MOSAIC: A Unified Trait Database to Complement Structured Population Models

Connor Bernard[1,†], Gabriel Silva Santos[1,2,3], Jacques A. Deere[1,4], Roberto Rodriguez-Caro[1,5], Pol Capdevila[1,6] Erik Kusch[7], Samuel J L Gascoigne[1], John Jackson[1], Roberto Salguero-Gómez[1,7,8]

[1] Department of Zoology, University of Oxford, 11a Mansfield Rd, OX13SZ, Oxford, United Kingdom

[2] Department of Ecology, Rio de Janeiro State University, Rio de Janeiro, Brazil

[3] Instituto Nacional da Mata Atlântica, INMA, Santa Teresa, Brazil.

[4] Department of Evolutionary and Population Biology, Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, 1012 WX Amsterdam, Netherlands

[5] Departamento de Biología Aplicada. Universidad Miguel Hernández. Av. Universidad, s/n, 03202 Elche (Alicante) Spain

[6] School of Biological Sciences, University of Bristol, 24 Tyndall Ave, Bristol BS8 1TQ, United Kingdom

[7] Center for Biodiversity Dynamics in a Changing World (BIOCHANGE), Section for Ecoinformatics & Biodiversity, Department of Biology, Aarhus University

[7] Centre for Biodiversity and Conservation Science, University of Queensland, St. Lucia, QLD, Australia

[8] Evolutionary Demography Laboratory, Max Plank Institute for Demographic Research, Rostock, Germany

[†] Corresponding author: connor.bernard@zoo.ox.ac.uk

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CONFLICT OF INTEREST STATEMENT

The authors report no conflicts of interest.

CONTRIBUTIONS

CB and RSG conceived the ideas; CB, RSG, GSS, JD, and PC designed the methodology; CB, GSS, JD, PC, and SJLG integrated databases; CB, GSS, and JD collected primary records data; EK led the climate data acquisition and analysis of geospatial data; and CB led the writing of the manuscript with assistance from JJ. All authors contributed critically to the drafts and gave final approval for publication.

DATA AVAILABILITY STATEMENT

The data in this paper and complete database are published open access in multiple formats (*e.g.*, .csv, .pdf, .R, .tree) on the MOSAIC website https://mosaicdatabase.web.ox.ac.uk and associated GitHub repository https://github.com/mosaicdatabase/mosaicdatabase.

Abstract (300/300)

1. The ecological sciences have joined the big data revolution. However, despite exponential growth in data availability, broader interoperability amongst datasets is still needed to unlock the potential of open access. The interface of demography and functional traits is well-positioned to benefit from said interoperability. Trait-based ecological approaches have been criticised because of their inability to predict fitness components, the core of demography; likewise, demographic approaches are data-hungry, and so using traits as ecological *shortcuts* to understanding and forecasting population viability could offer great value.
2. Here, we introduce MOSAIC, an open-access trait database that unlocks the demographic potential stored in the COMADRE, COMPADRE, and PADRINO open-access databases. MOSAIC data have been digitised and curated through a combination of existing datasets and additional taxonomic and/or trait records sourced from primary literature. In its first release, MOSAIC (v. 1.0.0) includes 14 trait fields for 300 animal and plant species: biomass, height, growth determination, regeneration, sexual dimorphism, mating system, hermaphrodism, sequential hermaphrodism, dispersal capacity, type of dispersal, mode of dispersal, dispersal classes, volancy, and aquatic habitat dependency. MOSAIC also includes species-level phylogenies for 1,359 species and population-specific climate data where locations are recorded.
3. Using MOSAIC, we highlight a taxonomic mismatch of widely used trait databases with existing structured population models. Despite millions of trait records available in open-access databases, taxonomic overlap between open-access demographic and trait databases is <5%. We identify where traits of interest to ecologists can benefit from

database integration and start to quantify traits that are poorly quantified (*e.g.,* growth determination, modularity).

