

DATA ARTICLE OPEN ACCESS

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

Maria Dornelas^{1,2}  | Laura H. Antão³  | Amanda E. Bates⁴  | Viviana Brambilla²  | Jonathan M. Chase^{5,6}  | Cher F. Y. Chow¹  | Ada Fontrodona-Eslava¹  | Anne E. Magurran¹  | Inês S. Martins^{1,7}  | Faye Moyes¹  | Alban Sagouis^{5,6}  | Samuel Adu-Acheampong⁸  | Daniel Acquah-Lamptey⁹  | Dušan Adam¹⁰  | Penelope A. Ajani¹¹  | Aitor Albaina¹²  | Pablo Almaraz¹³  | Jeongseop An¹⁴  | Roger Sigismund Anderson¹⁵  | Madelaine Jean Robertson Anderson¹⁶  | Alexsander Z. Antunes¹⁷  | Ivan Arismendi¹⁸  | Linda Armbrrecht¹⁹  | Pedro Aros-Mardones^{20,21}  | Sreejith Kalpuzha Ashtamoorthy²²  | Narayanan Ayyappan²³  | Gal Badihi²⁴  | Joseph J. Bailey²⁵  | Andrew H. Baird²⁶  | Mark Edward Baird²⁷  | Sreekumar Vadakkethil Balakrishnan²⁸  | José António L. Barão-Nóbrega²⁹  | Adi Barash^{30,31}  | Miguel Barbosa^{1,32}  | Jos Barlow³³  | Claus Bässler^{34,35}  | Matthieu Beaumont³⁶  | Natalie Beenaerts³⁷  | Tiago Octavio Begot³⁸  | Wallace Beiroz^{39,40}  | Ricardo Beldade⁴¹  | David M. Bell⁴²  | Alecia Bellgrove⁴³  | Jonathan Belmaker^{31,44}  | Lisandro Benedetti-Cecchi⁴⁵  | Cassandra E. Benkwitt³³  | Pamela Medina-van Berkum^{46,47}  | Brandon T. Bestelmeyer⁴⁸  | Matthew G. Betts⁴⁹  | Maxwell Kelvin Billah⁸  | Anne D. Bjorkman^{50,51}  | Magdalena Błażewicz⁵²  | Christopher P. Bloch⁵³  | Shane A. Blowes^{5,6}  | Antonio Bode⁵⁴  | Juliano A. Bogoni^{55,56}  | Thomas Bolger^{57,58}  | Timothy C. Bonebrake⁵⁹  | Erik Bonsdorff⁶⁰  | Roberta Bottarin⁶¹  | Luke N. Brokensha⁶²  | Rob W. Brooker⁶³  | Andrew J. Brooks⁶⁴  | Helge Bruehlheide^{5,65}  | Thiago Almeida Bueno⁶⁶  | Claire Laguionie^{67,68}  | Mariana Lopes Campagnoli⁶⁹  | James Cant^{1,70}  | Erica Pellegrini Caramaschi⁷¹  | Alexandre Caron⁷²  | Tadhg Carroll⁷  | Tancredi Caruso⁵⁷  | Juan Carvajal-Quintero^{5,73}  | Giuseppe Castaldelli⁷⁴  | Edward Castañeda-Moya⁷⁵  | Pedro V. Castilho⁷⁶  | Sonia Zanini Cechin⁷⁷  | Shahar Chaikin^{44,78}  | Uchangi Manjunatha Chandrashekara⁷⁹  | Tory J. Chase⁸⁰  | Chaolun Allen Chen⁸¹  | Jorge José Cherem⁸²  | Sei-Woong Choi⁸³  | Erica M. Christensen^{84,85,86}  | Alexander V. Christianini⁸⁷  | Jackson Wing Four Chu⁸⁸  | Peter Coad⁸⁹  | Carl Van Colen⁹⁰  | Lise Comte⁹¹  | Elisabeth J. Cooper⁹²  | J. Hans C. Cornelissen⁹³  | Eddy Cosson⁹⁴  | Unai Cotano⁹⁵  | Luc Crevecoeur⁹⁶  | Shannan Kyle Crow⁹⁷  | Graeme S. Cumming⁹⁸  | Vanessa S. Daga⁹⁶  | Gabriella Damasceno⁹⁹  | Gergana N. Daskalova¹⁰⁰  | Claire H. Davies²⁷  | Robert A. Davis¹⁰¹  | Frank P. Day¹⁰²  | Sussy De-La-Zerda¹⁰³  | Amy Elizabeth Deacon¹⁰⁴  | Indradatta de Castro-Arrazola^{105,106}  | Steven Degraer¹⁰⁷  | Kharran Deonarinesingh¹⁰⁴  | Juan C. Diaz-Ricaurte^{108,109}  | Christopher R. Dickman¹¹⁰  | Tara Dirilgen^{57,58,111}  | Ciaran John Dolan^{112,113}  | J. Emmett Duffy¹¹⁴  | Timothy E. Dunn¹¹⁵  | Giselda Durigan¹¹⁶  | Ciara Dwyer¹¹⁷  | Stevan Earl¹¹⁸  | Dor Edelist¹¹⁹  | Graham John Edgar¹²⁰  | Sally Edmondson¹²¹  | Ashley K. Elgin¹²²  | Kari Elsa Ellingsen¹²³  | Sarah C. Elmendorf^{124,125}  | Ruth S. Eriksen^{27,126,127}  | S. K. Morgan Ernest¹²⁸  | Ruben Escribano¹²⁹  | Paula Cabral Eterovick¹³⁰  | Brian S. Evans¹³¹  | Jason D. Everett^{132,133,134}  | Vesela Evtimova¹³⁵  | Dan A. Exton⁴⁷  | Andrew J. Fairbairn¹³⁶  | Felipe Moreli Fantacini¹³⁷  | Fabiano Turini Farah¹³⁸  | Fábio Zanella Farneda^{139,140}  | Mario E. Favila¹⁴¹  | Philippe Fernandez-Fournier¹⁴²  | Braulio Fernández-Zapata¹⁴³  | Diogo F. Ferreira^{144,145}  | Carola Ferronato¹⁴⁶  | Christopher R. du Feu¹⁴⁷  | Alessandra Fidelis¹⁴⁸  | David A. Fifield¹⁴⁹  | Vilmar Picinatto Filho¹⁵⁰  | Walter Mesquita Filho¹⁵¹  | Robert N. L. Fitt¹⁵²  | Carlos A. H. Flechtmann¹⁵³  | William R. Fraser¹⁵⁴  | Donna L. Fraser¹⁵⁴  | Lídia Freixas¹⁵⁵  | John Fryxell¹⁵⁶  | Garrett J. Fundakowski¹  | Scott Stanley Gabara¹⁵⁷  | Elise Gallois^{158,159}  | Mariana García Criado¹⁵⁸  | Emili García-Berthou¹⁶⁰  | Joaquim Garrabou^{161,162}  | Andrew R. Gates¹⁶³  | Roberto Cazzolla Gatti¹⁶⁴  | Anna Gavioli⁷⁴  | Tal Gavriel⁴⁴  | Benoit Gendreau-Berthiaume¹⁶⁵  | Xingli Giam¹⁶⁶  | Carina Gjerdrum¹⁶⁷  | Michael Glemnitz¹⁶⁸  | Jasmin Annica Godbold¹⁴³  | Daniel Gómez-Gras^{169,170,171}  | Rodrigo Barbosa Gonçalves³⁸  | Andy Goold¹⁴⁷  | Richard R. Gordon¹⁷²  | Menachem Goren³¹  | Fernando Vilas Boas Goulart¹⁷³  | William A. Gould¹⁷⁴  | Meagan M. Grabowski¹⁷⁵  | Nicholas A. J. Graham³³  | Maurício Eduardo Graipel¹⁷⁶  | Laura J. Grange^{143,177}  | Aaron C. Greenville¹¹⁰  | Gary D. Grossman¹⁷⁸  | Valeria A. Guinder¹⁴⁶  | Peter Haase^{179,180}  | Gary N. Haskins¹⁸¹  | Kris Havstad¹⁸²  | Luise Hermanutz¹⁸³  | Michael Julian Hames Hickford¹⁸⁴  | Pamela Hidalgo¹⁸⁵ 

For affiliations refer to page 8.

