we recommend sampling effort standardisation, in addition to spatial scale standardisation prior to analysis.

as date and coordinates, removal of non-organismal records and correction of taxonomic misspellings, as per the taxonomic standardisation procedure described below. To store data in long format, records of null, blank or zeroes for abundances were removed; however, given the criterion that all species in the sample are recorded, absences can be interpreted as a species not being detected, and these can be reconstructed for each species in each time series.

Data standardisation also involved the construction of sampling event identifiers ('SAMPLE_DESC' in the raw data table). These are concatenated strings based on the provided study methods and data fields to accurately represent survey designs across space and time, such as sampling frequency and grouped observations (e.g., year_month_site_quadrat). The construction of these identifiers is reported in the metadata Sample table ('SAMPLE_DESC_NAME'). The wide variety of sampling methods across the studies included in BioTIME is reflected in this field, with combinations of latitude, longitude, depth/elevation, date, transect, quadrat or trawl ID being common identifiers used. For some methods, for example, research cruise trawls, pitfall traps or camera traps, sampling was somewhat continuous. To represent the assemblage-level observations for these types of methods, samples were defined as constant time intervals (e.g., 1 week or 3 days depending on the nature of the data, but consistent within the time series). In the previous version of the database, we included a field to reflect whether observations took place in exactly the same location through time (e.g., in permanent plots), which has been deleted in this version of the database because of the difficulty in applying the concept consistently across taxa and methods (e.g., sessile vs. mobile taxa and destructive vs. observational data). Observation records are aggregated so that each sampling event contains only one abundance and/or biomass record per taxon, without any distinctions between life stage or sex, to ensure consistency across all datasets, and given that this was the resolution provided by the overwhelming majority of the studies. For studies added in BioTIME 2.0 where abundances and biomass are recorded at the individual level, records are not aggregated (i.e., abundance must be calculated by adding records of each species, and individual level sizes are kept within the database).