4. The MOSAIC database evidences the importance of improving interoperability in open-access efforts in ecology as well as the need for complementary digitisation to fill targeted taxonomic gaps. In addition, MOSAIC highlights emerging challenges associated with the disparity between locations where different trait records are sourced.

KEYWORDS

COMADRE, COMPADRE, functional traits, gap of knowledge, integral projection model (IPM), interoperability, matrix population model (MPM), open access, open traits, PADRINO.

"I'm not interested in your data; I'm interested in merging your data with other data.
Your data will never be as exciting as what I can merge it with."
—Sir Tim Berners-Lee (co-founder of the World Wide Web)

Introduction

The ecological sciences have recently joined the big data revolution (Farley, Dawson, Goring, & Williams, 2018; Marx, 2013; Reichman, Jones, & Schildhauer, 2011). Total species distribution records measure in the hundreds of millions (Maldonado et al., 2015; Troia & McManamay, 2016). Functional trait data exist for tens of thousands of species across the globe (Díaz et al., 2016; Enquist et al., 2019; Maitner et al., 2018). Similar gains have taken place in related fields, from big omics (Field et al., 2009) to global state-of-the-art climate models (*e.g.*, ERA-5 [https://www.ecmwf.int/en/forecasts/dataset/ecmwf-reanalysis-v5]) becoming available at fine spatial and temporal resolutions suitable for biological analyses (Davy & Kusch, 2021; Hersbach et al., 2020), and from behavioural trait data (Rowcliffe, Jansen, Kays, Kranstauber, & Carbone, 2016) to population data (Global Population Dynamics Database [https://knb.ecoinformatics.org/view/doi:10.5063/AA/nceas.167.15]; Human Mortality Database (J.R. Wilmoth, K. Andreev, D. Jdanov, 2007; mortality.org); Human Fertility Database (Jasilioniene et al., 2015; humanfertility.org); AnAge Database (De Magalhães & Costa, 2009); DATLife [Max Plank Institute of Demographic Research 2022; https://datlife.org/]). We have also seen growth datasets characterising phenomena at levels of biological complexity above the organismal level, including community ecology databases (BioTime (Dornelas et al., 2018); Web of Life (Fortuna, Ortega, & Bascompote, 2014); metaCommunity Ecology: Species, Traits, Environment and Space (CESTES) (Jeliazkov et al., 2020); Environmental Data Initiative [https://environmentaldatainitiative.org/]). The growth of records in ecology datasets and complementary environmental datasets is enabling us now to test ecological theory at larger and

more complex scales. In line with open-access growth, however, there is a recognised need to improve and coordinate data standards to guide the systematic collection and management of data across different trait collection programmes (Gallagher et al., 2020; Kissling et al., 2018; Wilkinson et al., 2016).

Despite the increasing availability of biological data, combining different datasets into common analyses is often hampered by the lack of complementarity between databases. Interoperable systems reflect the transformation of constituent data types into a standardised format of spatial, temporal, and measurement scales, accounting for differences in methods (Nadrowski et al., 2013). The need to improve interoperability across datasets is demonstrated by the widescale emergence of data harmonisation initiatives across fields of ecology (*e.g.,* Culina et al., 2018; Kattge et al., 2020; Schneider et al., 2019). In the past decade, dozens of initiatives have taken shape to both centralise data from existing datasets and to improve data interoperability: standardising units, scales, and terminology for comparative purposes (Edwards, Lane, & Nielsen, 2000; Maurer, Firestone, & Scriver, 2000). Unifying data formats and streamlining their integration unlocks the potential for existing datasets to answer questions that cut across levels of biological complexity. Linking together levels of biological complexity is critical for identifying how phenomena emerge and transmit across different levels of biological organisation, upscaling and downscaling through biological systems. For example, the critical linkages between genetics and biochemistry (The ENCODE Project Consortium, 2012; http://bigg.ucsd.edu/), biochemistry and physiology (Vitousek, Johnson, & Husak, 2018), and physiology and demography (Laughlin, Gremer, Adler, Mitchell, & Moore, 2020; Swenson et al., 2020) have benefitted from dataset integration.