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Pedro Higuchi¹⁸⁶ | Andrew S. Hoey²⁶ | Gert Van Hoey¹⁸⁷ | Annika Hofgaard¹⁸⁸ | Kristen T. Holeck¹⁸⁹ | Robert D. Hollister¹⁹⁰ | Richard T. Holmes¹⁹¹ | Mia Odell Hoogenboom¹⁹² | Joaquín Hortal¹⁹³ | Tammy Horton¹⁶³ | Chih-hao Hsieh¹⁹⁴ | Christine L. Huffard¹⁹⁵ | Ida-Maria Huikkonen¹⁹⁶ | Allen H. Hurlbert^{197,198} | Julian Hynes¹⁹⁹ | Pascal Irz²⁰⁰ | Natalia Macedo Ivanauskas²⁰¹ | Akemi Iwayama²⁰² | Darren K. James⁴⁸ | Ute Jandt^{5,65} | Anna M. Jazdzewska⁵² | Merlijn Jocque^{47,107,203} | Sophie T. Johnston⁹⁶ | Samuel E. I. Jones^{47,204} | Faith A. M. Jones²⁰⁵ | Julia A. Jones²⁰⁶ | Edite Jucevica²⁰⁷ | Ugis Kagainis^{208,209} | Maiko Kagami²¹⁰ | Jungwon Kang⁹⁶ | Xuejia Ke¹ | Erin Colleen Keeley²¹¹ | Rebecca Kinnear^{1,212,213} | Kari Klanderud²¹⁴ | Uwe Klink²¹⁵ | Roel van Klink^{5,6} | Stefan Klotz²¹⁶ | Carolien Knockaert²¹⁷ | Halvor Knutsen^{218,219} | Matti Koivula²²⁰ | Alessandra Kortz²²¹ | Peter Krieger²²² | Chao-Yang Kuo^{223,224} | David J. Kushner²²⁵ | Rosina Kyerematen⁸ | Raphaël Lagarde²²⁶ | Lesley T. Lancaster²²⁷ | Ori Frid Landau²²⁸ | Wouter Van Landuyt²⁰³ | Eric R. Larson²²⁹ | Mai Lazarus⁴⁴ | Cheol Min Lee²³⁰ | Jonathan S. Lefcheck²³¹ | Jonas J. Lembrechts^{232,233} | Renato A. Ferreira de Lima²³⁴ | Romulão Guimarães Lima²³⁵ | Nathália G. S. Lima²³⁶ | Cristina Linares^{170,171} | Sandra C. Lindstrom²³⁷ | Francisco Lloret²³⁸ | John David Lloyd²³⁹ | Cleonice Maria Cardoso Lobato²⁴⁰ | David M. Lodge²⁴¹ | Peter Richard Long²⁴² | Celeste López-Abbate¹⁴⁶ | Adrià López-Baucells²⁴³ | Julio Louzada²⁴⁴ | Maite Louzao²⁴⁵ | Antonella Lugliè^{246,247} | Micheli Ribeiro Luiz²⁴⁸ | S. Ellen Macdonald²⁴⁹ | Joshua S. Madin¹⁶⁹ | André Lincoln Barroso Magalhães²⁵⁰ | Rajindra Mahabir¹⁰⁴ | David Maphisa^{251,252,253,254} | Thomas Edward Martin^{47,255} | Marcio Martins¹⁰⁹ | Patrick T. Martone²⁵⁶ | Silvia Matesanz^{257,258} | Shin-ichiro S. Matsuzaki²⁵⁹ | Thomas J. Matthews^{260,261,262} | Iain McCombe Matthews¹ | Connie J. Maxwell⁴⁸ | Kent P. McFarland²⁶³ | Brian J. McGill^{264,265} | Diane Marie McKnight²⁶⁶ | Michael J. McWilliam¹ | Jason Meador²⁶⁷ | Henning Meesenburg²¹⁵ | Kristin Meier¹⁶⁸ | Viesturs Melecis²⁶⁸ | Peter L. Meserve²⁶⁹ | Christoph F. J. Meyer²⁷⁰ | Anders Michelsen²⁷¹ | Natali Oliva Roman Miiller²⁷² | Marco Milardi²⁷³ | Nataliya Milchakova²⁷⁴ | Robert J. Miller²⁷⁵ | Jonathan Millett²⁷⁶ | Tom Moens²⁷⁷ | Luciano F. A. Montag²⁷⁸ | Jon Moore^{279,280} | Jörg Müller^{281,282} | Akhil Murali²² | Shauna Ann Murray¹¹ | Isla H. Myers-Smith^{158,237} | Randall W. Myster²⁸³ | Masahiro Nakamura²⁸⁴ | Sasi Nayar²⁸⁵ | Francis Neat²⁸⁶ | James A. Nelson²⁸⁷ | Michael Paul Nelson⁴⁹ | Boris P. Nikolov¹³⁵ | Rym Nouioua²⁸⁸ | Collins Ayine Nsor²⁸⁹ | Michael O'Connor²⁹⁰ | Edward Adzesiwor Obodai⁹⁶ | Amy Marie Offland¹⁴⁷ | Romà Ogaya²⁹¹ | Hisako Ogura²⁹² | Thomas A. Okey^{293,294} | Julian D. Olden²⁹⁵ | Luiz Gustavo Rodrigues Oliveira-Santos²⁹⁶ | Jeffrey C. Oliver²⁹⁷ | Esben Moland Olsen^{218,219} | Vladimir G. Onipchenko²⁹⁸ | Daniel Oro²⁹⁹ | Davis Ozolins²⁰⁸ | Krzysztof Pabis⁵² | Bachisio Mario Padedda^{246,247} | Facundo X. Palacio³⁰⁰ | Alain Paquette³⁰¹ | Sinta Trilestari Pardede³⁰² | David M. Paterson²¹² | Sarah Pausina^{132,134} | Raphaël Pélissier^{303,304} | Steven C. Pennings³⁰⁵ | Josep Penuelas³⁰⁶ | Felipe Walter Pereira³⁰⁷ | Nivaldo Peroni⁵⁵ | Sergio Picó³⁰⁸ | Francesca Pilotto³⁰⁹ | Hudson Tercio Pinheiro³¹⁰ | Oscar Pizarro^{311,312} | Roberto Pizzolotto³¹³ | Francesco Pomati³¹⁴ | Paulo Santos Pompeu³¹⁵ | Dominique Ponton³¹⁶ | Eric Post³¹⁷ | Nicolas Poulet³¹⁸ | Juha Pöyry¹⁹⁶ | Steven J. Presley³¹⁹ | Herbert H. T. Prins³²⁰ | Pieter Provoost³²¹ | Kathleen L. Prudic^{322,323,324} | Vignesh Punjayil²² | Petr Pyšek^{221,325} | Pascal Querner³²⁶ | Juan Pablo Quimbayo³²⁷ | Indar W. Ramnarine¹⁰⁴ | Daniel C. Reed²⁷⁵ | Peter Bernard Reich^{328,329} | Suzanne M. Remillard⁴⁹ | Cerren Richards³³⁰ | Anthony James Richardson^{132,331,332} | Itai van Rijn⁴⁴ | Victor H. Rivera-Monroy³³³ | Christian Rixen^{334,335} | Kevin Peter Robinson^{112,113} | Ricardo Rocha⁷⁰ | Ricardo R. Rodrigues^{336,337} | Cassy Rodrigues¹⁴⁸ | Bjørn de Roos³³⁸ | Denise de C. de Rossa-Feres³³⁹ | Loreta Rosselli³⁴⁰ | Peter Charles Rothlisberg¹³² | Ana Rubio⁸⁹ | Lars G. Rudstam³⁴¹ | Catalina S. Ruz³⁴² | Nancy B. Rybicki³⁴³ | Gunther Van Ryckegem²⁰³ | Andrew L. Rypel^{344,345} | Jon P. Sadler²⁶⁰ | Victor Satoru Saito³⁴⁶ | Sofia Sal³⁴⁷ | Renato Portela Salomão^{348,349} | Nathan J. Sanders³⁵⁰ | Flavio A. M. Santos³⁵¹ | Tiago Gomes dos Santos³⁵² | Swapan Kumar Sarker³⁵³ | Sara E. Scanga³⁵⁴ | Marcus Schaub³⁵⁵ | Jochen Schmidt⁹⁷ | Inger Kappel Schmidt³⁵⁶ | Robert L. Schooley²²⁹ | Alfred Schultz⁹⁶ | Alberto Scotti^{61,357} | Amanda Serpell-Stevens¹⁶³ | Filipe C. Serrano¹⁰⁹ | Elizabeth H. Shadwick^{27,358} | Matthew Shaft³⁵⁹ | Thomas W. Sherry³⁶⁰ | Erika Mayumi Shimabukuro³⁶¹ | Jacek Siciński⁵² | Caya Sievers²¹² | Fernando Rodrigues da Silva³⁶² | Ana Carolina da Silva¹⁸⁶ | Juliana M. Silveira³⁶³ | Tadeu Siqueira^{364,365} | Arunkumar Kavidapadinjattathil Sivadasan²² | Prasad Theruvil Pambal Sivan²² | Agnija Skuja²⁰⁸ | Amalia L. Slaughter⁴⁸ | Jasper A. Slingsby³⁶⁶ | Joseph R. Smith¹⁴⁷ | Bruno Eleres Soares³⁶⁷ | Martin Solan¹⁴³ | Flaviana Maluf Souza³⁶⁸ | Gabriel B. G. Souza³⁶⁹ | Joshua L. Sprague¹⁵⁷ | Ulrich Stachow¹⁶⁸ | J. John Stadt³⁷⁰ | Christopher D. Stallings³⁷¹ | Radoslav Hristov Stanchev³⁷² | Emily H. Stanley³⁷³ | Brian M. Starzomski³⁷⁴ | Jose Mauro Sterza³⁷⁵ | Maarten Stevens²⁰³ | F. Gary Stiles³⁷⁶ | Stefan Stoll³⁷⁷ | Rick D. Stuart-Smith^{120,378} | Yzel Rondon Suárez³⁷⁹ | Laura Super³⁸⁰ | Sarah R. Supp³⁸¹ | Tapio Sutela³⁸² | Iain M. Suthers^{383,384} | Anna Suuronen¹⁹⁶ | Kerrie M. Swadling³⁸⁵ | Daniel K. Szydlowski³⁷³ | Hisatomo Taki³⁸⁶ | Sara Jeanne Snell Taylor¹⁹⁷ | Pablo A. Tedesco³⁸⁷ | Nils Teichert³⁸⁸ | Akira Terui³⁸⁹ | Gary P. Thiede³⁹⁰ | Anne Thimonier³⁹¹ | Oliver Thomas⁴⁷ | Peter Allan Thompson²⁷ | Simon Thorr^{9,392,393} | Jeremy S. Tiemann³⁹⁴ | Luís Felipe Toledo³⁹⁵ | Anne Tolvanen³⁸² | Maria Teresa Zugliani Toniato³⁹⁶ | Ignasi Torre¹⁵⁵ | Marcos Adriano Tortato⁸² | Kumiko Totsu²⁵⁹ | Andrew Trant³⁹⁷ | Robert R. Twilley³³³ | Hirokazu Urabe³⁹⁸ | Pierre Valade³⁹⁹ | Nelson Valdivia^{400,401} | Martha Isabel Vallejo⁴⁰² | Thomas J. Valone⁴⁰³ | Jan Vanaverbeke¹⁰⁷ | Tiago Silveira Vasconcelos⁴⁰⁴ | Teppo Vehanen²²⁰ | Fábio Venturoli⁴⁰⁵ | Hans M. Verheye⁴⁰⁶ | Hendrik Jannes Wietse Vermeulen³³⁸ | Arne Verstraeten²⁰³ | Marcelo Vianna⁴⁰⁷ | Rui Vieira^{408,409} | João Paulo Santos Vieira-Alencar⁴¹⁰ | Marc Vilella¹⁵⁵ | Jean Ricardo Simões Vitule⁴¹¹ | Lien Van Vu^{412,413}

Robert B. Waide⁴¹⁴  | Paige S. Warren⁴¹⁵  | Joseph Paul Wayman²⁶⁰  | Sara L. Webb^{416,417} | Benjamin Weigel^{60,418}  | Ellen A. R. Welti⁴¹⁹  | Fritha West^{359,420}  | Fulgor Westermann⁴²¹ | Matthew A. Whalen⁴²²  | Ethan P. White¹²⁸  | Claire E. Widdicombe⁴²³  | Richard Williams⁴²⁴ | Mark Williamson⁴²⁵ | Michael R. Willig³¹⁹  | Sonja Wipf³³⁵  | Eric J. Woehler⁴²⁶  | Alje Woldering³³⁸ | Kerry D. Woods^{427,428}  | Wu-Bing Xu^{5,6,429}  | Ruthy Yahel⁴³⁰  | Zeren Yang¹ | Kyle J. A. Zawada⁴³¹  | Camila Zornosa-Torres³⁹⁵  | Assaf Zvuloni²²⁸

Correspondence: BioTIME core Team (biotimeproj@st-andrews.ac.uk)

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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 organisational 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

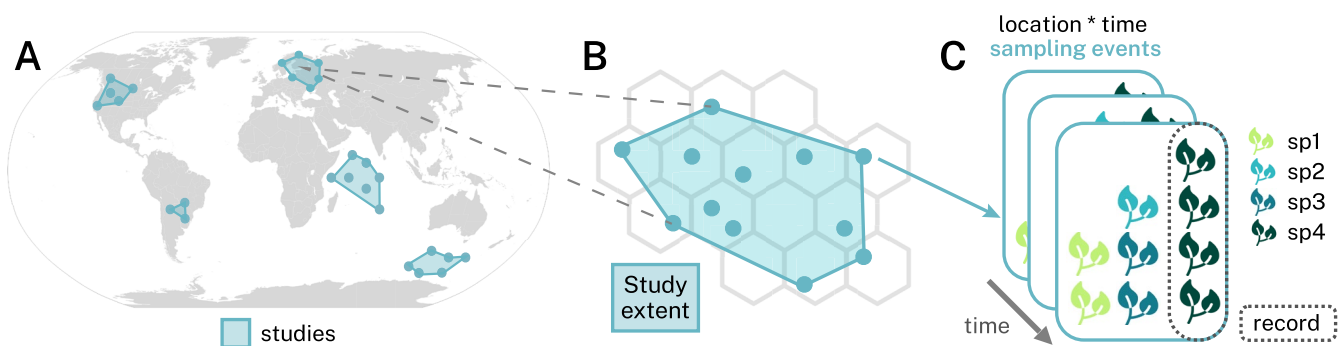


FIGURE 1 | Hierarchical structure of the BioTIME database. (A) Studies are defined by a sampling methodology which is constant over time, and have a minimum of one site and two sampling events in different years, with at least one sampling location each. (B) Study spatial extent was determined by the 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).