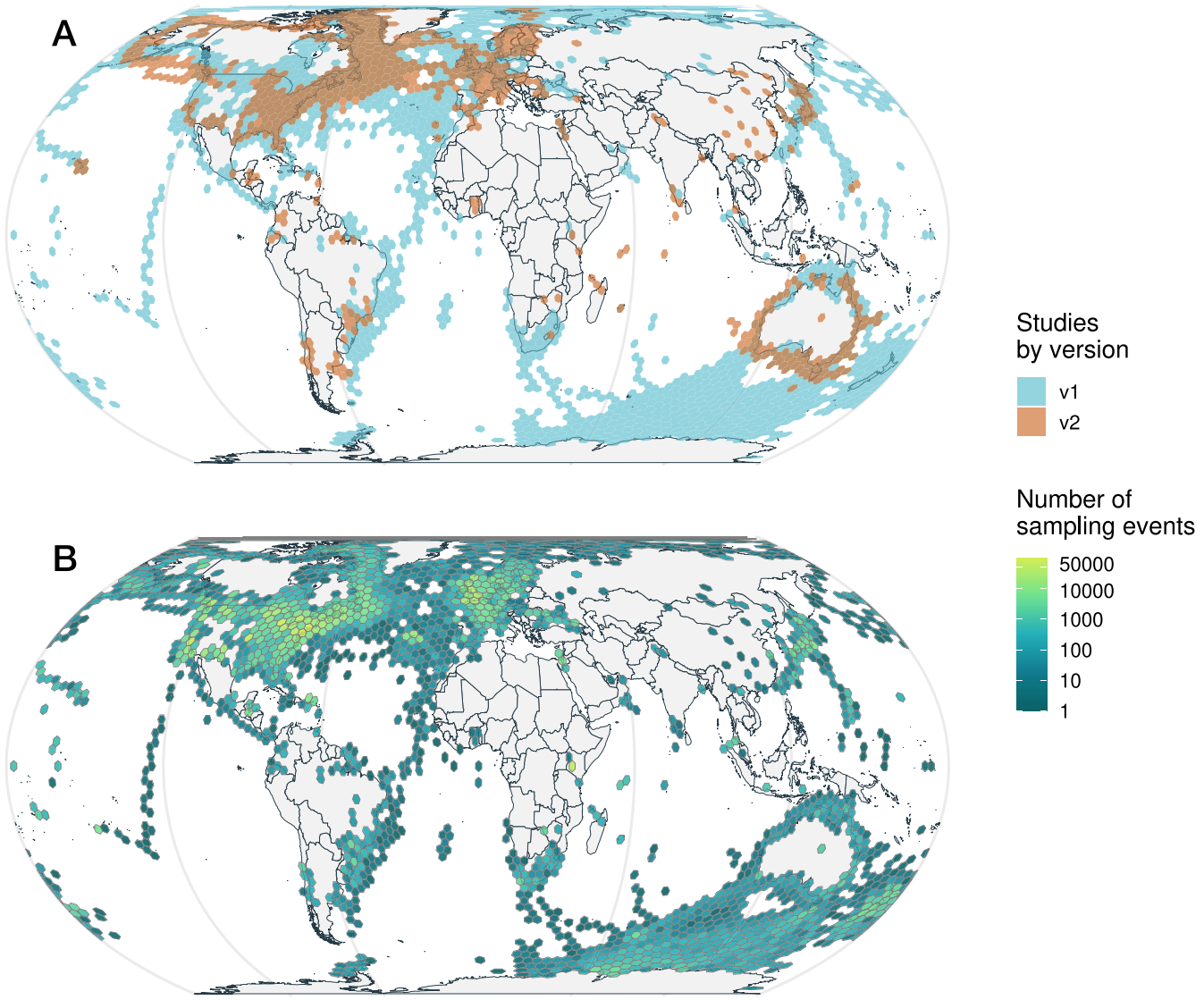

FIGURE 2 | Map showing BioTIME sampling locations. Each grid cell is approximately 75,000 km^2. Panel A shows the geographic distribution of studies added to BioTIME version 2.0. Panel B shows the spatial density of sampling events in version 2.0 of the database.

For version 2.0 of the database, records underwent a more rigorous standardisation of taxonomic classification. Specifically, all taxonomic records in the entire database were validated with either the *taxize* (Chamberlain and Szöcs 2013) or the *worrms* R packages (Chamberlain and Vanhoorne 2024). When using the *taxize* package, we used the classification() function and chose the Global Biodiversity Information Facility (GBIF) database as the first option to update the taxonomy, with the Integrated Taxonomic Information System (ITIS) as a second option should no matches be found. To ensure better representation of known marine species, we used the wm_records_names() function from the *worrms* package. We checked first for matches at the species level, then genus and, finally, family. If no valid names were found, we performed manual checks to the lowest resolution possible. Where species were identified as common names, we first ran them through the comm2Sci() function in *taxize*, before completing the checks as described above. BioTIME 2.0 contains two species tables: one which contains species as provided in the original data, and one with the standardised taxonomic classification, including species, genus, family, order, class, phylum and kingdom. Including the two tables ensures standardisation can be reproduced as taxonomy is updated. Nevertheless, it is worth noting that while lumping species that are synonymised is possible, splitting species beyond the data originally recorded is not.

BioTIME is designed to facilitate biodiversity analyses at the assemblage level, and hence any unidentified taxonomic records were kept to the lowest taxonomic resolution reported in the raw data. Records of unidentified taxa that were distinguished by the data collectors were kept separate (e.g., unknown beetle sp1, unknown beetle sp2) and are consistent within studies; therefore, these records can be used to estimate diversity metrics within the study, but cannot contribute to population assessments across studies (i.e., there is no way to determine whether populations of the same species appear in other studies). The standardised version of the database has 97% of the taxa identified to at least family and 74% to species level.

For spatial information, latitudes and longitudes of each study were mapped to check they matched location descriptions. Spatial extent was estimated as the area of the convex hull encompassing all the spatial coordinates (Figure 1) and grain size from the reported methods for each study. Changes made during the curation process were recorded in the curation table and confirmed with the data providers. For all studies revised or added to this database version, code used in data curation is available from the BioTIME Github repository (https://github.com/bioTIMEHub/BioTIME). The curated version of the data was shared with the data providers who agreed to the changes made.