The limitations of global-scale datasets are shifting away from data availability and toward data interoperability. The global-scale integration of functional traits is headed in this direction. Momentum toward data integration is evidenced by recent database initiatives (*e.g.,* Guerrero-Ramírez et al., 2021) and global networks that, like the Open Trait Network (https://opentraits.org/), aim to standardise and integrate trait data across taxa (Gallagher et al., 2020). Despite major improvements in the consolidation and accessibility of trait data, there is not yet a single-source centralised database spanning behaviour, physiology, habitat, and other trait data for a wide range of species. Existing databases are often linked by taxonomy (*e.g.,* FishBase (Froese & Pauly, 2010), CoralTraits (Madin et al., 2016), MammalBase (Lintulaakso, 2013), AmphiBio (Oliveira, São-Pedro, Santos-Barrera, Penone, & Costa, 2017)); trait type (*e.g.,* TreeOfSex (The Tree of Sex Consortium 2014), TreeBase (Boettiger & Temple Lang, 2012), Xylum Functional Traits (Borghetti, Gentilesca, Colangelo, Ripullone, & Rita, 2020)); data type (*e.g.,* GBIF (https://www.gbif.org/), MOL (Jetz, Thomas, Joy, Hartmann, & Mooers, 2012), TetraDensity (Santini, Isaac, & Ficetola, 2018)); or a combination of the taxonomies and traits (WooDiv (Monnet et al., 2021), CarniDiet (Middleton, Svensson, Scharlemann, Faurby, & Sandom, 2021)). A number of other databases take a more general approach in their thematic scope, but are still constrained to a limited set of traits and taxonomy (*e.g.,* Amniote (Myhrvold et al., 2015), Pantheria (Jones et al., 2009), BIEN (Enquist, Condit, Peet, Schildhauer, & Thiers, 2016; Maitner et al., 2018), TRY (Kattge et al., 2020)). MOSAIC offers a platform that integrates databases in the remit of species with structured population models across their ecological traits.

Here, we introduce MOSAIC, a centralized database of trait data across the Tree of Life. MOSAIC is an open-access database that complements the existing demographic data available in the COMPADRE Plant Matrix Database (Salguero-Gómez et al., 2015), COMADRE Animal

Matrix Database (Salguero-Gómez et al., 2016), and the new PADRINO IPM Database (Levin et al., BioRxiv; doi: 10.1101/2022.03.02.482673; https://levisc8.github.io/RPadrino/). MOSAIC v. 1.0.0 includes 14 frequently used traits that encompass morphological, reproductive, dispersal, and habitat type attributes for some 300 species of animals and plants. Additional traits will be added in the future (see *Future Direction, below*). MOSAIC allows users to integrate structured population data to probe larger questions through the collection, curation, and complementarity of relevant contextual data.

Methods

Scope and Coverage of MOSAIC

The MOSAIC database (Version 1.0.0) includes 14 key trait records across 300 species (Fig. 1). MOSAIC is designed to provide complementary data for analysis in connection with structured population models: matrix population models (MPMs, Caswell, 2000), where state variables are discrete (*e.g.*, age (Morris et al., 2008), ontogeny/development (Smallegange, Deere, & Coulson, 2014), discrete classes of size (Crouse, Crowder, & Caswell, 1987)), and integral projection models (IPMs, Easterling, Ellner, & Dixon, 2000), where the state variables are continuous (*e.g.,* size (Jongejans, Shea, Skarpaas, Kelly, & Ellner, 2011), mass (Ozgul et al., 2010), parasite load (Metcalf, Graham, Martinez-Bakker, & Childs, 2016)). The traits included in MOSAIC 1.0.0 were identified by the MOSAIC team as a set of physical, physiological, geographic, and behavioural attributes of most immediate relevance to demographic research (see Table 1; more information at https://mosaicdatabase.web.ox.ac.uk). Traits were also selected in consideration of the lack of standardised and centralised databases for certain traits (*e.g.,* volancy, modularity, and growth indeterminacy; see Fig. 2 for trait variance and taxonomic structure of