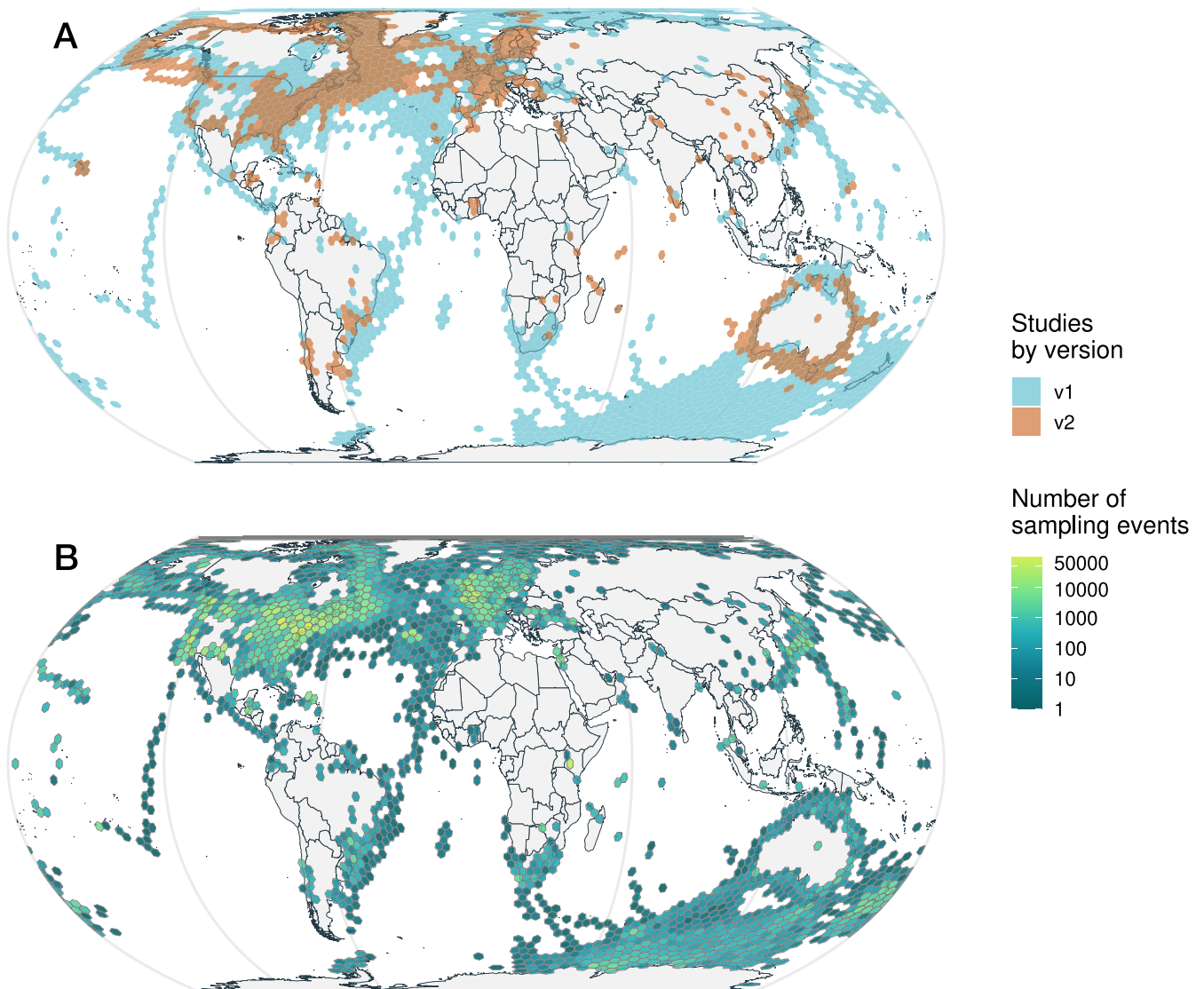


FIGURE 2 | Map showing BioTIME sampling locations. Each grid cell is approximately 75,000 km². Panel A shows the geographic distribution of studies added to BioTIME version 2.0. Panel B shows the spatial density of sampling events in version 2.0 of the database.

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 *worms* 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 *worms* 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

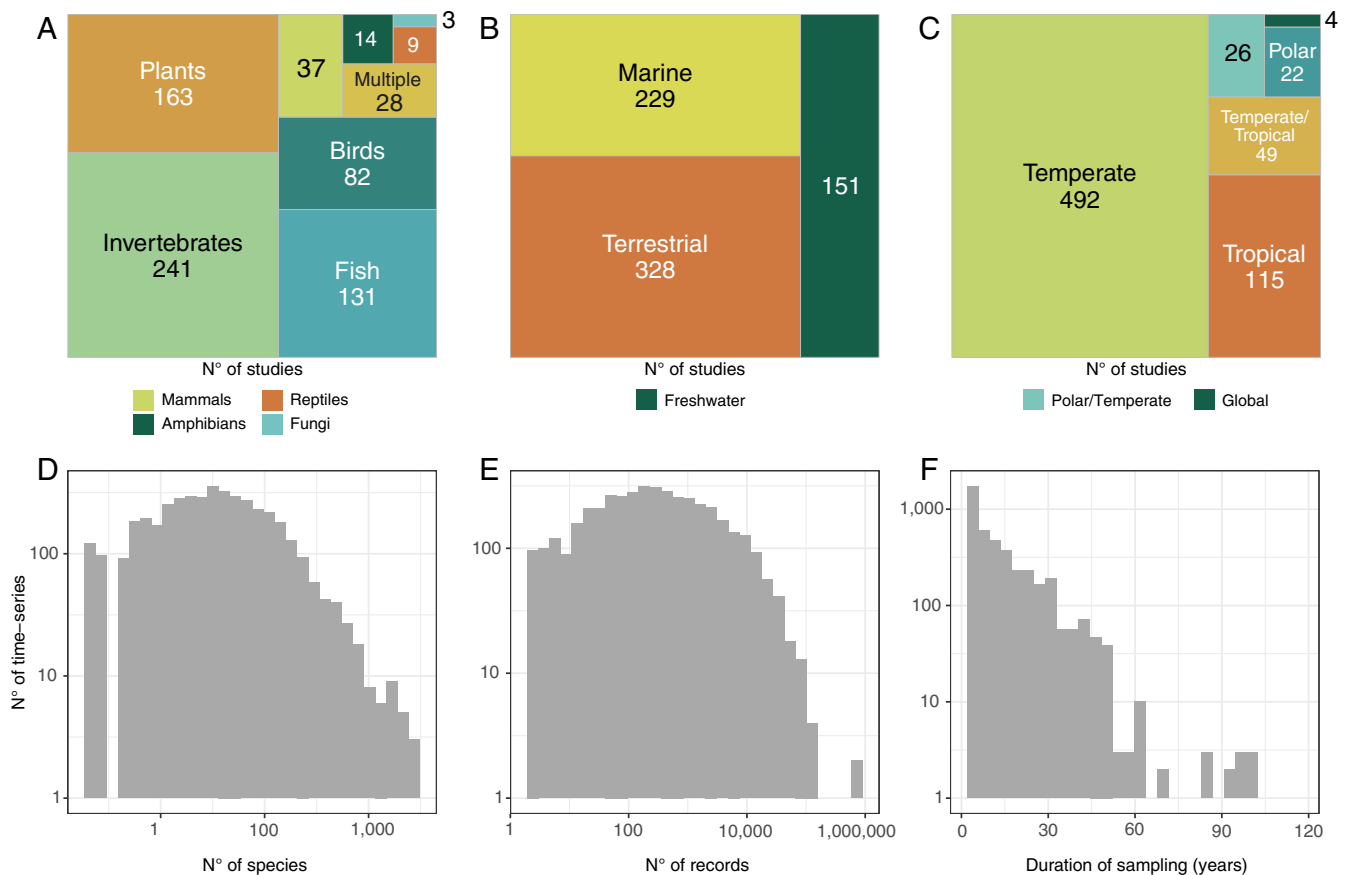


FIGURE 3 | Plots illustrating the proportion of studies that fall into the different classifications of: (A) Taxa, (B) Realm and (C) Climate. (D) species richness, (E) total number of records and (E) duration of sampling across time series. Note that time series were defined using the BioTIMER package, 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 km².

