

BioTIME: A database of biodiversity time series for the Anthropocene

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Funding information

European Research Council and EU, Grant/Award Number: AdG-250189, PoC-727440 and ERC-SyG-2013-610028; Natural Environmental Research Council, Grant/Award Number: NE/L002531/1; National Science Foundation, Grant/Award Number: DEB-1237733, DEB-1456729, 9714103, 0632263, 0856516, 1432277, DEB-9705814, BSR-8811902, DEB 9411973, DEB 0080538, DEB 0218039, DEB 0620910, DEB 0963447, DEB-1546686, DEB-129764, OCE 95-21184, OCE-

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.

0099226, OCE-03-52343, OCE-0623874, OCE-1031061, OCE-1336206 and DEB-1354563; National Science Foundation (LTER), Grant/Award Number: DEB-1235828, DEB-1440297, DBI-0620409, DEB-9910514, DEB-1237517, OCE-0417412, OCE-1026851, OCE-1236905, OCE-1637396, DEB-1440409, DEB-0832652, DEB-0936498, DEB-0620652, DEB-1234162 and DEB-0823293; Fundação para a Ciência e Tecnologia, Grant/Award Number: POPH/FSE SFRH/BD/90469/2012, SFRH/BD/84030/2012, PTDC/BIA-BIC/111184/2009; SFRH/BD/80488/2011 and PD/BD/52597/2014; Ciência sem Fronteiras/CAPEs, Grant/Award Number: 1091/13-1; Instituto Milenio de Oceanografia, Grant/Award Number: IC120019; ARC Centre of Excellence, Grant/Award Number: CE0561432; NSERC Canada; CONICYT/FONDECYT, Grant/Award Number: 1160026, ICM PO5-002, CONICYT/FONDECYT, 11110351, 1151094, 1070808 and 1130511; RSF, Grant/Award Number: 14-50-00029; Gordon and Betty Moore Foundation, Grant/Award Number: GBMF4563; Catalan Government; Marie Curie Individual Fellowship, Grant/Award Number: QLK5-CT2002-51518 and MERG-CT-2004-022065; CNPq, Grant/Award Number: 306170/2015-9, 475434/2010-2, 403809/2012-6 and 561897/2010; FAPESP (São Paulo Research Foundation), Grant/Award Number: 2015/10714-6, 2015/06743-0, 2008/10049-9, 2013/50714-0 and 1999/09635-0 e 2013/50718-5; EU CLIMMOOR, Grant/Award Number: ENV4-CT97-0694; VULCAN, Grant/Award Number: EVK2-CT-2000-00094; Spanish, Grant/Award Number: REN2000-0278/CCI, REN2001-003/GLO and CGL2016-79835-P; Catalan, Grant/Award Number: AGAUR SGR-2014-453 and SGR-2017-1005; DFG, Grant/Award Number: 120/10-2; Polar Continental Shelf Program; CENPES - PETROBRAS; FAPERJ, Grant/Award Number: E-26/110.114/2013; German Academic Exchange Service; sDiv; iDiv; New Zealand Department of Conservation; Wellcome Trust, Grant/Award Number: 105621/Z/14/Z; Smithsonian Atherton Seidell Fund; Botanic Gardens and Parks Authority; Research Council of Norway; Conselleria de Innovació, Hisenda i Economia; Yukon Government Herschel Island-Qikiqtaruk Territorial Park; UK Natural Environment Research Council ShrubTundra Grant, Grant/Award Number: NE/M016323/1; IPY; Memorial University; ArcticNet. DOI: 10.13039/50110000027. Netherlands Organization for Scientific Research in the Tropics NWO, grant W84-194. Ciências sem Fronteiras and Coordenação de Pessoal de Nível Superior (CAPES, Brazil), Grant/Award Number: 1091/13-1. National Science Foundation (LTER), Award Number: OCE-9982105, OCE-0620276, OCE-1232779.