select traits excluded from existing databases). Importantly, we note that MOSAIC is not a general dataset for analysis of functional traits, as this is available through other extensive repositories (*e.g.,* TRY (Kattge et al., 2020), BIEN (Enquist et al., 2016; Maitner et al., 2018)). Instead, the focus of MOSAIC is on providing taxonomic coverage to species with open-access structured population models available in the COMADRE (Salguero-Gómez et al., 2016), COMPADRE (Salguero-Gómez et al., 2015), and PADRINO databases (Levin et al. forthcoming) (See Fig. 3 and Fig. 4 for spatial scope and taxonomic scope with respect to structured population databases, respectively). MOSAIC provides a much-needed interoperability between existing databases that are germane to demography. By doing so, MOSAIC helps to fill critical data needs of population ecologists and functional trait ecologists (see Fig. 5 for relevant covariance structure). Although demographically motivated, MOSAIC affords opportunities for data to address novel questions more broadly across ecology, evolution, and conservation biology.

Accessing MOSAIC

A guide for downloading the MOSAIC database can be accessed on the MOSAIC portal (https://mosaicdatabase.web.ox.ac.uk). The MOSAIC database is open access and can be downloaded into R using a few lines of code (see: https://mosaicdatabase.web.ox.ac.uk/download-database), which download the MOSAIC data object as an S4 object (Rda file). The database can also be downloaded from GitHub directly as an (.Rda) or comma separated value (.csv) file and loaded into R manually.

The MOSAIC portal hosts information pages and downloadable files about the database. Users can download the *MOSAIC User Guide*, *vignettes*, and *data collection protocols* from the portal webpage (https://mosaicdatabase.web.ox.ac.uk/vignettes and https://mosaicdatabase.web.ox.ac.uk/user-guide). The *User Guide* specifies the classifications,

187 precision, and data types for each trait field. The MOSAIC *User Guide* details the metadata on the
188 structure of data for each trait (*e.g.,* species, genus, mosaic index). An updated list of the databases
189 that are directly or indirectly addressed by the MOSAIC database is maintained on the MOSAIC
190 portal.

191 **Data Sources**

192 MOSAIC is both a *meta*-database (a database of databases) and a database in its own right,
193 containing new trait records from primary literature (Fig. 1). The MOSAIC database contains
194 records centralised from existing datasets where functional traits relevant to population ecologists
195 can be openly accessed and redistributed (*e.g.,* BIEN (Enquist et al., 2016; Maitner et al., 2018)).
196 The records reflected in the MOSAIC database do not encompass the entirety of the source
197 databases but are instead partial facsimiles of those databases that reflect records relevant to
198 population databases (COMADRE, COMPADRE, PADRINO). MOSAIC has three major
199 components: (1) trait records sourced from existing databases (22%); (2) trait records newly
200 procured through searching the primary literature (71%); and (3) trait record markers that direct
201 users to additional records that are not included in the MOSAIC database (7%). MOSAIC trait
202 markers exist for one of two reasons: the database containing the records of interest does not allow
203 records to be accessed or limits redistribution rights behind individual registration and/or specific
204 use applications; or records in other databases contain multiple records for a species, which do not
205 currently fit within the data structure of version 1.0.0 of MOSAIC (see *Future Targets for*
206 *MOSAIC*).

207 In addition to identifying whether a trait record is new, the "MOSAIC" attribute field also
208 identifies whether the attribute field (*i.e.,* trait name) is part of an existing database. For example,
209 the MOSAIC field might indicate that a record for specific leaf area is new for a specific species,

and also that the attribute is part of databases such as TRY (Kattge et al., 2020) or BIEN (Enquist et al., 2016; Maitner et al., 2018). By contrast, a new species record for volancy would indicate that there are currently no databases that systematically collect data on volancy attributes and therefore that all volancy records in the MOSAIC database are new.