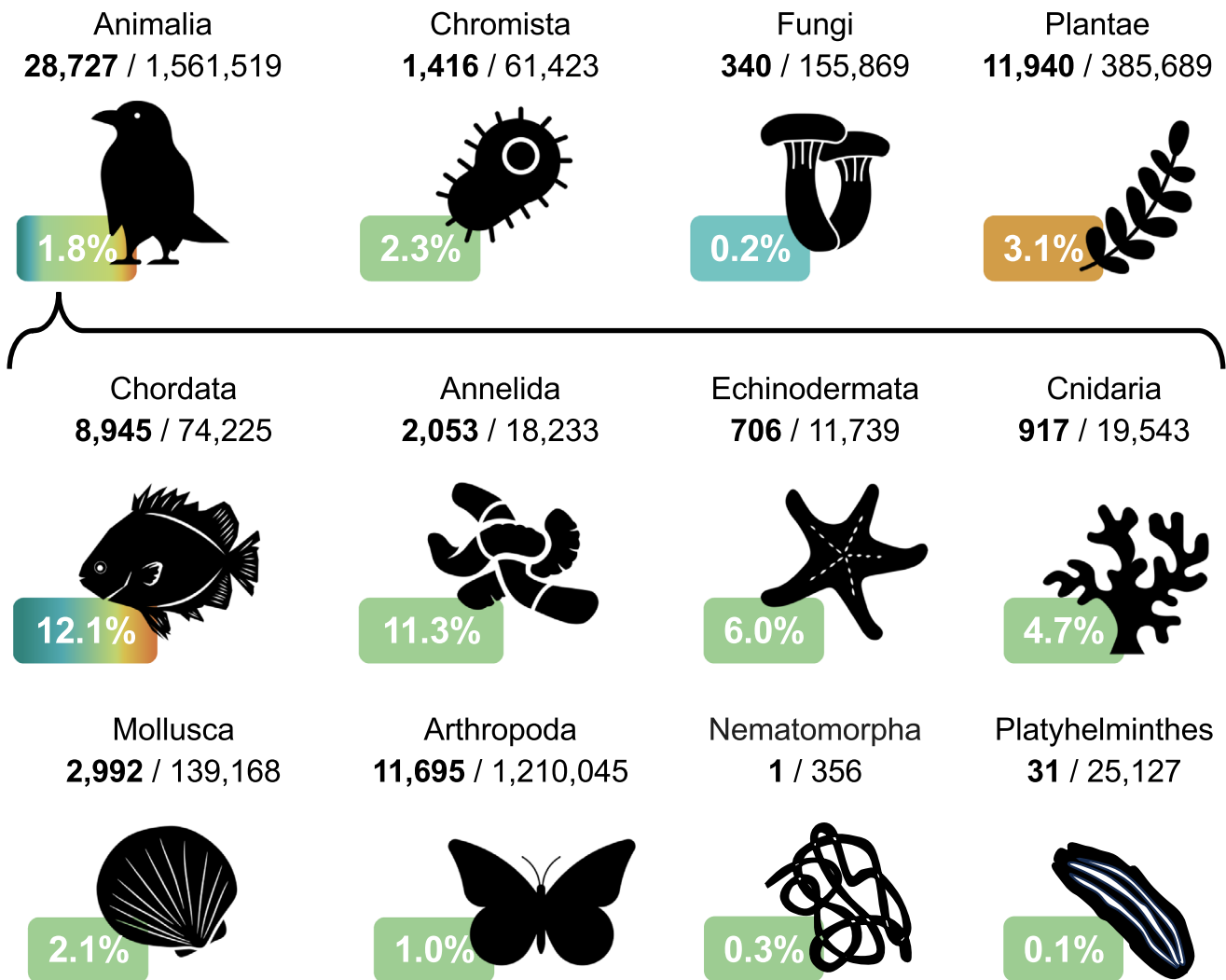


FIGURE 4 | Proportional representation of different taxonomic units in BioTIME 2.0. For each taxon, we provide the number of species included in the database relative to the number of species known to science according to the Catalogue of Life (Bánki et al. 2024) accessed on 17 December 2024. Note how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

recurred 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 km², 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.

This version of the database is made publicly available in a SQL version and as a .csv query through Zenodo ([10.5281/zenodo.10932823](https://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.

Affiliations

¹Centre for Biological Diversity, School of Biology, University of St Andrews, Fife, UK | ²MARE—Centro de Ciências do Mar e do Ambiente, Faculdade de Ciências, Universidade de Lisboa, Lisboa, Portugal | ³Research Centre for Ecological Change, Organismal and Evolutionary Biology Research Programme, Faculty of Biological and Environmental Sciences, University of Helsinki, Helsinki, Finland | ⁴Department of Biology, University of Victoria, Victoria, British Columbia, Canada | ⁵German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany | ⁶Department of Computer Science, Martin Luther University Halle-Wittenberg, Halle (Saale), Germany | ⁷Leverhulme Centre for Anthropocene Biodiversity, Department of Biology, University of York, York, UK | ⁸Department of Animal Biology and Conservation Science, University of Ghana, Accra, Ghana | ⁹Philipps Universität Marburg, Marburg, Germany | ¹⁰Department of Forest Ecology, Silva Tarouca Research Institute, Brno, Czech Republic | ¹¹School of Life Sciences, University of Technology Sydney, Sydney, New South Wales, Australia | ¹²Zoology and Animal Cell Biology Department, University of the Basque Country (UPV/EHU), Leioa, Spain | ¹³Grupo de Oceanografía de Ecosistemas, Instituto de Ciencias Marinas de Andalucía, CSIC, Campus Universitario de Puerto Real, Puerto Real, Spain | ¹⁴National Institute of Ecology, Secheon, Republic of Korea | ¹⁵African Regional Postgraduate Programme in Insect Science, University of Ghana, Accra, Ghana | ¹⁶Département de

Biologie, Université de Sherbrooke, Sherbrooke, Quebec, Canada | ¹⁷Núcleo de Conservação da Biodiversidade, Instituto de Pesquisas Ambientais, Secretaria de Meio Ambiente, Infraestrutura e Logística do Estado de São Paulo, São Paulo, Brazil | ¹⁸Department of Fisheries, Wildlife, and Conservation Sciences, Oregon State University, Corvallis, Oregon, USA | ¹⁹Institute for Marine and Antarctic Studies, Ecology & Biodiversity Centre, University of Tasmania, Hobart, Tasmania, Australia | ²⁰Graduate Program in Oceanography, Department of Oceanography, Faculty of Natural Sciences and Oceanography, University of Concepción, Concepción, Chile | ²¹Millennium Institute of Oceanography (IMO), Concepción, Chile | ²²Forest Ecology Department, KSCSTE-Kerala Forest Research Institute, Peechi, Kerala, India | ²³Department of Ecology, French Institute of Pondicherry, Pondicherry, India | ²⁴School of Psychology and Neuroscience, University of St Andrews, Fife, UK | ²⁵School of Life Sciences, Faculty of Science & Engineering, Anglia Ruskin University, Cambridge, UK | ²⁶College of Science and Engineering, James Cook University, Townsville, Queensland, Australia | ²⁷CSIRO Environment, Hobart, Tasmania, Australia | ²⁸Kerala Forest Research Institute, Peechi, Kerala, India | ²⁹Operarión Wallacea—Wallace House, Lincolnshire, UK | ³⁰Sharks in Israel, NGO, Israel | ³¹The Steinhart Museum of Natural History, Tel Aviv University, Tel Aviv, Israel | ³²Department of Biology, University of Aveiro, Aveiro, Portugal | ³³Lancaster Environment Centre, Lancaster University, Lancaster, UK | ³⁴Ecology of Fungi, Bayreuth Center of Ecology and Environmental Research (BayCEER), University of Bayreuth, Bayreuth, Germany | ³⁵Bavarian Forest National Park, Grafenau, Germany | ³⁶Environnement et Changement Climatique Canada, Quebec, Québec, Canada | ³⁷Centre for Environmental Sciences, Hasselt University, Hasselt, Belgium | ³⁸Universidade Federal do Paraná, Curitiba, Brazil | ³⁹Programa de Pós-Graduação em Ecologia e Monitoramento Ambiental, Departamento de Engenharia e Meio Ambiente, Centro de Ciências Aplicadas e Educação, Universidade Federal da Paraíba—Campus IV, Rio Tinto, Paraíba, Brazil | ⁴⁰Programa de Pós-Graduação em Ecologia e Evolução, Universidade Estadual de Feira de Santana, Feira de Santana, Bahia, Brazil | ⁴¹Estación Costera de Investigaciones Marinas, Facultad de Ciencias Biológicas, Pontificia Universidad Católica de Chile, Santiago, Chile | ⁴²USDA Forest Service, Pacific Northwest Research Station, Portland, Oregon, USA | ⁴³School of Life and Environmental Sciences, Deakin Marine Research and Innovation Centre, Deakin University, Warrnambool, Victoria, Australia | ⁴⁴School of Zoology, George S. Wise Faculty of Life Sciences, Tel Aviv University, Tel Aviv, Israel | ⁴⁵Department of Biology, University of Pisa, URL CoNISMa, Pisa, Italy | ⁴⁶Department of Biochemistry, Max Planck Institute for Chemical Ecology, Jena, Germany | ⁴⁷Operation Wallacea, Wallace House, Spilsby, UK | ⁴⁸USDA-ARS Range Management Research Unit, Jornada Experimental Range, Las Cruces, New Mexico, USA | ⁴⁹Department of Forest Ecosystems and Society, Oregon State University, Corvallis, Oregon, USA | ⁵⁰Department of Biological and Environmental Sciences, University of Gothenburg, Gothenburg, Sweden | ⁵¹Gothenburg Global Biodiversity Centre, Gothenburg, Sweden | ⁵²Faculty of Biology and Environmental Protection, Department of Invertebrate Zoology and Hydrobiology, University of Lodz, Lodz, Poland | ⁵³Department of Biological Sciences, Bridgewater State University, Bridgewater, Massachusetts, USA | ⁵⁴Instituto Español de Oceanografía (IEO-CSIC), Centro Oceanográfico de A Coruña, A Coruña, Spain | ⁵⁵Universidade Federal de Santa Catarina, Florianópolis, Brazil | ⁵⁶Universidade Do Estado de Mato Grosso, Cáceres, Brazil | ⁵⁷School of Biology and Environmental Science, University College Dublin, Dublin, Ireland | ⁵⁸Earth Institute, University College Dublin, Dublin, Ireland | ⁵⁹School of Biological Sciences, The University of Hong Kong, Hong Kong SAR, China | ⁶⁰Environmental and Marine Biology, Faculty of Science and Engineering, Åbo Akademi University, Åbo, Finland | ⁶¹Institute for Alpine Environment, EURAC Research, Bozen, Italy | ⁶²Institute for Marine and Antarctic Studies, Australian Antarctic Partnership Program, Australian Antarctic Division, Hobart, Tasmania, Australia | ⁶³The James Hutton Institute, Aberdeen, UK | ⁶⁴Coastal Research Center, Marine Science Institute, University of California,