In this version, 16 studies previously included in BioTIME v1.0 were removed, as additional information revealed they did not meet some of the criteria for inclusion in the database (File S4). Additionally, 49 studies included in BioTIME v1.0 were

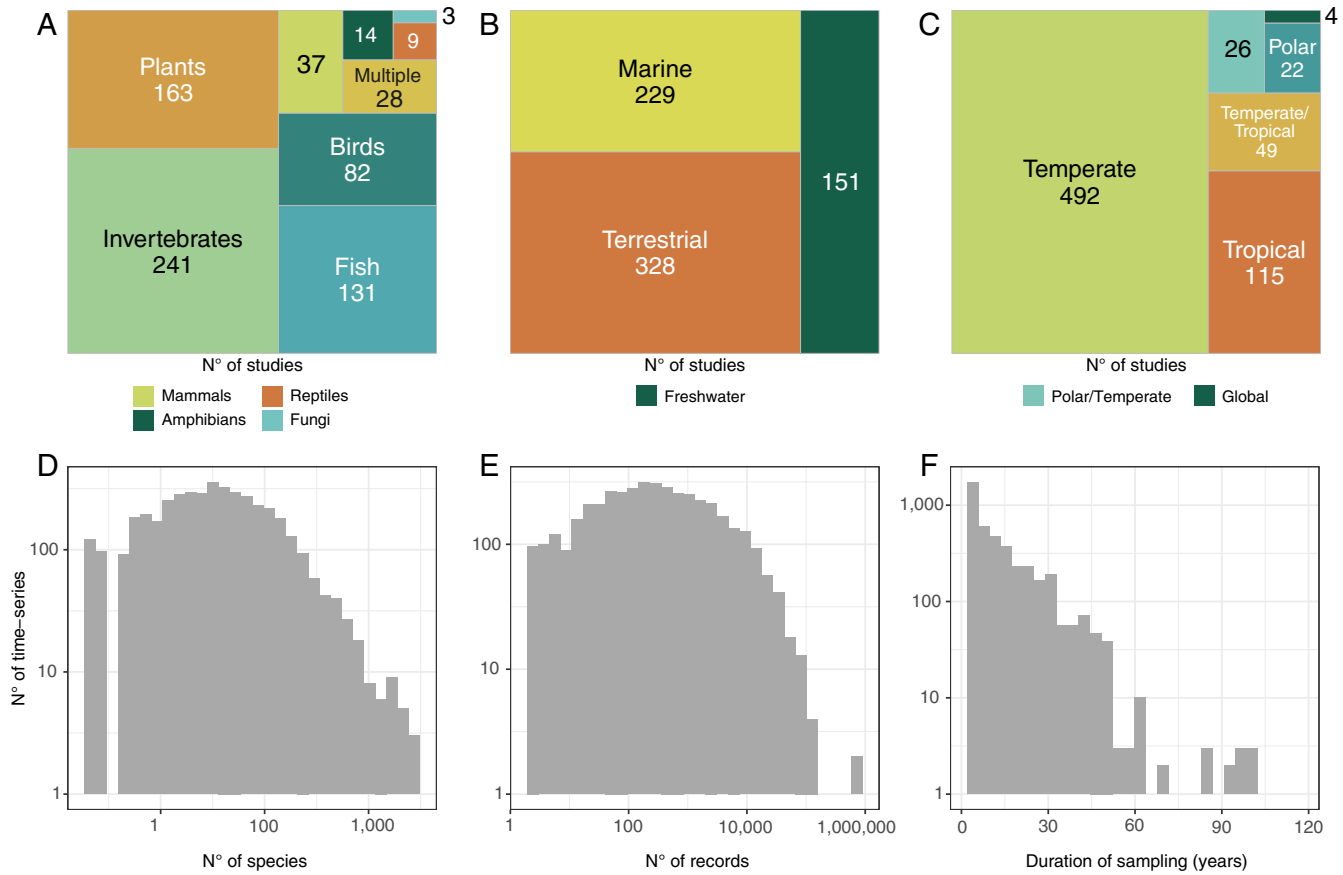

FIGURE 3 | Plots illustrating the proportion of studies that fall into the different classifications of: (A) Taxa, (B) Realm and (C) Climate. (D) species richness, (E) total number of records and (E) duration of sampling across time series. Note that time series were defined using the BioTIMEr package, where functions are now available to help users identify, separate and standardise BioTIME data based on location (latitude/longitude); here, we implemented a grain of 75,000 km^2.