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 km² (158 cm²) to 100 km² (1,000,000,000,000 cm²).

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

FCT - SFRH / BPD / 82259 / 2011. U.S. Fish and Wildlife Service/State Wildlife federal grant number T-15. Australian Research Council Centre of Excellence for Coral Reef Studies (CE140100020). Australian Research Council Future Fellowship FT110100609. M.B., A.J., K.P., J.S. received financial support from internal funds of University of Łódź. NSF DEB 1353139. Catalan Government fellowships (DURSI): 1998FI-00596, 2001BEAI200208, MEC D Post-doctoral fellowship EX2002-0022. National Science Foundation Award OPP-1440435. FONDECYT 1141037 and FON-DAP 15150003 (IDEAL). CNPq Grant 306595-2014-1

Editor: Thomas Hickler

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://ecological-data.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

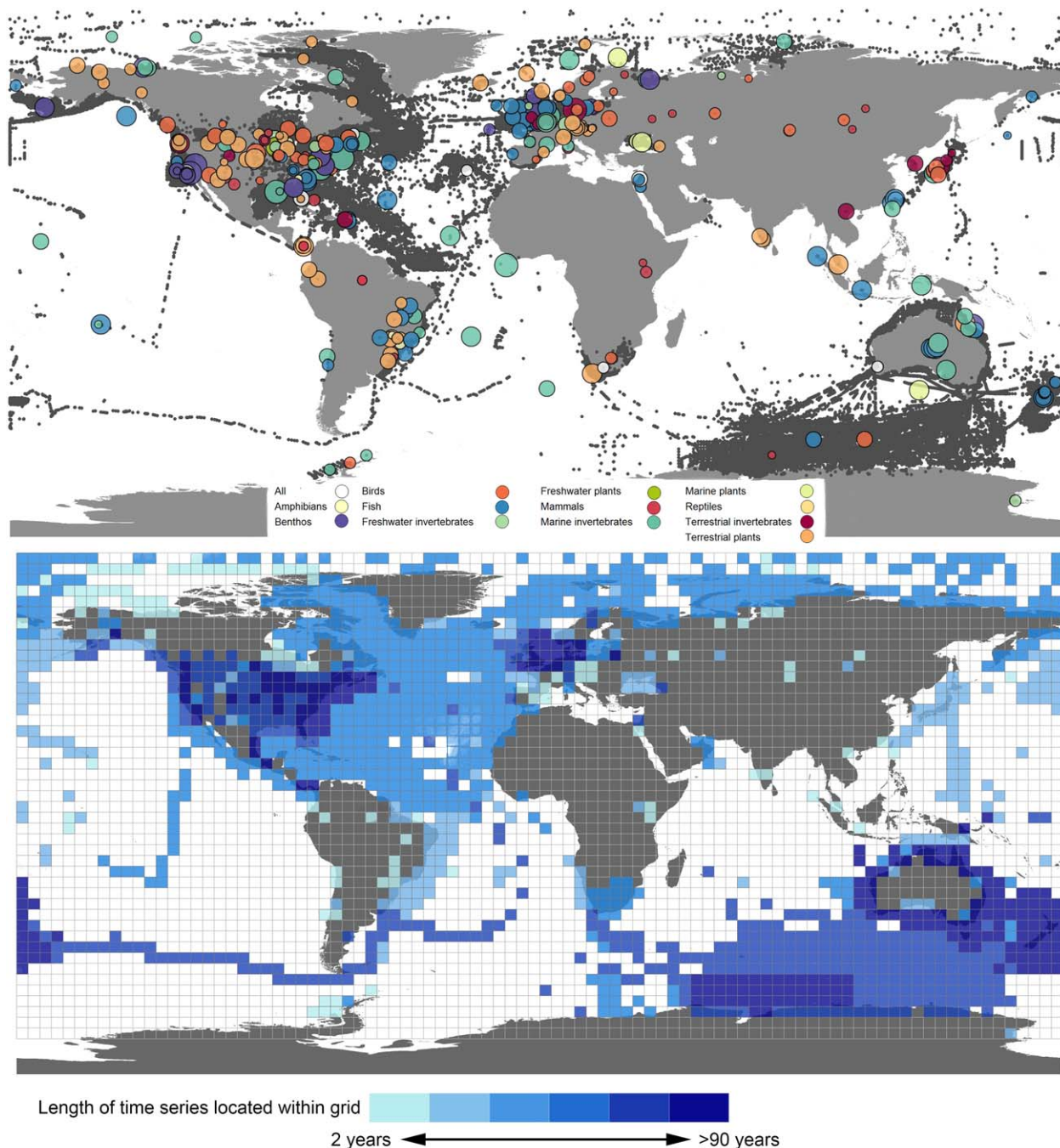


FIGURE 1 Top: Geographical locations of all the records included in BioTIME in dark grey, with central points per study shown as circles of different colour and size, according to taxa and number of species. Bottom: Map overlaid with $\sim 4^\circ$ grid cells coloured by the length of the full or partial 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>).