Santa Barbara, California, USA | ⁶⁵Martin Luther University Halle-Wittenberg, Institute of Biology/Geobotany and Botanical Garden, Halle (Saale), Germany | ⁶⁶ESALQ University of São Paulo, LERF (Laboratório de Ecologia e Restauração Florestal), Piracicaba, Brazil | ⁶⁷Museum National d'Histoire Naturelle, Paris, France | ⁶⁸CNAM Intechmer, LUSAC, Tourlaville, France | ⁶⁹Programa de Pós-Graduação em Ecologia e Recursos Naturais—UFScar, São Paulo, Brazil | ⁷⁰Department of Biology, University of Oxford, Oxford, UK | ⁷¹Universidade Federal do Rio de Janeiro, Instituto de Biologia, Laboratório de Ecologia de Peixes, Rio de Janeiro, Brazil | ⁷²ASTRE, CIRAD, INRA, MUSE, University of Montpellier, Montpellier, France, Forêts et Sociétés, Univ Montpellier, CIRAD, Montpellier, France | ⁷³Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada | ⁷⁴Department of Environmental and Prevention Sciences, University of Ferrara, Ferrara, Italy | ⁷⁵Institute of Environment, Florida International University, Miami, Florida, USA | ⁷⁶Santa Catarina State University—UDESC, Florianópolis, Brazil | ⁷⁷Programa de Pós Graduação em Biodiversidade Animal: Universidade Federal de Santa Maria, Santa Maria, Brazil | ⁷⁸Biogeography and Global Change Department, National Museum of Natural Sciences, CSIC, Madrid, Spain | ⁷⁹Kerala Forest Research Institute, Peechi, Kerala, India | ⁸⁰Department of Environmental Studies and Sciences, Skidmore College, Saratoga Springs, New York, USA | ⁸¹Biodiversity Research Center, Academia Sinica, Taipei, Taiwan | ⁸²Instituto Tabuleiro, Florianópolis, Santa Catarina, Brazil | ⁸³Mokpo National University, Muan, Jeonnam, South Korea | ⁸⁴New Mexico State University, Las Cruces, New Mexico, USA | ⁸⁵USDA-ARS-Jornada Experimental Range, Las Cruces, New Mexico, USA | ⁸⁶U.S. Geological Survey, Fort Collins Science Center, Fort Collins, Colorado, USA | ⁸⁷Department of Environmental Sciences, Universidade Federal de São Carlos, Sorocaba, Brazil | ⁸⁸St. Andrews Biological Station, Fisheries and Oceans Canada, St. Andrews, New Brunswick, Canada | ⁸⁹Hornsby Shire Council, Hornsby, New South Wales, Australia | ⁹⁰Marine Biology Research Group, Ghent University, Gent, Belgium | ⁹¹Conservation Science Partners, Truckee, California, USA | ⁹²Department of Arctic and Marine Biology, UiT-The Arctic University of Norway, Tromsø, Norway | ⁹³Systems Ecology, A-LIFE, Vrije Universiteit, Amsterdam, the Netherlands | ⁹⁴Office Français de la Biodiversité (OFB), DSUED, France | ⁹⁵AZTI Marine Research Division, Basque Research and Technology Alliance (BRTA), Sukarrieta, Spain | ⁹⁶Unaffiliated | ⁹⁷National Institute of Water and Atmospheric Research (NIWA), Auckland, New Zealand | ⁹⁸Oceans Institute, University of Western Australia, Crawley, Western Australia, Australia | ⁹⁹Universidade Estadual Paulista (Unesp), Instituto de Biociências, Rio Claro, Brazil | ¹⁰⁰Department of Conservation Biology, University of Goettingen, Goettingen, Germany | ¹⁰¹School of Science, Edith Cowan University, Joondalup, Western Australia, Australia | ¹⁰²Department of Biological Sciences, Old Dominion University, Norfolk, Virginia, USA | ¹⁰³Asociación Bogotana de Ornitología, Colombia | ¹⁰⁴Department of Life Sciences, The University of the West Indies, St Augustine, Trinidad and Tobago | ¹⁰⁵Department of Biogeography and Global Change, Museo Nacional de Ciencias Naturales (MNCN-CSIC), Madrid, Spain | ¹⁰⁶Departamento de Zoología, Facultad de Ciencias, Universidad de Granada, Granada, Spain | ¹⁰⁷Royal Belgian Institute of Natural Sciences (RBINS), Brussels, Belgium | ¹⁰⁸Semillero de Investigación en Ecofisiología y Biogeografía de Vertebrados, Grupo de investigación en Biodiversidad y Desarrollo Amazónico (BYDA), Centro de Investigaciones Amazónicas Macaigual—César Augusto Estrada González, Universidad de la Amazonia, Florencia, Caquetá, Colombia | ¹⁰⁹Departamento de Ecologia, Instituto de Biociências, Universidade de São Paulo, São Paulo, Brazil | ¹¹⁰School of Life and Environmental Sciences, The University of Sydney, Darlington, New South Wales, Australia | ¹¹¹Department of Biology, Maynooth University, Co. Kildare, Ireland | ¹¹²Cetacean Research & Rescue Unit, Banff, UK | ¹¹³Centre for Ecology & Conservation, University of Exeter, Cornwall, UK | ¹¹⁴Smithsonian MarineGEO, Smithsonian Environmental Research Center, Edgewater, Maryland, USA | ¹¹⁵Joint Nature Conservation Committee, Aberdeen, UK | ¹¹⁶Instituto de

Pesquisas Ambientais, Universidade Estadual de Campinas, Campinas, Brazil | ¹¹⁷Centre for Environmental and Climate Science, Lund University, Lund, Sweden | ¹¹⁸Arizona State University, Central Arizona-Phoenix Long-Term Ecological Research, Tempe, Arizona, USA | ¹¹⁹Ruppin Academic Center, University of Haifa, Haifa, Israel | ¹²⁰Institute for Marine and Antarctic Studies, University of Tasmania, Hobart, Tasmania, Australia | ¹²¹Geography and Environment, Loughborough University, Loughborough, UK | ¹²²National Oceanic and Atmospheric Administration Great Lakes Environmental Research Laboratory, Muskegon, Michigan, USA | ¹²³Norwegian Institute for Nature Research (NINA), Tromsø, Norway | ¹²⁴Institute of Arctic and Alpine Research, University of Colorado, Boulder, Colorado, USA | ¹²⁵Department of Ecology and Evolutionary Biology, University of Colorado, Boulder, Colorado, USA | ¹²⁶Institute of Marine and Antarctic Studies (IMAS), Battery Point, Tasmania, Australia | ¹²⁷Australian Antarctic Program Partnership (AAPP), Hobart, Tasmania, Australia | ¹²⁸Department of Wildlife Ecology and Conservation, University of Florida, Gainesville, Florida, USA | ¹²⁹Instituto Milenio de Oceanografía, Departamento de Oceanografía, Universidad de Concepción, Concepción, Chile | ¹³⁰Universität Hamburg Fachbereich Biologie Institut für Zell-Und Systembiologie der Tiere Martin-Luther-King-Platz, Hamburg, Germany | ¹³¹Migratory Bird Center, Smithsonian's National Zoo and Conservation Institute, Washington, DC, USA | ¹³²CSIRO Environment, Queensland Biosciences Precinct, St Lucia, Queensland, Australia | ¹³³Centre for Marine Science and Innovation, School of Biological, Earth and Environmental Sciences, University of New South Wales, Sydney, New South Wales, Australia | ¹³⁴School of Environment, University of Queensland, Brisbane, Queensland, Australia | ¹³⁵Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Sofia, Bulgaria | ¹³⁶Terrestrial Ecology Research Group, Department of Life Science Systems, School of Life Sciences, Technical University of Munich, Freising, Germany | ¹³⁷Instituto Ambiental Brüderthal, Brusque, Brazil | ¹³⁸Re.Green, Piracicaba, Brazil | ¹³⁹Center of Biological Sciences, Department of Animal and Plant Biology, State University of Londrina, Londrina, Brazil | ¹⁴⁰Biological Dynamics of Forest Fragments Project, National Institute for Amazonian Research and Smithsonian Tropical Research Institute, Manaus, Brazil | ¹⁴¹Instituto de Ecología, A.C., Red de Ecoetología, Mexico | ¹⁴²Department of Biological Sciences, Simon Fraser University, Burnaby, British Columbia, Canada | ¹⁴³School of Ocean and Earth Science, National Oceanography Centre, Southampton, University of Southampton, Southampton, UK | ¹⁴⁴CIBIO-InBIO, Research Centre in Biodiversity and Genetic Resources, University of Porto, Vairão, Portugal | ¹⁴⁵BIOPOLIS Program in Genomics, Biodiversity and Land Planning, CIBIO, Vairão, Portugal | ¹⁴⁶Instituto Argentino de Oceanografía (IADO-CONICET), Universidad Nacional del Sur (UNS), Bahía Blanca, Argentina | ¹⁴⁷Treswell Wood Integrated Population Monitoring Group (TWIG), Retford, United Kingdom | ¹⁴⁸Lab of Vegetation Ecology, Universidade Estadual Paulista (UNESP), Instituto de Biociências, Rio Claro, Brazil | ¹⁴⁹Environment and Climate Change Canada, Canada | ¹⁵⁰SUMATRA Inteligência Ambiental, Lages, Brazil | ¹⁵¹Departamento de Entomologia e Acarologia, Escola Superior de Agricultura Luiz de Queiroz, Universidade de São Paulo (USP), Piracicaba, Brazil | ¹⁵²Liverpool John Moores University, School of Biological and Environmental Sciences, Liverpool, UK | ¹⁵³Department of Plant Protection, UNESP, Ilha Solteira, Brazil | ¹⁵⁴Polar Oceans Research Group, Sheridan, Montana, USA | ¹⁵⁵BiBio Research Group, Natural Sciences Museum of Granollers, Granollers, Spain | ¹⁵⁶Department of Integrative Biology, University of Guelph, Guelph, Ontario, Canada | ¹⁵⁷Channel Islands National Park, Ventura, California, USA | ¹⁵⁸School of Geosciences, The University of Edinburgh, Edinburgh, UK | ¹⁵⁹Natural History Museum, London, UK | ¹⁶⁰GRECO, Institute of Aquatic Ecology, University of Girona, Girona, Spain | ¹⁶¹Institut de Ciències del Mar-CSIC, Barcelona, Spain | ¹⁶²CNRS, IRD, MIO, Université de Toulon, Aix Marseille Univ, Marseille, France | ¹⁶³National Oceanography Centre, Southampton, UK | ¹⁶⁴Department of Biological, Geological, and Environmental Sciences (BiGeA), University of Bologna, Bologna, Italy | ¹⁶⁵Université

