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DATA PAPER

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BioTIME: A database of biodiversity time series for the Anthropocene

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Abstract

Motivation: The BioTIME database contains raw data on species identities and abundances in ecological assemblages through time. These data enable users to calculate temporal trends in biodiversity within and amongst assemblages using a broad range of metrics. BioTIME is being developed as a community-led open-source database of biodiversity time series. Our goal is to accelerate and facilitate quantitative analysis of temporal patterns of biodiversity in the Anthropocene.

Main types of variables included: The database contains 8,777,413 species abundance records, from assemblages consistently sampled for a minimum of 2 years, which need not necessarily be consecutive. In addition, the database contains metadata relating to sampling methodology and contextual information about each record.

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Spatial location and grain: BioTIME is a global database of 547,161 unique sampling locations spanning the marine, freshwater and terrestrial realms. Grain size varies across datasets from 0.0000000158 km^2 (158 cm^2) to 100 km^2 (1,000,000,000,000 cm^2).

Time period and grain: BioTIME records span from 1874 to 2016. The minimal temporal grain across all datasets in BioTIME is a year.

Major taxa and level of measurement: BioTIME includes data from 44,440 species across the plant and animal kingdoms, ranging from plants, plankton and terrestrial invertebrates to small and large vertebrates.

Software format: .csv and .SQL.

KEYWORDS

biodiversity, global, spatial, species richness, temporal, turnover

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1 | BACKGROUND

Quantifying changes in biodiversity in the Anthropocene is a key challenge of our time given the paucity of temporal and spatial data for most taxa on Earth. The nature and extent of the reorganization of natural assemblages are currently controversial because conflicting estimates of biodiversity change have been obtained using different methodological approaches and for different regions, time periods and taxa. Some reports suggest alarming and systematic biodiversity loss. For example, estimates of global extinction rates place global losses orders of magnitude above background rates (Pereira, Navarro, & Martins, 2012). In addition, estimates of population trends for vertebrates suggest average declines of the order of 60% in the past 30 years (Collen et al., 2009). Nonetheless, analyses based on spatial variation yield more modest declines in the range of 8% (Newbold et al., 2015). In contrast, some analyses of assemblage time series consistently detect no systematic trend in temporal α-diversity (such as species richness), on average, across local communities (Brown, Ernest, Parody, & Haskell, 2001; Dornelas et al., 2014; Vellend et al., 2013, 2016), but instead uncover substantial variation in composition (temporal β-diversity; i.e., temporal turnover), including both losses and gains of species (Dornelas et al., 2014; Magurran, Dornelas, Moyes, Gotelli, & McGill, 2015). Spatially structured gains and losses are also predicted from climate change projections (García Molinos et al., 2016). Some of these discrepancies are a result of differences in the temporal and spatial scales at which analyses were performed (McGill, Dornelas, Gotelli, & Magurran, 2014), whereas other differences may be attributable to the organizational level on which an analysis is focused (e.g., population vs. community). Clearly, more research is needed into how populations, communities and ecosystems are changing in the face of widespread human influence on the planet (Waters et al., 2016). Here, we introduce BioTIME, a curated database of biodiversity time series, with the goal of facilitating and promoting research in this area.

Biodiversity is a multifaceted concept, which can be measured in many different ways. Similar to the approach of essential biodiversity variables (Pereira et al., 2013), we focus on assembling data that maximize the number of metrics that can be calculated. Specifically, BioTIME is composed of species abundance records for assemblages that have been sampled through time with a consistent methodology. The focus on assemblages differentiates BioTIME from population databases, such as the Global Population Dynamics Database (https://www.imperial.ac.uk/cpb/gpdd2/secure/login.aspx) and the Living Planet Index database (http://www.livingplanetindex.org/home/index), and enables users to quantify patterns at different organizational levels, including both the assemblage and the population level. BioTIME complements the PREDICTS database (http://www.predicts.org.uk/) in providing time series rather than space for time comparisons. Moreover, most previous databases have been either terrestrial (e.g., vertebrates, GPDD; vegetation, sPlot; multiple taxa, PREDICTS) or marine (e.g., OBIS), whereas BioTIME includes marine, freshwater and terrestrial realms; hence, it facilitates comparisons across realms. Finally, previous databases are not specifically focused on temporal assemblage data, which means that BioTIME fills an important gap in allowing spatial and temporal comparisons. In addition, coupling BioTIME with additional information will allow analyses of temporal change in phylogenetic diversity and trait diversity alongside taxonomic diversity.