Organisation of Sources in MOSAIC

The MOSAIC attribute field is a factorial variable with three levels: MOSAIC-A, MOSAIC-B, and MOSAIC-C. The first of these levels, MOSAIC-A (Fig. 1), labels only records that reflect existing databases (*i.e.*, provenance of an existing data acquisition service); the second, MOSAIC-B, labels new records collected by the MOSAIC team that are in a trait field within the scope of an existing database initiative (*e.g.,* specific leaf area in BIEN); and the third, MOSAIC-C, labels new records collected by the MOSAIC team on traits for which there is not currently a database initiative centralising records. If a datum has been adopted from another dataset or database, then the relevant source is referenced in the *Database* attribute column. Note that this value will be "NA" for all MOSAIC-C records, logically. Over time, data sharing will move records in MOSAIC-B to MOSAIC-A as the MOSAIC-B traits are assimilated in the database networks that specialise on an existing trait (*i.e.,* data feedback; see Fig. 1).

Sources and Provenance of Records

Because of existing limitations on data access, some datasets cannot be transferred into MOSAIC. Where data exist outside of the MOSAIC platform, but have restricted access, the MOSAIC database directs users toward the appropriate database on a trait and taxa-specific level (see `metaMOSAIC`). The *MOSAIC User Guide* (Appendix S1) explains differences between data gaps that are yet to be reviewed and those that are true gaps (*e.g.,* volancy/flight capability of plants). Data were obtained through searching peer-reviewed records of ISI Web of Science,

Scopus, and Google Scholar using key words pertinent to the species name and trait field in question (see Appendix S2 for a list of keywords queried). The MOSAIC team also searched the archives of data repositories, including the Dryad digital repository (http://datadryad.org; see Appendix S3 for a complete list of repositories reviewed – to be maintained hereafter on the MOSAIC portal), and reviewed in detail journal archives that have a high occurrence of data publishing, including *Nature Scientific Data*, *Methods in Ecology and Evolution*, and *Journal of Ecology*. MOSAIC also reflects a review of data from data aggregating servers, such as the open traits network (https://opentraits.org/), the ecological data wiki (https://ecologicaldata.org/), environmental data initiative (https://environmentaldatainitiative.org/), and databases that aggregate other databases (*e.g.,* BIEN (Enquist et al., 2016; Maitner et al., 2018) and TRY (Kattge et al., 2020)). The complete set of key words used in this review is detailed in a supplement to the *User Guide* posted on the MOSAIC portal. A current list of databases reviewed in the development of MOSAIC is included in Appendix S3. Suggested data sources and key terms can be submitted through the MOSAIC data portal.

Database Navigation

The *User Guide* contains detailed information on navigating the MOSAIC R data object. In general, the data object can be queried with the syntax: `mosaic@trait.name@values[[mosaic.index]]`. In the aforementioned syntax, the `trait.name` and `mosaic.index` should reflect one trait and one or more species index values in the respective locations (*e.g.,* `mosaic@volancy@value[[93]]`). The complete set of records for a trait can be viewed and assigned by calling the trait from the mosaic object without an index specified (*e.g.,* `mosaic@volancy@value`). The mosaic index value reflects a unique identifier that can be linked from COMADRE, COMPADRE, and PADRINO through the index