du Québec en Outaouais, Gatineau, Québec, Canada | ¹⁶⁶University of Tennessee, Knoxville, Tennessee, USA | ¹⁶⁷Canadian Wildlife Service, Environment and Climate Change, Sackville, Canada | ¹⁶⁸Leibniz Centre for Agricultural Landscape Research (Germany), Müncheberg, Germany | ¹⁶⁹Hawai'i Institute of Marine Biology, University of Hawai'i at Mānoa, Honolulu, Hawai'i, USA | ¹⁷⁰Departament Evolutionary Biology, Ecology and Environmental Sciences, Universitat de Barcelona (UB), Barcelona, Spain | ¹⁷¹Institut de Recerca de la Biodiversitat (IRBio), Universitat de Barcelona (UB), Barcelona, Spain | ¹⁷²Department of Environment, Yukon Parks, Inuvik, Northwest Territories, Canada | ¹⁷³Sefaz/SP, São Paulo, Brazil | ¹⁷⁴USDA Forest Service Research and Development, Río Piedras, Puerto Rico | ¹⁷⁵MG Consulting, Yukon, Northwest Territories, Canada | ¹⁷⁶Ecology and Zoology Department, Federal University of Santa Catarina, Florianópolis, Santa Catarina, Brazil | ¹⁷⁷School of Ocean Sciences, Bangor University, Bangor, UK | ¹⁷⁸Warnell School of Forestry & Natural Resources, University of Georgia, Athens, Georgia, USA | ¹⁷⁹Department of River Ecology and Conservation, Senckenberg Research Institute and Natural History Museum Frankfurt, Frankfurt am Main, Germany | ¹⁸⁰Faculty of Biology, University of Duisburg-Essen, Duisburg, Germany | ¹⁸¹Cetacean Research and Rescue Unit, Banff, UK | ¹⁸²USDA-ARS, Jornada Experimental Range, Las Cruces, New Mexico, USA | ¹⁸³Depth of Biology Memorial University, St. John's, Newfoundland, Canada | ¹⁸⁴National Institute of Water and Atmospheric Research, Christchurch, New Zealand | ¹⁸⁵Departamento de Oceanografía, Instituto Milenio de Oceanografía (IMO), Facultad de Ciencias Naturales y Oceanográficas, Universidad de Concepción, Concepción, Chile | ¹⁸⁶Universidade Do Estado de Santa Catarina, Lages, Brazil | ¹⁸⁷Department of Aquatic Environment and Quality, Flanders Research Institute for Agriculture, Fisheries and Food, Oostende, Belgium | ¹⁸⁸Norwegian Institute for Nature Research, Trondheim, Norway | ¹⁸⁹Cornell Biological Field Station, Cornell University, Ithaca, New York, USA | ¹⁹⁰Biology Department, Grand Valley State University, Allendale, Michigan, USA | ¹⁹¹Department of Biological Sciences, Dartmouth College, Hanover, New Hampshire, USA | ¹⁹²James Cook University, Townsville, Queensland, Australia | ¹⁹³Department of Biogeography and Global Change, Museo Nacional de Ciencias Naturales (MNCN-CSIC), Madrid, Spain | ¹⁹⁴Institute of Oceanography, National Taiwan University, Taipei, Taiwan | ¹⁹⁵Monterey Bay Aquarium Research Institute, Moss Landing, California, USA | ¹⁹⁶Finnish Environment Institute (SYKE), Nature Solutions, Helsinki, Finland | ¹⁹⁷Department of Biology, University of North Carolina, Chapel Hill, North Carolina, USA | ¹⁹⁸Environment, Energy and Ecology Program, University of North Carolina, Chapel Hill, North Carolina, USA | ¹⁹⁹University of Ghana, Hynes & Associates International, Western University, London, Canada | ²⁰⁰Office Français de la Biodiversité, Direction Régionale Bretagne, Cesson-Sévigné, France | ²⁰¹Instituto de Pesquisas Ambientais, São Paulo, Brazil | ²⁰²Chiba Prefectural Environmental Research Center, Tokyo Bay, Japan | ²⁰³Research Institute for Nature and Forest (INBO), Brussels, Belgium | ²⁰⁴School of Biological Sciences, Georgia Institute of Technology, Atlanta, Georgia, USA | ²⁰⁵Department of Wildlife, Fish and Environmental Studies, Swedish University of Agricultural Sciences, Umeå, Sweden | ²⁰⁶Geography, College of Earth, Ocean, and Atmospheric Sciences, Oregon State University, Corvallis, Oregon, USA | ²⁰⁷Institute of Biology, University of Latvia, Riga, Latvia | ²⁰⁸Institute of Biology, University of Latvia, Riga, Latvia | ²⁰⁹Department of Zoology and Animal Ecology, Faculty of Biology, University of Latvia, Riga, Latvia | ²¹⁰Yokohama National University, Yokohama, Japan | ²¹¹National Science Foundation's McMurdo Dry Valley's Long-Term Ecological Research Project (NSF McMurdo Dry Valley LTER), Institute of Arctic and Alpine Research (INSTAAR), College of Engineering, University of Colorado, Boulder, Colorado, USA | ²¹²Scottish Oceans Institute, School of Biology, University of St. Andrews, St Andrews, UK | ²¹³Shetland Oil Terminal Environmental Advisory Group (SOTEAG), St Andrews, UK | ²¹⁴Faculty of Environmental Sciences and Natural Resource Management, Norwegian University of Life Sciences, Ås, Norway | ²¹⁵Northwest

German Forest Research Institute, Göttingen, Germany | ²¹⁶Department of Community Ecology, Helmholtz Centre for Environmental Research—UFZ, Halle (Saale), Germany | ²¹⁷Flanders Marine Institute (VLIZ), Oostende, Belgium | ²¹⁸Institute of Marine Research, Flødevigen, Norway | ²¹⁹Centre for Coastal Research (CCR), Department of Natural Sciences, University of Agder, Kristiansand, Norway | ²²⁰Natural Resources Institute Finland (Luke), Helsinki, Finland | ²²¹Department of Invasion Ecology, Czech Academy of Sciences, Institute of Botany, Průhonice, Czech Republic | ²²²Field Station Fabrikschleichach, Department of Animal Ecology and Tropical Biology Biocenter, University of Würzburg, Rauhenebrach, Germany | ²²³Industry-Academy Cooperation Division, National Museum of Marine Science and Technology, Keelung, Taiwan | ²²⁴Taiwan Association for Marine Environmental Education, Taipei, Taiwan | ²²⁵Channel Islands National Park, National Park Service, Ventura, California, USA | ²²⁶Centre de Formation et de Recherche sur les Environnements Méditerranéens, Université de Perpignan Via Domitia—CNRS, Perpignan, France | ²²⁷University of Aberdeen School of Biological Sciences, University of Aberdeen, Aberdeen, UK | ²²⁸Israel Nature and Parks Authority, Jerusalem, Israel | ²²⁹Department of Natural Resources and Environmental Sciences, University of Illinois, Urbana, Illinois, USA | ²³⁰California Department of Food and Agriculture, Sacramento, California, USA | ²³¹University of Maryland Center for Environmental Science, Cambridge, Maryland, USA | ²³²Plants and Ecosystems, University of Antwerp, Antwerp, Belgium | ²³³Ecology & Biodiversity, University of Utrecht, Utrecht, the Netherlands | ²³⁴Departamento de Ciências Biológicas, ESALQ, Universidade de São Paulo, Piracicaba, Brazil | ²³⁵Programa de Pós-Graduação em Ecologia, Biology Institute, Federal University of Rio de Janeiro, Rio de Janeiro, Brazil | ²³⁶Universidade Federal de Minas Gerais, Minas Gerais, Brazil | ²³⁷University of British Columbia, Vancouver, British Columbia, USA | ²³⁸CREAF, Univ Autònoma Barcelona, Barcelona, Spain | ²³⁹Western EcoSystems Technology Inc, Cheyenne, Wyoming, USA | ²⁴⁰Pós-doutorado do Programa de pós-graduação em Ecologia, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil | ²⁴¹Department of Ecology and Evolutionary Biology, Cornell Atkinson Center for Sustainability, Ithaca, New York, USA | ²⁴²Oxford Brookes University, Oxford, UK | ²⁴³Natural Sciences Museum of Granollers, Granollers, Spain | ²⁴⁴Departamento de Ecologia e Conservação, Universidade Federal de Lavras, Lavras, Brazil | ²⁴⁵AZTI, Marine Research, Basque Research and Technology Alliance (BRTA), Pasaia, Spain | ²⁴⁶NBFC, National Biodiversity Future Center, Palermo, Italy | ²⁴⁷Department of Architecture, Design and Urban Planning, University of Sassari, Sassari, Italy | ²⁴⁸Instituto Felinos do Aguai, Siderópolis, Brazil | ²⁴⁹Department of Renewable Resources, University of Alberta, Edmonton, Alberta, Canada | ²⁵⁰Programa de Pós-Graduação em Ecologia de Biomas Tropicais, Universidade Federal de Ouro Preto, Ouro Preto, Brazil | ²⁵¹South African National Biodiversity Institute, Claremont, South Africa | ²⁵²Statistics in Ecology, Environment and Conservation, Department of Statistical Sciences, University of Cape Town, Rondebosch, South Africa | ²⁵³Animal Demography Unit, Department of Biological Sciences, University of Cape Town, Rondebosch, South Africa | ²⁵⁴BirdLife South Africa, Parklands, South Africa | ²⁵⁵School of Environmental and Natural Sciences, College of Environmental Sciences and Engineering, Bangor University, Bangor, UK | ²⁵⁶Botany Department and Biodiversity Research Centre, University of British Columbia, Vancouver, British Columbia, Canada | ²⁵⁷Instituto de Investigación en Cambio Global (ICG-URJC), Universidad Rey Juan Carlos, Móstoles, Spain | ²⁵⁸Área de Biodiversidad y Conservación, Universidad Rey Juan Carlos, Móstoles, Spain | ²⁵⁹Biodiversity Division, National Institute for Environmental Studies, Japan | ²⁶⁰School of Geography, Earth and Environmental Sciences, University of Birmingham, Birmingham, UK | ²⁶¹CE3C—Centre for Ecology, Evolution and Environmental Changes/Azorean Biodiversity Group/CHANGE—Global Change and Sustainability Institute and Universidade dos Açores—Faculty of Agricultural Sciences and Environment, Angra do Heroísmo, Portugal | ²⁶²Birmingham Institute of Forest Research, University of Birmingham, Birmingham,