The goals of the BioTIME database are as follows: (a) to assemble and format raw species abundance data for assemblages consistently sampled through time; (b) to encourage re-use of these data through open-source access of standardized and curated versions of the data; and (c) to promote appropriate crediting of data sources. These goals are in line with best practice in promoting maximal use of ecological data (Costello et al., 2014; White et al., 2013) and highlight data gaps to funding agencies. In addition, we hope that BioTIME will engage ecologists in the collection, standardization, sharing and quality control of assemblage-level species abundance data, particularly in poorly sampled parts of the world, and highlight the value of such data to funding agencies.

2 | METHODS

The BioTIME database is composed of 11 tables: a main table containing the core observations (records), and 10 tables that provide contextual information as described below and in Supporting Information Figure S1. There are five main levels of organization: record, sample, plot, site and study. A record is our fundamental unit of observation of the abundance of a species in a sample. A sample includes all the records that belong to the same sampling event; for example, a quadrat on the seashore, a single plankton tow or a bird transect. A sample is defined by a single location and a single date. If the exact location has been repeatedly sampled through time, then all the samples that correspond to that location belong to the same plot. Multiple samples and plots can be located in the same area, which we term a site. Finally, the highest observational unit is a study, which is defined by having a regular and consistent sampling methodology. Sources of data in which the sampling methodology changed during the course of the study were classified as separate studies. Every organizational level has contextual variables that are kept either in dedicated tables or are part of the main table (see Supporting Information Figure S1 for a complete list of the fields in each table). In addition, the database also includes tables with information relating to the sampling methodology, and treatments associated with some samples when applicable, citation information, contacts and licenses for each study, and the curation steps performed on each study before it was entered in the database.

2.1 | Data acquisition

Searches began in 2010, and data were acquired from a variety of sources: literature searches, large databases [specifically, OBIS (www.iobis.org/), GBIF (www.gbif.org/) and Ecological Data Wiki (https://ecologicaldata.org/)], through personal networking and through broadcasted data requests at conferences and on social media. We have used four main criteria for data inclusion on BioTIME: (a) abundance observations come from samples of assemblages where all individuals within the sample were counted and identified (i.e., assemblage rather than population data); (b) most of the individuals were identified to species; (c) sampling methods were constant through time; and (d) the time series spans a minimum of 2 years. The last condition was changed relative to the initial criteria because it became apparent that it would allow better spatial representation given the many locations that have been surveyed historically and then resurveyed. Each study is kept separate within the database and has a specific license from the CC spectrum, whose terms must be observed (https://creativecommons.org/). A static version of the database is released with this publication (http://biotime.st-andrews.ac.uk and https://zenodo.org/record/1095627). However, data entry and curation is ongoing (http://biotime.st-andrews.ac.uk/contribute.php), and we expect the database to keep growing in the foreseeable future. We plan to release static updates of the database periodically.

2.2 | Data curation and quality control

Before inclusion in the database, data were subjected to standardization in a curation process described specifically for each study in the curation table of the database. Specifically, these were checked for the presence of the following: duplicates within each study and against the entire database; species with zero abundance; and non-organismal records, all of which were removed. Abundances of zero for a particular population can be inferred from their absence from samples in the study. Additionally, species names were checked for typographic errors and misspellings, and a standardized notation was used for records of morphospecies and species complexes. Most records were included as provided and may not always conform to the latest nomenclature. Furthermore, latitudes and longitudes were checked for their location relative to other descriptors (e.g., country or marine vs. terrestrial). Finally, the grain and extent of each study were calculated from information in the methods where available, or by applying a convex hull algorithm to locations of the samples.