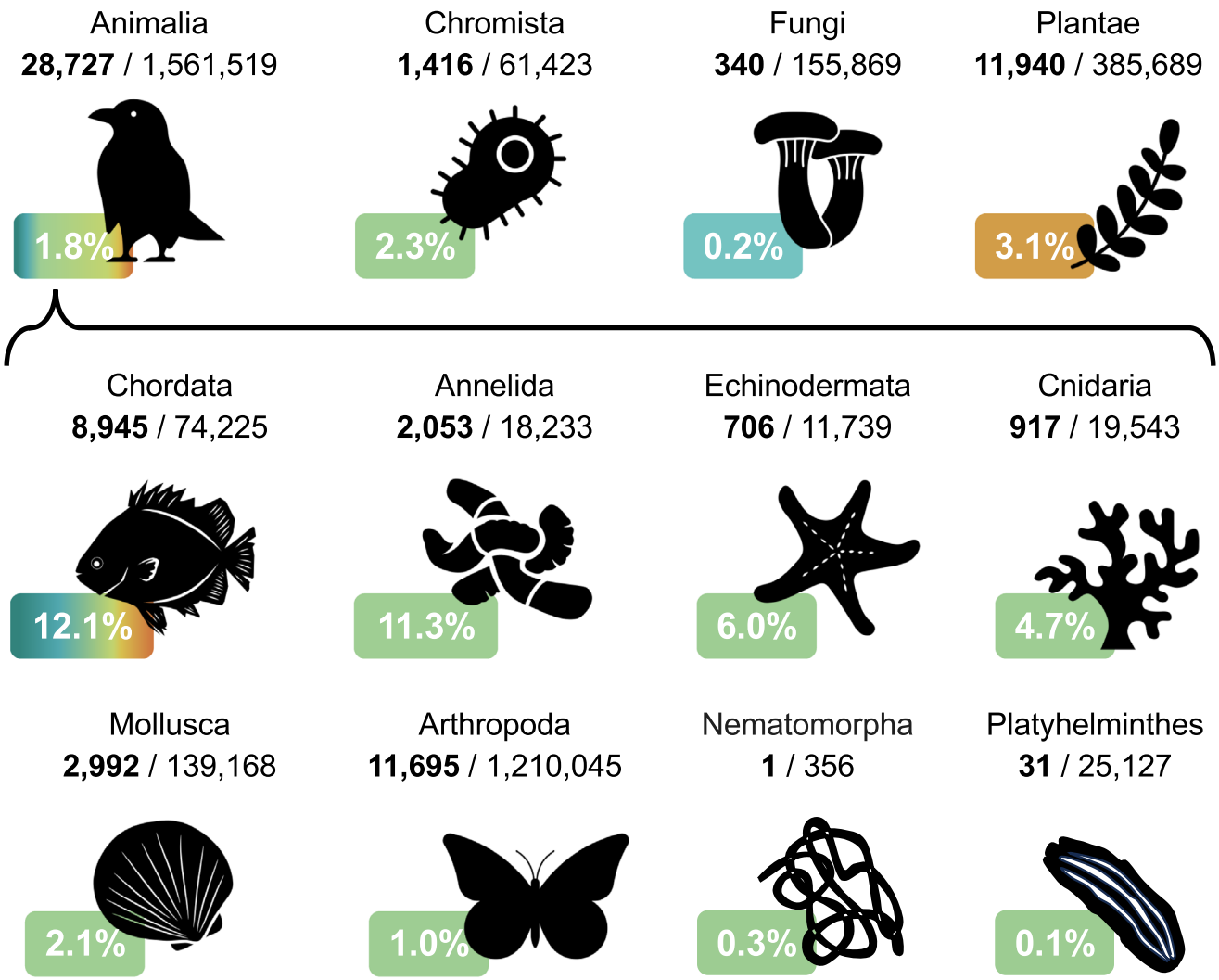

FIGURE 4 | Proportional representation of different taxonomic units in BioTIME 2.0. For each taxon, we provide the number of species included in the database relative to the number of species known to science according to the Catalogue of Life (Bánki et al. 2024) accessed on 17 December 2024. Note how coverage is much higher in some groups (e.g., sharks 37.2%) than others (e.g., insects 0.92%).