UK | ²⁶³Vermont Center for Ecostudies, Hartford, Vermont, USA | ²⁶⁴School of Biology and Ecology, University of Maine, Orono, Maine, USA | ²⁶⁵Mitchell Center for Sustainability Solutions, University of Maine, Orono, Maine, USA | ²⁶⁶University of Colorado-Boulder, Boulder, Colorado, USA | ²⁶⁷Mainspring Conservation Trust, Franklin, North Carolina, USA | ²⁶⁸Institute of Biology, Faculty of Medicine and Life Sciences, University of Latvia, Riga, Latvia | ²⁶⁹Northern Illinois University, University of Idaho, Moscow, Idaho, USA | ²⁷⁰School of Science, Engineering and Environment, University of Salford, Manchester, UK | ²⁷¹Department of Biology, University of Copenhagen, Copenhagen Ø, Denmark | ²⁷²Programa de Pós Graduação em Ecologia e Conservação, Universidade Federal do Paraná, Laboratório de Ecologia e Conservação, Parana, Brazil | ²⁷³Southern Indian Ocean Fisheries Agreement (SIOFA), Le Port, France | ²⁷⁴Institute of Biology of the Southern Seas (IBSS), Russian Academy of Sciences, Sevastopol, Russia | ²⁷⁵Marine Science Institute, University of California, Santa Barbara, California, USA | ²⁷⁶Geography and Environment, Loughborough University, Leicestershire, UK | ²⁷⁷Biology Department, Marine Biology Lab, Ghent University, Gent, Belgium | ²⁷⁸Universidade Federal do Pará, Belém, Brazil | ²⁷⁹Aquatic Survey & Monitoring Ltd. (ASML), Durham, UK | ²⁸⁰Shetland Oil Terminal Environmental Advisory Group (SOTEAG), St Andrews, UK | ²⁸¹Field Station Fabrikschleichach, Department of Animal Ecology and Tropical Biology, Biocenter, University of Würzburg, Rauhenebrach, Germany | ²⁸²Bavarian Forest National Park, Grafenau, Germany | ²⁸³Biology Department, Oklahoma State University, Oklahoma City, Oklahoma, USA | ²⁸⁴Wakayama Experimental Forest, Field Science Center for Northern Biosphere, Hokkaido University, Wakayama, Japan | ²⁸⁵South Australian Research and Development Institute, Flinders University, Adelaide, South Australia, Australia | ²⁸⁶World Maritime University, Malmo, Sweden | ²⁸⁷Department of Marine Sciences, University of Georgia, Athens, Georgia, USA | ²⁸⁸Department of Botany and Biodiversity Research, Faculty of Life Sciences, University of Vienna, Vienna, Austria | ²⁸⁹Department of Forest Resources Technology, Faculty of Renewable Natural Resources, Kwame University of Science and Technology, Kumasi, Ghana | ²⁹⁰University of Aberdeen, Aberdeen, UK | ²⁹¹Global Ecology Unit, CSIC-CREAF-UAB, Bellaterra, Catalonia, Spain, CREAF, Cerdanyola del Vallès, Catalonia, Spain | ²⁹²Chiba Prefectural Environmental Research Center, Tokyo Bay, Japan | ²⁹³Ocean Integrity Research, Victoria, British Columbia, Canada | ²⁹⁴School of Environmental Studies, University of Victoria, Victoria, British Columbia, Canada | ²⁹⁵School of Aquatic and Fishery Sciences, University of Washington, Seattle, Washington, USA | ²⁹⁶Lab of Movement and Population Ecology, Biosciences Institute, Federal University of Mato Grosso do Sul, Campo Grande, Brazil | ²⁹⁷University Libraries, University of Arizona, Tucson, Arizona, USA | ²⁹⁸Moscow Lomonosov State University, Moscow, Russia | ²⁹⁹Centre d'Estudis Avançats de Blanes (CEAB-CSIC), Blanes, Spain | ³⁰⁰Sección Ornitológia, Museo de La Plata, Universidad Nacional de La Plata, and Consejo Nacional de Investigaciones Científicas y Técnicas, Buenos Aires, Argentina | ³⁰¹Centre for Forest Research, Département des Sciences Biologiques, Université du Québec à Montréal, Montreal, Québec, Canada | ³⁰²Wildlife Conservation Society Indonesia Marine Program, Bogor, West Java, Indonesia | ³⁰³UMR AMAP, IRD, CIRAD, CNRS, INRA, Université de Montpellier, Montpellier, France | ³⁰⁴Ecology Department, French Institute of Pondicherry, CNRS, MEAE, Puducherry, India | ³⁰⁵University of Houston, Houston, Texas, USA | ³⁰⁶Centro de Investigación Ecológica y Aplicaciones Forestales, CSIC, Global Ecology Unit, CREAF-CSIC-UAB, Bellaterra 08193, Barcelona, Catalonia, Spain, Cerdanyola del Vallès 08193, Barcelona, Catalonia, Spain | ³⁰⁷Programa de Pós-Graduação em Ecologia e Evolução, Departamento de Ecologia, Campus Samambaia, Universidade Federal de Goiás (UFG), Goiânia, Brazil | ³⁰⁸Instituto de Investigación Marina (INMAR), Departamento de Biología, Universidad de Cádiz, Puerto Real, Spain | ³⁰⁹Norwegian Institute for Nature Research (NINA), Oslo, Norway | ³¹⁰Center for Marine Biology, University of São Paulo, São Sebastião, Brazil | ³¹¹Department of Marine Technology, Norwegian University of Science and Technology (NTNU), Trondheim, Norway | ³¹²Australian Centre of Field Robotics,

University of Sydney, Sydney, New South Wales, Australia | ³¹³Università Della Calabria, Dipartimento Biologia Ecologia Scienze Della Terra, Rende, Italy | ³¹⁴Department of Aquatic Ecology, Eawag: Swiss Federal Institute of Aquatic Science and Technology, Dübendorf, Switzerland | ³¹⁵Department of Ecology and Conservation, Federal University of Lavras, Lavras, Brazil | ³¹⁶Institut de Recherche pour le Développement (IRD), UMR ENTROPIE, Perpignan, France | ³¹⁷Department of Wildlife, Fish, and Conservation Biology, University of California, Davis, California, USA | ³¹⁸Pôle Ecohydraulique, Office Français pour la Biodiversité Institut des Mécaniques des Fluides (OFB-IMFT), Toulouse, France | ³¹⁹Institute of the Environment, Center for Environmental Sciences & Engineering, Department of Ecology & Evolutionary Biology, University of Connecticut, Storrs, Connecticut, USA | ³²⁰Department of Animal Sciences, Wageningen University, Wageningen, the Netherlands | ³²¹Intergovernmental Oceanographic Commission of UNESCO, Oostende, Belgium | ³²²School of Natural Resources and the Environment, University of Arizona, Tucson, Arizona, USA | ³²³Arizona Institute for Resilience, University of Arizona, Tucson, Arizona, USA | ³²⁴BIO5 Institute, University of Arizona, Tucson, Arizona, USA | ³²⁵Department of Ecology, Faculty of Science, Charles University, Prague, Czech Republic | ³²⁶Natural History Museum Vienna, Vienna, Austria | ³²⁷BioScales Lab, Department of Biology, University of Miami, Miami, Florida, USA | ³²⁸Institute for Global Change Biology and School of Environment and Sustainability, University of Michigan, Ann Arbor, Michigan, USA | ³²⁹Department of Forest Resources, University of Minnesota, Minneapolis, Minnesota, USA | ³³⁰Department of Ocean Sciences, Memorial University of Newfoundland, St. John's, Canada | ³³¹School of the Environment, University of Queensland, St Lucia, Queensland, Australia | ³³²Centre for Biodiversity and Conservation Science (CBCS), The University of Queensland, St Lucia, Queensland, Australia | ³³³Department of Oceanography and Coastal Sciences, College of Coast and Environment, Louisiana State University, Baton Rouge, Louisiana, USA | ³³⁴Climate Change, Extremes and Natural Hazards in Alpine Regions Research Centre, CERC, Davos Dorf, Switzerland | ³³⁵WSL Institute for Snow and Avalanche Research SLF, Davos, Switzerland | ³³⁶Department of Biological Sciences, University of São Paulo, Piracicaba, Brazil | ³³⁷Re.Green, Rio de Janeiro, Brazil | ³³⁸Willem Beijerinck Biologisch Station (WBBS) Foundation, Loon, the Netherlands | ³³⁹Departamento de Ciências Biológicas, UNESP—São Paulo State University, Campus São José do Rio Preto, Brazil | ³⁴⁰Universidad de Ciencias Aplicadas y Ambientales UDCA, Asociación Bogotana de Ornitología, Provincia de Cartagena, Colombia | ³⁴¹Department of Natural Resources and the Environment, Cornell University, New York, New York, USA | ³⁴²Subtidal Ecology Laboratory, Estación Costera de Investigaciones Marinas, Departamento de Ecología, Facultad de Ciencias Biológicas, Pontificia Universidad Católica de Chile, Santiago, Chile | ³⁴³George Mason University, Fairfax, Virginia, USA | ³⁴⁴Department of Wildlife, Fish and Conservation Biology, University of California Davis, Davis, California, USA | ³⁴⁵Center for Watershed Sciences, University of California Davis, Davis, California, USA | ³⁴⁶Environmental Sciences Department, Federal University of São Carlos (UFSCar), São Paulo, Brazil | ³⁴⁷Department of Life Sciences, Imperial College London, Berkshire, UK | ³⁴⁸Universidad Nacional Autónoma de México, Facultad de Estudios Superiores Iztacala, Tlalnepantla, Mexico | ³⁴⁹Instituto Nacional de Pesquisas da Amazônia, Manaus, Brazil | ³⁵⁰Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, Michigan, USA | ³⁵¹Departamento de Biologia Vegetal, UNICAMP, Campinas, Brazil | ³⁵²Universidade Federal de Santa Maria (UFSM), Santa Maria, Brazil | ³⁵³Department of Forestry and Environmental Science, School of Agriculture and Mineral Sciences, Shahjalal University of Science and Technology, Sylhet, Bangladesh | ³⁵⁴Biology Department, Utica University, Utica, New York, USA | ³⁵⁵Swiss Federal Institute for Forest, Snow and Landscape Research WSL, Birmensdorf, Switzerland | ³⁵⁶Department of Geosciences and Natural Resource Management, University of Copenhagen, Frederiksberg, Denmark | ³⁵⁷APEM Ltd, Stockport, UK | ³⁵⁸Australian Antarctic Program Partnership, Hobart, Tasmania,