3 | DESCRIPTION OF DATA

In total, the version of BioTIME released with this paper includes 8,777,413 records, across 547,161 unique locations, gathered from 361 studies (Figure 1; see Appendix for a full list of citations). These observations span the Poles to the Equator, from depths of *c.* 5,000 m to elevations of *c.* 4,000 m above sea level, and include the terrestrial, freshwater and marine realms. The database includes records spanning 21 out of 26 ecoregions [WWF; (http://www.worldwildlife.org/biomes)]. Nonetheless, there are spatial biases in the distribution of sampling locations, with most studies occurring in Europe, North America and Australia. This geographical bias has persisted despite the growth of the database. For example, a comparison between Supporting Information Figure S2 and the data included in the study by Dornelas et al. (2014) displays only small differences, despite the database having more than tripled its size in the interim. It is our hope that this geographical bias will decrease over time via targeted searches and data recruitment.

There are 44,440 taxa in BioTIME. The majority of these (88.8%) are species, but some organisms are identified only to coarser taxonomic levels, such as genus. BioTIME includes assemblages across the animal and plant kingdoms, ranging from mammals to microscopic plankton. As with the spatial distribution, there are also taxonomic biases in the data in BioTIME (Figure 2). Almost 70% of records fall into one of four categories: terrestrial plants, birds, fish and marine invertebrates, with fish accounting for 28% of the total database.

BioTIME records span 118 years (from 1874 to 2016), with the longest time series having 97 years and an average duration of 13 years. In more detail, 56.5% of studies contain up to 10 years of data, 42% between 10 and 50 years and 1.4% $>$ 50 years.

4 | USAGE NOTES

Version 1.0 of the BioTIME database can be downloaded from https://zenodo.org/record/1095627 or from http://biotime.st-andrews.ac.uk/. The use of data contained in BioTIME should cite original data citations in addition to the present paper. There is considerable variation in the spatial and temporal grain and extent among studies, which must be considered in any analysis of BioTIME data. Moreover, the number of samples was often not constant through time within studies; consequently, we recommend the use of sample-based rarefaction and provide R code to query the database, implement sample-based rarefaction and calculate a suite of biodiversity metrics. Specifically, we provide a tutorial guiding users to interact with both formats of the database (.csv and .sql; Allaire et al., 2015; Becker, Wilks, & Brownrigg, 2014; Oksanen et al., 2013; Ooms, James, DebRoy, Wickham, & Horner, 2015; R Development Core Team, 2013; Wickham, 2009; Wickham & Francois, 2015). Please note that for interacting with the .sql version of the database, users will have to set up a connection with