field of mosaic (*e.g.,* `comadre@data$MatrixID[comadre@data$SpeciesAccepted=="Alces alces"]`). Associated metadata for each record can be queried by the following syntax: `mosaic@trait.name@metadatafield[[mosaic.index]]`. Here, the `metadatafield` should reflect one metadata element (*e.g.,* `mosaic@volancy@author[[93]]`). The complete metadata for a species can be viewed using the `mos_meta()` function or searched manually by slots, or by querying rows of the database in the comma separated value format (https://mosaicdatabase.web.ox.ac.uk/navigating-mosaic). See the *User Guide* (Appendix S1) for more information. The database is organised to be readily subsetted, including compatibility with Tidyverse package (Wikham et al. 2019) syntax (see *Navigating MOSAIC*; https://mosaicdatabase.web.ox.ac.uk/vignettes, also in Appendix S4). The MOSAIC object can be searched in `R` by taxonomy, trait, locality, duration of study, sex, and other metadata fields applicable to COMADRE, COMPADRE, and PADRINO (see *vignettes*, above, also Appendix SX). Trait values in the database are measured in standardised units of measure for each trait (Table 1). Species names are specified in conformance with the Catalogue of Life (www.catalogueoflife.org), also consistent with the COMPADRE, COMADRE, and PADRINO databases. The *User Guide* provides specific guidelines for querying fields within the data object in R and for negotiating the dataset in finer detail (https://mosaicdatabase.web.ox.ac.uk/user-guide).

Error Reporting

The MOSAIC portal has an *Error Report* page for reporting potentially erroneous records, or to query additional questions (https://mosaicdatabase.web.ox.ac.uk/suggested-additions-error-reporting; but see also FAQ: https://mosaicdatabase.web.ox.ac.uk/frequently-asked-questions).

Potential errors can be reported anonymously or with contact information (*e.g.*, name, email). Decisions on reported errors will be disclosed on the Error Report page (https://mosaicdatabase.web.ox.ac.uk/suggested-additions-error-reporting) and to the reporting party if contact information is included in the request. If it is not possible to submit errors via the portal, users can also to reach out by email to: mosaicdatabase@biology.ox.ac.uk.

Recommended Records

The MOSAIC portal has a *Recommended Records* page (https://mosaicdatabase.web.ox.ac.uk/suggestion-additions) for reporting suggested records that are not included in the MOSAIC database. Recommendations can be made with or without contact information. Contact information will be used exclusively for clarifying questions and updating the commenter when records are included. MOSAIC will report decisions on the *Recommendations Incorporated* page (https://mosaicdatabase.web.ox.ac.uk/suggestion-additions). Users may also request new data fields to be prioritised in future rollouts. Given the realities of limiting resources, The MOSAIC team will do their best to include the requested records in future versions. Likewise, we also welcome submissions of data collected by individuals via mosaicdatabase@biology.ox.ac.uk.

***metaMOSAIC*: licensed data, access limitations, and restricted redistribution of existing records and databases**

Not all datasets permit open use, dissemination, and redistribution of their trait data. Where limitations on the data collation and redistribution apply, there may be application procedures, registration, and other actions necessary for an individual to obtain access to specific trait records for analysis (*e.g., TRY*). MOSAIC centralises the metadata for datasets that do not allow data to be redistributed to help navigate to relevant data resources outside the scope of open access. Records

in limited access databases can be searched in MOSAIC by taxonomic group and by trait. MOSAIC links researchers to application materials for requesting access to those limited-access databases. The data access of licensed or non-open-access databases is stored in a data object called `metaMOSAIC` that is an extension of the MOSAIC database. The MOSAIC dataset thus provides data where it is accessible and `metaMOSAIC` guides researchers to where data exist with registration. When searching fields in the MOSAIC database, the `metaMOSAIC` adjunct dataset indicates if data are available in these ancillary sources (see *User Guide* in Appendix S1 for more information) and provide links to pertinent sources and data through the provider. `metaMOSAIC` is part of the main database object accessible through the MOSAIC portal.

Database Updates

The MOSAIC database will be updated as new data are added to the COMADRE, COMPADRE, and PADRINO databases. Updates of the MOSAIC database will account for newly discovered data sources and new literature that adds to or changes the species-level traits in the database, as well as correct errors from earlier versions. New MOSAIC versions will be released periodically with a notice published on the website, in the data object metadata, the mosaic GitHub page (https://github.com/mosaicdatabase), and through updates in associated packages in conformance with standard semantic versioning (a three-part version code reflecting major, minor, and patch updates, in respective positions). Updates will be published to the mosaic portal (https://mosaicdatabase.web.ox.ac.uk), social media (Twitter: @mosaicdatabase), and GitHub (https://github.com/mosaicdatabase). The MOSAIC portal includes a location for submission of recommendations for additions or suggested changes to the database.