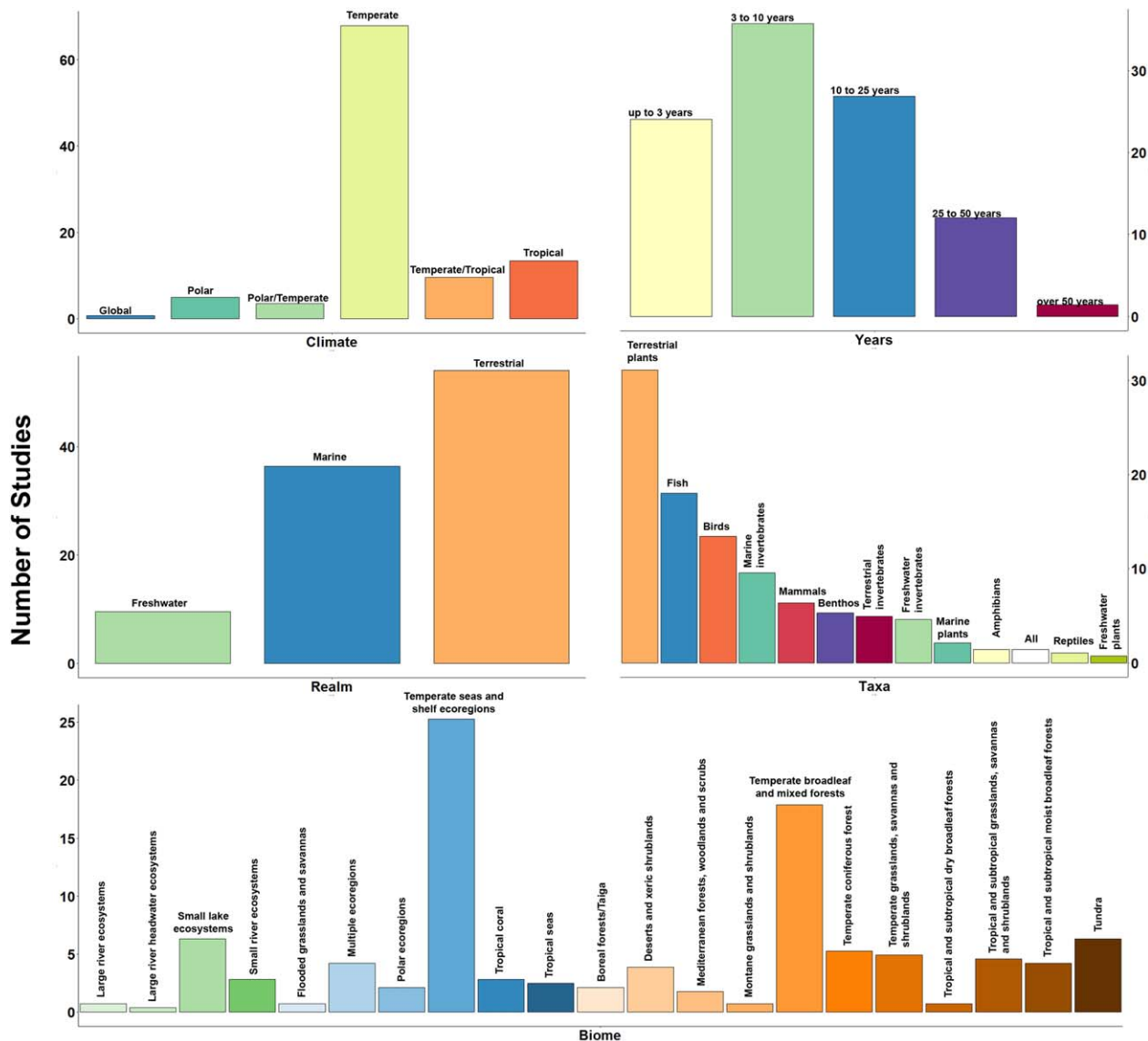


FIGURE 2 Proportion of studies that fall into the different classifications of: Climate, number of years sampled, realm, taxa and biome

ACKNOWLEDGMENTS

European Research Council and EU: A.E.M., M.D. and F.M. are grateful for the support of the ERC grants BioTIME [AdG-250189] and BioCHANGE [PoC-727440]. J.P. and M.E. acknowledge the financial support from the ERC Synergy grant ERC-SyG-2013-306 610028 IMBALANCE-P, Spanish CGL2016-79835-P and Catalan SGR-2017-1005. Long-term sampling of Calafuria rocky shores (L.B.-C.) has been supported by various E.U. projects, in addition to the University of Pisa and the Census of Marine Life. Natural Environmental Research Council: C.W. is grateful for the support of the Natural Environmental Research Council [grant number NE/L002531/1]. The Porcupine Abyssal Plain Sustained Observatory is funded by the U.K. Natural Environment Research Council. We thank the Atlantic Meridional Program (supported by the U.K. Natural Environment Research Council through the Atlantic Meridional Transect consortium) and the L4 programme (funded under the U.K.

NERC Oceans 2025 programme as part of Theme 10, Sustained Observations). C.E.W. thanks the U.K.'s Natural Environment Research Council for funding the Western Channel Observatory's plankton time-series through the National Capability programme. National Science Foundation (NSF): S.K.M.E. acknowledges the U.S. National Science Foundation for funding data collection. S.R.S. was supported by NSF grant 1400911. The research of F.P.D. was funded by NSF grant DEB-1237733. D.A.K. thanks the National Science Foundation (most recently DEB-1456729) for their support. This material (R.D.H.) is based upon work supported by the National Science Foundation under Grant No. 9714103, 0632263, 0856516, and 1432277. K.D.W. thanks the U.S. Forest Service, National Science Foundation and Andrew W. Mellon Foundation. Research (M. W., R.B.W. and C.B.) was supported by grants DEB-9705814, BSR-8811902, DEB 9411973, DEB 0080538, DEB 0218039, DEB 0620910, DEB 0963447, DEB-1546686 and DEB-129764 from the