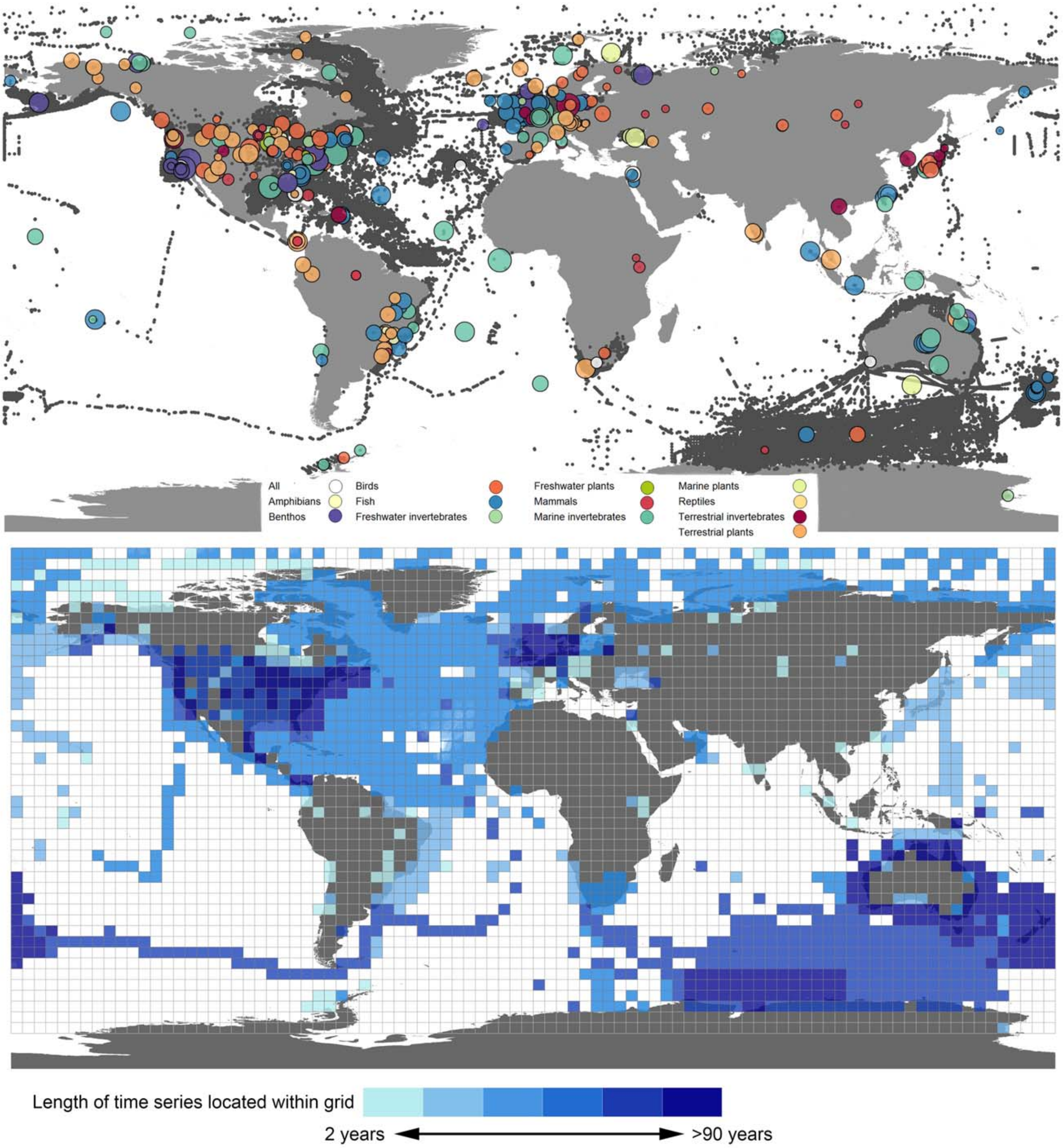

FIGURE 1 Top: Geographical locations of all the records included in BioTIME in dark grey, with central points per study shown as circles of different colour and size, according to taxa and number of species. Bottom: Map overlaid with ~4° grid cells coloured by the length of the full or partial time series contained within each cell

the server where they have installed the SQL database. For interacting with the .csv version, users have to download both the data and the metadata csv files, making sure that all the paths to these files are modified accordingly.

The data included in the present paper represent the subset of data within the BioTIME database for which we were able to secure licences to republish. The additional studies held in the full database have been obtained from publicly available data and are listed in Supporting Information Table S1. In total, BioTIME currently holds 387 studies, containing 12,623,386 records from a total of 652,675 distinct geographical locations, and 45,093 species. These records span a total of 124 years from 1858 to 2016 inclusive. We will continue to interact with data providers in order to increase data availability and to recruit additional data. Instructions on how to contribute to future releases can be found here (http://biotime.st-andrews.ac.uk/contribute.php).