Future Targets of MOSAIC

Versioning

MOSAIC database updates and version history will be posted to the MOSAIC portal in the future.

Taxonomic Scope

Future versions of MOSAIC are scheduled for expansion to include 50 core traits across some 1,500 species (the current entirety of COMPADRE, COMADRE, and PADRINO; *MOSAIC target traits*; see *User Guide* [Appendix S1]). The MOSAIC core traits list will guide the future roll-out of attributes gathered and stewarded by the MOSAIC team (available on the MOSAIC portal website; see below), but additional trait suggestions can be submitted through the online portal.

Interspecific Variation in Hierarchical Data Structures

Future versions of the MOSAIC database will adopt a hierarchical file structure that will accommodate multiple records per species. Once records for COMADRE, COMPADRE, and PADRINO are fully populated across the MOSAIC traits with mean, pooled, or other representative quantities (*e.g.,* mean leaf size for all plants or adult bodymass of animals), secondary records will be added. Existing trait databases may contain multiple records per species (see, for example, structure of COMADRE (Salguero-Gómez et al., 2016), COMPADRE (Salguero-Gómez et al., 2015), BIEN (Enquist et al., 2016; Maitner et al., 2018), TRY (Kattge et al., 2020)), although some databases host a single record per species' trait, such as age and growth rate for animals in AnAge (De Magalhães & Costa, 2009). To facilitate research into intra-specific trait variation (Albert, 2015; Messier, McGill, & Lechowicz, 2010; Siefert et al., 2015), MOSAIC provides provenance of records, whether records were subject to selection or merger (means or pooling), and fields that identify whether multiple records are known to exist. Where records for a given species were isolated from existing databases, mean values are often retrieved, and the

348 database sourcing additional data is noted in the database under the attributed field ("Additional
349 Trait Data Available" field).

350 *citMOSAIC: Citizen Science*

351 In addition to `metaMosaic`, which guides users to licenced data not reported in the
352 MOSAIC database, MOSAIC plans to roll out a database of identical structure to MOSAIC that
353 gathers information from citizen science datasets. Like MOSAIC, citMOSAIC will have three
354 components (citMOSAIC-A, citMOSAIC-B, citMOSAIC-C), reflecting the same relationship of
355 databases and fields to MOSAIC (see https://mosaicdatabase.web.ox.ac.uk/citizen-mosaic for
356 more information). citMOSAIC will be kept independent of the main MOSAIC database to avoid
357 conflation of peer reviewed literature from citizen science data. Where appropriate to use datasets
358 together, the metadata, query functionality, and design of citMOSAIC will mirror that of MOSAIC
359 to promote interoperation of databases. citMOSAIC will be downloadable from the MOSAIC
360 portal website.

361 **Cautionary Notes**

362 Records in the MOSAIC database are gathered and standardised under the protocols
363 detailed in the *User Guide* (Appendix S1; also available through the MOSAIC portal). Users
364 should be attentive to the precision, levels, and context of data in MOSAIC when used for analysis.
365 For those records in the dataset that come from multiple individuals, we present them as statistical
366 components (*e.g.,* minimum, maximum, or mean trait values). Functional traits in MOSAIC may
367 be estimated from populations studied in COMADRE, COMPADRE, PADRINO, or other
368 databases (Table S3). The potential temporal and spatial mismatch between databases that are
369 linked in an analysis merits close attention (Csergő et al., 2017). The studies in the MOSAIC
370 database also include research conducted by different investigators using independent tools,

371 technologies, sample designs, and study methods. The influence of research methods and
372 instruments on the error values in the dataset may require additional consideration for potential
373 bias, noise, and imprecision. Where more than one life history trait value exists for a given species,
374 MOSAIC users will need to determine whether averaging or selective filtering to one study is most
375 appropriate in view of the specifics of the given research question. In certain cases, trait values for
376 a species might only be available for a single st/age and therefore may not provide a complete
377 picture of the trait variation amongst st/ages. Users are encouraged to be cautious when
378 contextualising the scope of representation of the values in the database and their analyses.