recurated as more metadata or new data became available—all these changes are reported in File S4.

The contact table includes publicly available contact information for data contributors (name and/or email) to allow users to reach out to the original contributors with any queries regarding data usage. These data were processed in compliance with both UK and EU General Data Protection Regulations (GDPR). A data protection statement explaining the lawful basis for the use and processing of these data is now available on the database website: https://biotime.st-andrews.ac.uk/usageGuidelines.php.

4 | Description of Data

BioTIME 2.0 includes 708 studies distributed across 553,253 locations, with almost twice as many studies and 11.3% more locations relative to the previous version (Figure 2). The database now includes 11,989,233 records from 56,400 taxa (36.7% and 26.7% increase from version 1.0, respectively) from across the tree of life, collected over 1,603,067 sampling events across the marine, freshwater and terrestrial realms (Figure 3). Temporally, the database spans 1874 to 2023, with median time series length being 7 years. With a grid resolution of 75,000 km^2, the database currently includes 4,301 time series in total, of which, 2390 have durations longer than 5 years, 1,745 longer than 10, 893 longer than 20, and 37 longer than 50 years (Figure 3). Despite efforts to improve representation, both spatial and taxonomic biases persist (Figures 2 and 4, File S5). Spatial biases persist in the database and are especially evident in the terrestrial realm, despite targeted searches having improved spatial representation. The marine realm has better representation, both spatial (in terms of latitudes and longitudes) and regarding global change space (Daskalova et al. 2020). However, as inherently more three-dimensional and given the features of sampling in marine habitats, it is likely that a smaller proportion of the marine realm is represented in our database compared with the terrestrial realm.

5 | Usage Notes

This version of the database is made publicly available in a SQL version and as a .csv query through Zenodo (10.5281/zenodo.10932823) and BioTIME's website (https://biotime.st-andrews.ac.uk) under a CC-BY licence (https://creativecommons.org/). The data are, hence, free to use with attribution via citation of this paper. In addition, each study has a licence associated with a spectrum of governmental, Creative Commons and Data Commons licences. The database is also GDPR compliant. Citations for data sources of individual studies are provided in the metadata table citation and are also listed in File S3.

To facilitate comparisons across studies, we recommend standardising the spatial extent of the time series by gridding the data into constant area polygons prior to analysis. In addition, as the number of samples may change through time, we recommend sampling effort standardisation. To facilitate the use of the database, the release of BioTIME 2.0 is accompanied by an R package, BioTIMEr (Sagouis 2024). The package provides functions to deal with these spatial and temporal issues—namely to spatially grid the studies into constant extent cells and subsample time-series so that sampling effort (specifically number of samples) is constant through time. In addition, the package includes functions to calculate several metrics of alpha diversity and compositional change over time. A vignette is supplied to illustrate the use of each function.

The extended efforts in data standardisation aimed to facilitate integration with other databases. For example, the taxonomic standardisation should streamline integration with trait or phylogenetic data, and for this purpose, the standardised species name is preferable. In contrast, to reflect the species names as recognised by the observers at the time of observation, or to update as taxonomy changes, the original species names are preferable.

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Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

A static stable release of BioTIME version 2.0 can be found in Zenodo (https://doi.org/10.5281/zenodo.10932823). Code used in data curation and standardisation can be found at github.com/bioTIMEHub/BioTIME. The R package BioTIMEr is available in CRAN and can be found at github.com/bioTIMEHub/BioTIMEr.

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Supporting Information

Additional supporting information can be found online in the Supporting Information section.