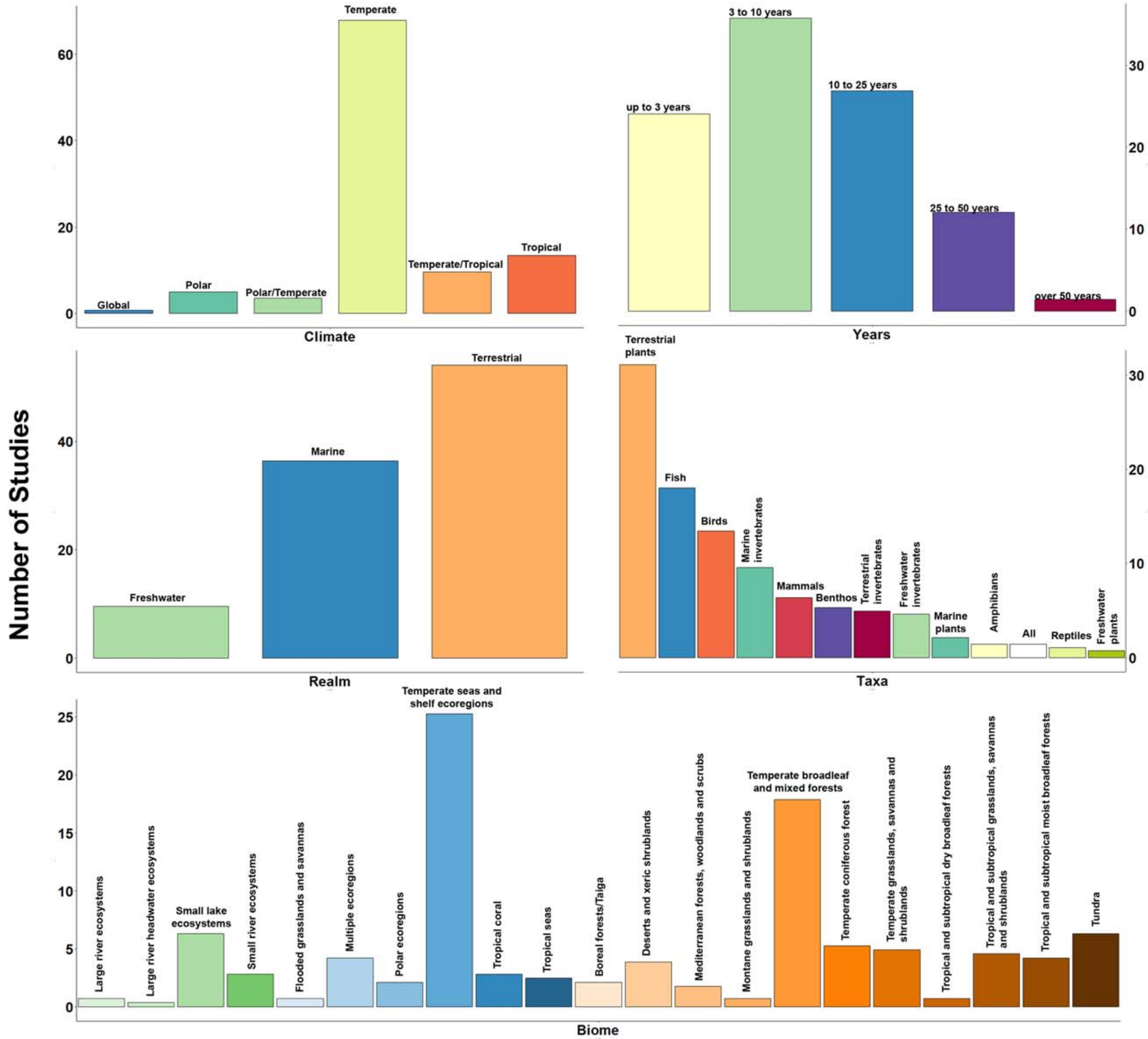

FIGURE 2 Proportion of studies that fall into the different classifications of: Climate, number of years sampled, realm, taxa and biome

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DATA ACCESSIBILITY

The BioTIME database is accessible through the BioTIME website (http://biotime.st-andrews.ac.uk) and through the Zenodo repository (https://zenodo.org/record/1095627).

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BIOSKETCH

The **BioTIME consortium** emerged from the ERC project BioTIME in 2010. The consortium currently includes 271 authors distributed among 35 countries engaged in collecting biodiversity time series data and committed to sharing it for wider use. We hope that the BioTIME database allows analysis of large-scale patterns of biodiversity change and contributes to giving credit to the data collectors, without whom synthesis would not be possible.

SUPPORTING INFORMATION

Additional Supporting Information may be found online in the supporting information tab for this article.

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