Australia | ³⁵⁹The Whitelands Project CIC, Hampshire, UK | ³⁶⁰Professor Emeritus, Department of Ecology and Evolutionary Biology, Tulane University, New Orleans, Louisiana, USA: Visiting Scholar, Department of Biological Sciences, Dartmouth College, Hanover, New Hampshire, USA | ³⁶¹Biodiversity and Biostatistics Department, Institute of Biosciences, Sao Paulo State University (UNESP), Botucatu, Brazil | ³⁶²Laboratório de Ecologia Teórica: Integrando Tempo, Biologia e Espaço (LET.IT.BE), Departamento de Ciências Ambientais, Universidade Federal de São Carlos, Sorocaba, Brazil | ³⁶³Lancaster University, Lancaster, UK | ³⁶⁴Institute of Biosciences, São Paulo State University (UNESP), São Paulo, Brazil | ³⁶⁵School of Biological Sciences, University of Canterbury, Christchurch, New Zealand | ³⁶⁶Department of Biological Sciences and Centre for Statistics in Ecology, Environment and Conservation, University of Cape Town, Cape Town, South Africa, Fynbos Node, South African Environmental Observation Network, Centre for Biodiversity Conservation, Cape Town, South Africa | ³⁶⁷Institute of Environmental Change and Society, University of Regina, Regina, Saskatchewan, Canada | ³⁶⁸Instituto de Pesquisas Ambientais, São Paulo, Brazil | ³⁶⁹Programa de Pós-Graduação em Ecologia: Teoria, Aplicação e Valores (EcoTAV), Universidade Federal da Bahia, Instituto e Biologia, Salvador, Bahia, Brazil | ³⁷⁰Alberta Forestry and Parks, Forestry Division, Edmonton, Alberta, Canada | ³⁷¹College of Marine Science, University of South Florida, St. Petersburg, Florida, USA | ³⁷²Executive Environment Agency, Sofia, Bulgaria | ³⁷³Center for Limnology, University of Wisconsin-Madison, Madison, Wisconsin, USA | ³⁷⁴School of Environmental Studies, University of Victoria, Victoria, British Columbia, Canada | ³⁷⁵Ethica Ambiental, Vila Velha, Brazil | ³⁷⁶Ethica Ambiental, Universidad Nacional de Colombia, Bogotá DC, Colombia | ³⁷⁷University of Applied Sciences Trier, Environmental Campus Birkenfeld, Hoppstädten-Weiersbach, Germany | ³⁷⁸Reef Life Survey Foundation, Battery Point, Tasmania, Australia | ³⁷⁹Laboratório de Ecologia/CERNA, Universidade Estadual de Mato Grosso do Sul (UEMS), Dourados, Brazil | ³⁸⁰The University of British Columbia, Vancouver, British Columbia, Canada | ³⁸¹Data Analytics Program, Denison University, Granville, Ohio, USA | ³⁸²Natural Resources Institute Finland, Oulu, Finland | ³⁸³University of New South Wales, Sydney, New South Wales, Australia | ³⁸⁴Sydney Institute of Marine Science, Mosman, New South Wales, Australia | ³⁸⁵Institute for Marine and Antarctic Studies, Australian Antarctic Program Partnership, Battery Point, Tasmania, Australia | ³⁸⁶Department of Forest Entomology, Forestry and Forest Products Research Institute, Ibaraki, Japan | ³⁸⁷Centre de Recherche sur la Biodiversité et l'Environnement (CRBE), Université de Toulouse, CNRS, IRD, Toulouse INP, Université Toulouse 3—Paul Sabatier (UT3), Toulouse, France | ³⁸⁸Museum National d'Histoire Naturelle, Station Marine de Dinard, CRESCO, Dinard, France | ³⁸⁹Department of Biology, University of North Carolina Greensboro, Greensboro, North Carolina, USA | ³⁹⁰Department of Watershed Sciences, Ecology Center, Utah State University, Logan, Utah, USA | ³⁹¹Swiss Federal Institute for Forest, Snow and Landscape Research WSL, Birmensdorf, Switzerland | ³⁹²Hessian Agency for Nature Conservation, Environment and Geology, Biodiversity Center, Giessen, Germany | ³⁹³Czech Academy of Sciences, Biology Centre, Institute of Entomology, České Budějovice, Czech Republic | ³⁹⁴Illinois Natural History Survey, Prairie Research Institute, University of Illinois, Champaign, Illinois, USA | ³⁹⁵Universidade Estadual de Campinas (Unicamp), Campinas, Brazil | ³⁹⁶Instituto de Pesquisas Ambientais, São Paulo, Brazil | ³⁹⁷School of Environment, Resources and Sustainability, University of Waterloo, Waterloo, Ontario, Canada | ³⁹⁸Salmon and Freshwater Fisheries Research Institute, Hokkaido Research Organization, Eniwa, Japan | ³⁹⁹Ocea Consult, Saint Pierre, La Réunion, France | ⁴⁰⁰Instituto de Ciencias Marinas y Limnológicas, Facultad de Ciencias, Universidad Austral de Chile, Valdivia, Chile | ⁴⁰¹Centro FONDAP de Investigación de Dinámicas de Ecosistemas Marinos de Altas Latitudes (IDEAL) Instituto de Ciencias Ambientales y Evolutivas, Universidad Austral de Chile, Valdivia, Chile | ⁴⁰²Universidad Militar Nueva Granada, Programa de Biología Aplicada, Grupo de Investigación Diversitas, Bogotá, Colombia | ⁴⁰³Department of Biology, Saint Louis University, Saint

Louis, Missouri, USA | ⁴⁰⁴Departamento de Ciências Biológicas, Universidade Estadual Paulista (UNESP), Bauru, Brazil | ⁴⁰⁵Escola de Agronomia, Universidade Federal de Goiás, Goiânia, Brazil | ⁴⁰⁶Department of Biological Sciences, University of Cape Town, Cape Town, South Africa | ⁴⁰⁷Instituto de Biologia, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil | ⁴⁰⁸Centre for Environment, Fisheries & Aquaculture Science, Lowestoft Laboratory, Suffolk, UK | ⁴⁰⁹School of Environmental Sciences, University of East Anglia, Norwich, UK | ⁴¹⁰Centro de Ciências Naturais e Humanas, Universidade Federal Do ABC (UFABC), São Bernardo do Campo, Brazil | ⁴¹¹Laboratório de Ecologia e Conservação, Setor de Tecnologia, Universidade Federal Do Paraná, Curitiba, Brazil | ⁴¹²Vietnam National Museum of Nature, Vietnam Academy of Science and Technology (VAST), Hanoi, Vietnam | ⁴¹³Graduate University of Science and Technology, Vietnam Academy of Science and Technology (VAST), Hanoi, Vietnam | ⁴¹⁴Department of Biology, University of New Mexico, Albuquerque, New Mexico, USA | ⁴¹⁵Department of Environmental Conservation, University of Massachusetts, Amherst, Massachusetts, USA | ⁴¹⁶Biology Department, Drew University, Madison, New Jersey, USA | ⁴¹⁷Environmental Studies Department, Drew University, Madison, New Jersey, USA | ⁴¹⁸INRAE, EABX, Cestas, France | ⁴¹⁹Conservation Ecology Center, Smithsonian's National zoo and Conservation Biology Institute, Front Royal, Virginia, USA | ⁴²⁰School of Geography and Sustainable Development, University of St Andrews, St Andrews, UK | ⁴²¹Landesamt für Umwelt Rheinland-Pfalz, Mainz, Germany | ⁴²²Virginia State University, Petersburg, Virginia, USA | ⁴²³Plymouth Marine Laboratory, Prospect Place, Plymouth, UK | ⁴²⁴Australian Antarctic Division, Kingston, Tasmania, Australia | ⁴²⁵Department of Biology, University of York, York, UK | ⁴²⁶Australasian Seabird Group, BirdLife Australia, Hobart, Tasmania, Australia | ⁴²⁷Natural Sciences, Bennington College, Bennington, Vermont, USA | ⁴²⁸Huron Mountain Wildlife Foundation, Big Bay, Michigan, USA | ⁴²⁹State Key Laboratory of Vegetation and Environmental Change, Institute of Botany, Beijing, China | ⁴³⁰Science Division, Israel Nature and Parks Authority, Yerushalayim, Israel | ⁴³¹School of Natural Sciences, Macquarie University, Sydney, New South Wales, Australia

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Candidate, University of British Columbia, with the assistance of the team wrote up the first draft of this README file and did data file curation—including making data summary files and completing data cleaning—as part of a Living Data Project (LDP), Canadian Institute of Ecology and Evolution, data rescue paid internship supported by NSERC CREATE (<https://www.ciee-icee.ca/ldp.html>). In addition to the team, there was cohort support from LDP graduate students and postdocs. See more here about the principles and rationale behind data rescue: Bledsoe, E. K. et al. (2022). Data rescue: saving environmental data from extinction. *Proceedings of the Royal Society B*, 289(1979), 20220938. <https://doi.org/10.1098/rspb.2022.0938>. Funding to LTT was provided by two UK Natural Environment Research Council PhD studentships (including through the Quadrant Doctoral Training Program) and a PhD studentship funded by the Saudi Royal Embassy. L.V.V. was supported by the Vietnam Ministry of Science and Technology (ĐTĐL.CN-113/21) and Earthwatch Institute. The dataset by L. Armbrrecht originated from PhD research, which was supervised by Leanne Armand, Moninya Roughan and David Raftos. We thank the NMSC for providing RV Circe and the OEH for enabling the use of RV Bombora. We thank P. Ajani and T. Ingleton for support with phytoplankton identification. Throughout the many field campaigns, we thank T. Ingleton, P. Davies, R. Gardiner, A. Cox, B. Morris, D. Kricke, A. Waite, T. Sullivan, V. Rossi, J. Wood, T. Austin, M. Doblin, C. Robinson, A. Mantovanelli, A. Schaeffer, A. Grobler, W. Godinho, A. Wilkins and S. Milburn for assistance. The field work was partially funded by a grant from the Australian Research Council, DP 1093510 (to MR). L.A. was funded by Macquarie University, the Australian Biological Resources Study, the Australian Marine Sciences Association and the Linnean Society of NSW. IMOS is supported by the Australian Government through the National Collaborative Research Infrastructure Strategy and the Super Science Initiative. L.B.C. acknowledges the contribution by the European Union's Horizon 2023 Research and Innovation Program under grant agreement no.: 101060072 ACTNOW and grant agreement no.: 101058956 Marine SABRES. RivFishTIME has been developed as part of the international working group sYNGEO—The geography of synchrony in dendritic networks kindly supported by sDiv, the Synthesis Centre of the German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, funded by the German Research Foundation (FZT 118). L. Rosselli and colleagues thank the Asociación Bogotana de Ornitología and all observers that participated in the Sabana de Bogotá Christmas Bird Counts. We also thank landowners and institutions that permitted access to the areas during the decades of CBC. Juanita Niño, Julián Pinzón and Stefany Velásquez-Licona of the UDCA helped with organising the data. For the Chingaza study, we are grateful to the Sistema de Parques Nacionales Naturales de Colombia for help with logistics and fieldwork and for granting permits. The Empresa de Acueducto de Bogotá helped with logistics in 1991–1992. For companionship and valuable help in the field, we thank P. Camargo, F. Avellaneda, J. Candil, L. G. Linares, N. Moreno, R. Pulido, L. Tellez and the students of the UDCA. C. Garzon-Sanabria helped with data organisation. We thank G. Castañeda for his enthusiastic support in transportation in the field. The Chingaza project was funded by Universidad de Ciencias Aplicadas y Ambientales UDCA, Universidad Nacional de Colombia and resources from Patrimonio Autonomo Fondo Nacional de Financiamiento para la Ciencia, la Tecnología y la Innovación, Francisco Jose de Caldas. L. Crevecoeur thanks Marc Janssen. Research Productivity Grant (CNPq) (process #302881/2022-0). Grants and fellowships were provided to L.F.T. by São Paulo Research Foundation (FAPESP #2022/11096-8) and the National Council for Scientific and Technological Development (CNPq #302834/2020-6). We thank ArcticNet, Weston Northern Grants. M. Lazarus and colleagues would like to thank the Israeli Nature and Park Authority and all present and past Belmaker laboratory members who participated in data collection. M. Kagami was funded by JSPS_KAKEN(16H02943). M. Vianna acknowledges FAPERJ (E26/200.934/2022) and CNPq (302398/2022-8) for financial support. Marcio Martins thanks the Fundação de Amparo à Pesquisa do Estado de São Paulo (Fapesp) for research grants (#2015/21259-8, #2018/14091-1 and #2020/12658-4) and Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) for research fellowships

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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.