National Science Foundation to the Department of Environmental Science, University of Puerto Rico, and to the International Institute of Tropical Forestry USDA Forest Service, as part of the Luquillo Long-Term Ecological Research Program. The U.S. Forest Service (Department of Agriculture) and the University of Puerto Rico gave additional support. J.E.D. thanks the U.S. National Science Foundation for support with grants OCE 95-21184, OCE-0099226, OCE 03-52343, OCE-0623874, OCE-1031061 and OCE-1336206. Data compilation and cleaning by A.H.H., B.S.E. and S.J.S. was funded by NSF grant DEB-1354563 to A.H.H. W.A.G. thanks the AON ITEX program (awards 1432982, 0856710 and 1504381). All research at the U.S. Forest Service International Institute of Tropical Forestry is done in collaboration with the University of Puerto Rico. National Science Foundation (LTER): Jornada LTER, Research Site Manager – New Mexico State University. Datasets were provided by the Jornada Basin Long-Term Ecological Research (LTER) project. Funding for these data was provided by the U.S. National Science Foundation (Grant DEB-1235828). C.G. was supported under Cooperative Agreement #DEB-1440297, NTL LTER. Support for A.L. R. was provided under Cooperative Agreement #DEB-1440297, NTL-LTER. Data collection (E.H.S.) was supported by the National Science Foundation #DEB-1440297, NTL LTER. J.J. is grateful for funding to the H. J. Andrews Long-Term Ecological Research program from the U.S. National Science Foundation; U.S. Forest Service support of the H. J. Andrews Experimental Forest. V.H.R.-M. and R. R.T. thank NSF-Florida Coastal Everglades Long-Term Ecological Research (FCE-LTER) program (grant nos DBI-0620409, DEB-9910514 and DEB-1237517). D.C.R. is grateful for support from the NSF's LTER Program. D.C.R. thanks the U.S. National Science Foundation for supporting the Santa Barbara Coastal Long-Term Ecological Research (SBC-LTER) program. Data (A.J.B. and R.C.) were provided by the Moorea Coral Reef Long-Term Ecological Research Program (OCE-0417412, OCE-1026851, OCE-1236905 and OCE-1637396). D.L. thanks the Jornada Basin LTER Program and the Sevilleta LTER Program. Data (J.J., M.N. and S.M.R.) were provided by the H. J. Andrews Experimental Forest research program, funded by the NSF's LTER Program (DEB-1440409), U.S. Forest Service Pacific Northwest Research Station and Oregon State University. The authors are grateful to the LTER program for the data they provide. This includes material based upon work supported under Cooperative Agreements DEB-0832652 and DEB-0936498, and by grants from the LTER including DEB-0620652 and DEB-1234162; further support was provided by the Cedar Creek Ecosystem Science Reserve and the University of Minnesota. J.F.C. acknowledges funding from NSF (DEB-0823293) from the LTER to the Coweeta LTER Program at the University of Georgia. Other funding: L.H.A. was supported by Fundação para a Ciência e Tecnologia, Portugal (POPH/FSE SFRH/BD/90469/2012). A.R.K. is funded by Ciências sem Fronteiras and Coordenação de Pessoal de Nível Superior (CAPES, Brazil), Grant/Award Number: 1091/13-1. R.E. is grateful for support by Instituto Milenio de Oceanografía IC120019. A.H.B. is grateful for ARC Centre of Excellence (Grant CE0561432). R.P.V. is currently supported by a doctoral grant from Fundação para a

Ciência e Tecnologia, Portugal (SFRH/BD/84030/2012). J.J. is grateful for funding for data collection from NSERC Canada. J.R.G. is grateful for the support from CONICYT/FONDECYT no. 1160026, ICM PO5-002, CONICYT/FPB-23. A.P.M. is grateful for the support of FONDECYT Grants 11110351 and 1151094. A.A. and V.O. thank RSF (14-50-00029). E.P.W. is supported by the Gordon and Betty Moore Foundation's Data-Driven Discovery Initiative Grant GBMF4563. J.M.A. was supported by FI/FIAP (1998FI-00596) and BE (2001BEAI200208) fellowships from the Catalan Government (DURSI) during the fieldwork and by a MECD-Post-doctoral fellowship (EX2002-0022), a Marie Curie Individual Fellowship (QLK5-CT2002-51518) and Marie Curie project MARIBA (MERG-CT-2004-022065) afterwards. A.F. receives a scholarship from CNPq (306170/2015-9); G.D. receives a scholarship from FAPESP (2015/10714-6); projects to collect data received financial support from FAPESP (São Paulo Research Foundation) (2015/06743-0, 2008/10049-9), CNPq (475434/2010-2) and DFG (German Research Foundation, Project PF 120/10-2). F.L. acknowledges support from EU CLIMOOD ENV4-CT97-0694, VULCAN EVK2-CT-2000-00094), Spanish REN2000-0278/CCI and REN2001-003/GLO, and Catalanian AGAUR 2014 SGR 453. Y.R.S. is grateful for funding from FUNDECT, CNPq. F.R.S. is grateful for the support of the São Paulo Research Foundation (FAPESP, Proc. 2013/50714-0). D.A.K. is grateful for the support of FONDECYT (most recently, no. 1070808). E.L. acknowledges funding from NSERC and logistical support from Polar Continental Shelf Program. P.H. is grateful for the support of FONDECYT no. 1130511. G.B.G.S. and M.V. thank the staff who assisted in the field and laboratory research from the Laboratory of Fishery Biology and Technology. This study was part of the programme 'Environmental Assessment of Guanabara Bay' coordinated and funded by CENPES – PETROBRAS, which has given permission for the publication of the results. This study was also supported by the Long Term Ecological Programme (PELD programme – CNPq 403809/2012-6) and by FAPERJ (Thematic Programme, process E-26/110.114/2013). G.B.G.S. was funded by CAPES/Brazil. C.M. is grateful for the support of the German Academic Exchange Service (DAAD) and the German Research Foundation (DFG). H.B. and U.J. acknowledge the support of sDiv, the Synthesis Centre of the German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig. C.F.J.M., R.R. and A.L.-B. acknowledge funding from Fundação para a Ciência e Tecnologia, Portugal (PTDC/BIA-BIC/111184/2009, SFRH/BD/80488/2011 and PD/BD/52597/2014, respectively). F.Z.F. was funded by CAPES/Brazil. T.J.W. acknowledges support from the New Zealand Department of Conservation. General acknowledgments: Bioinformatics and Computational Biology analyses were supported by the University of St Andrews Bioinformatics Unit, which is funded by a Wellcome Trust ISSF award (grant 105621/Z/14/Z). We would like to acknowledge Richard Osman for his work in the Woods Hole study, and the Smithsonian Atherton Seidell Fund, which provides funds within the Smithsonian to make old studies and publications more available. Any use of trade, firm or product names is for descriptive purposes only and does not imply endorsement by the

U.S. Government. This study (P.B.) was performed under the auspices of Utah State University IACUC protocol number 1539. L.V.V. thanks Earthwatch Institute and their volunteers. R.A.D. and T.S.D. thank the Botanic Gardens and Parks Authority for the financial and logistical support, without which their reptile monitoring project would not be possible. R.S.S. and G.E. thank the Reef Life Survey volunteer divers. P.H. thanks Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq). F.H. acknowledges the EWHALE laboratory, Biology and Wildlife Department, Institute of Arctic Biology. H.K. thanks the Ministry of Trade, Industry and Fisheries. A.H. is supported by the Research Council of Norway. J.S. thanks the many researchers and field assistants who over the years contributed to the collection and curation of data for the studies presented in this database. S.K.C. thanks the City of Boulder Department of Open Space and Mountain Parks. N.A. thanks Karnataka Forest Department and IFP staff Messrs. S. Aravajy, S. Ramalingam, N. Barathan, G. Orukaimani, G. Jayapalan, K. Anthapa Gowda, Obbaya Gowda and Manoj Gowda. M.L. and J.M.A. wish to thank all participants in the MEDITS series cruises on board R/V Cornide de Saavedra, both scientists and crew (Spanish Institute of Oceanography), for all their help and support, and especially Pere Abelló and Luis Gil de Sola. Thanks to Daniel Oro and the Population Ecology research team at the Institut Mediterrani d'Estudis Avançats (IMEDEA, CSIC-UIB). M.L. was supported by a fellowship of Conselleria de Innovació, Hisenda i Economia (Govern de les Illes Balears). R.K., D.P. and J.M. acknowledge SOTEAG (Shetland Oil Terminal Environmental Advisory Group) for providing access to the dataset. We thank SOTEAG (Shetland Oil Terminal Advisory group) for providing data from the long term rocky shore monitoring programme after dataset. We thank Jake Goheen and Rob Pringle for providing data from the UHURU herbivore-exclusion experiment in central Kenya. J.S.M. thanks the Australian Research Council. J.S.M. thanks the staff of Lizard Island Research Station. F.P. would like to thank the Waserversorgung Zurich for collecting and allowing access to the data. Data (C.H.D.) was sourced from the Integrated Marine Observing System (IMOS); IMOS is a national collaborative research infrastructure, supported by the Australian Government. J.M.A. would like to thank the Spanish Institute of Oceanography (IEO), Pere Abelló, Luis Gil de Sola and Daniel Oro. M.T.Z.T. thanks Dr Ary Teixeira de Oliveira-Filho. I.H.M.-S. thanks the Herschel Island-Qikiqtaruk Territorial Park management and, in particular, Cameron D. Eckert, Catherine Kennedy, Dorothy Cooley and Jill F. Johnstone for establishing the ITEX protocols for plant composition monitoring on Qikiqtaruk. We thank the Herschel Island-Qikiqtaruk Territorial Park rangers for data collection logistical support, including in particular Richard Gordon, Edward McLeod, Sam McLeod, Ricky Joe, Paden Lennie, Deon Arey and LeeJohn Meyook. We thank the researchers and field assistants who helped with data collection, including Haydn Thomas, Sandra Angers-Blondie, Jakob Assmann, Meagan Grabowski, Catherine Henry, Annika Trimble, Louise Beveridge, Clara Flintrop, Santeri Lehtonen, Joe Boyle, John Godlee and Eleanor Walker. Funding was provided by the Yukon Government Herschel Island-Qikiqtaruk Territorial Park and the U.K. Natural Environment Research Council

ShrubTundra Grant NE/M016323/1. We thank the Inuvialuit People for the opportunity to conduct research on their traditional lands. L. H. and L.S.C. are grateful for the support of IPY, Memorial University and ArcticNet for funding. T.J.C. thanks the LIRS Trimodal Mapping Study. M.H. thanks the staff of Lizard Island Research Station. R.R.S. would like to thank E. E. de Assis, Santa Genebra and E. E. Caetetus and acknowledges funding from FAPESP (projetos temáticos: 1999/09635-0 and 2013/50718-5) and CNPq (Processo: 561897/2010). F.C. thanks SIBELCO Ltda. of Brazil for the logistic support in the accomplishment of the field work. We acknowledge the thousands of U.S. and Canadian volunteers who annually perform the North American Breeding Bird survey, as well as those who manage the program at the U.S. Geological Survey (USGS). The term 'Anthropocene' is not formally recognized by the USGS as a description of geological time. We use it here informally. We hope that data providers will continue to share their data (and any new updates) with OBIS and GBIF and encourage them to correct any errors identified by BioTIME. D.A., D.J., K.K., T.V. acknowledges support from Czech Science Foundation, project No. 16-18022S and from Czech Ministry of Environment, project No. 170368. We thank Jan Wittcock and other colleagues who assisted in the sampling and compilation of the macrobenthic data and the Belgian Federal Science Policy Office who funded MACROBEL through the programme 'Sustainable management of the North Sea' (SPSD I MN/02/96). M. B., A.J., K.P., J.S. received financial support from internal funds of University of Łódź. W.R.F. thanks the National Science Foundation for support through award OPP-1440435. N.V. thanks CONICYT grants FONDECYT 1141037 and FONDAP 15150003 (IDEAL).

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.

How to cite this article: Dornelas M, Antão LH, Moyes F, et al. BioTIME: A database of biodiversity time series for the Anthropocene. *Global Ecol Biogeogr*. 2018;27:760–786. <https://doi.org/10.1111/geb.12729>

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