379 **Representation, Variance, and Bias in MOSAIC v1.0.0**

380 MOSAIC can help to mechanistically examine the causes and correlates of demographic
381 variability across the thousands of animal and plant species housed in COMPADRE, COMADRE,
382 and PADRINO. In its version 1.0.0, MOSAIC contains a high degree of variance in trait values
383 known to shape demographic outcomes across major taxonomic groups. For example, determinant
384 growth is present for 0% of Amphibians and Birds and 100% of Bivalves, while volancy is present
385 for 0% in Reptiles, Amphibians, and Bony Fish and 77% in Birds (Fig. 2). Animal adult biomass
386 and plant height follow lognormal trait distributions (see Appendix S5). 11% of mammals are
387 indeterminate growers *vs.* 54% of reptiles and 0% birds, and 95% of mammals are monogamous
388 compared to 100% of reptiles and 20% of birds in MOSAIC. Recent studies have examined how
389 different vital rates are explained by functional traits (e.g., Carmona, Bello, Azcarate, Mason, &
390 Peco 2019; Pistón et al. 2018; Adler et al. 2014; Poorter et al. 2008). However, understanding how
391 trait variation across taxa translates to demographically influential properties remains
392 underdeveloped.

393 MOSAIC's initial release (v1.0.0) includes records for all major regions of the globe for
394 which we have structured population models (Fig.3). Nevertheless, species trait values are not
395 necessarily gathered from the same localities as population models (see *future directions* for more
396 information on systematising spatial mismatch). This is an important consideration for users of
397 MOSAIC (and more generally of trait-based approaches) wishing to bring together functional traits
398 and demographic rates, as traits and vital rates are known to vary considerably within the same
399 species across spatial scales (Violle et al. 2012; Albert et al. 2010; Bolnick et al. 2011). Moreover,
400 while there is at least one trait for each of these locations, the data density remains variable. Thus,
401 records are not necessarily representative of the global spread or the full spatial scope of MOSAIC.
402 For example, the highest complete coverage for MOSAIC traits is concentrated toward localities
403 with the with the longest-term demographic models (see COMPADRE locations associated with
404 MOSAIC records).

405 Phylogenetically, the initial release of MOSAIC is somewhat limited. Version 1.0.0 covers
406 300 of the 1,400 species currently available in COMPADRE, COMADRE and PADRINO.
407 However, MOSAIC trait data are well distributed across clades (Fig. 4). While there is not a highly
408 skewed phylogenetic concentration with respect to the existing structured population models or
409 clustering of records into small groups across the Tree of Life, phylogenetic density of MOSAIC
410 records remains low. Therefore, information from the MOSAIC database may be limited for a
411 given genus or order and, as such, should be approached with caution. In future versions of
412 MOSAIC, the phylogenetic bias is expected to diminish with more samples and stronger
413 phylogenetic representation.

414 Covariance across traits is also an important source of confound in existing analyses linking
415 traits and vital rates. Positive and negative correlations across traits that have independent

416 influences on vital rates can create apparent associations of demographic properties with traits,
417 spuriously functionalising non-functional traits (McElreath 2021). Disentangling the relevance of
418 key axes of trait variation for their demographic influences demands a clear quantification of the
419 direction and strength networks of trait associations, trade-offs, and demographic consequences.
420 Population biologists seek to understand not only how individual traits relate to different aspects
421 of demographic performance (*e.g.,* population growth rate, risk of quasi-extinction, *etc.*), but also
422 understanding how trait syndromes shape those demographic outcomes. MOSAIC presents a
423 highly varied covariance structure in trait values for the examined 300 species. For example,
424 without *a priori* expectation, indeterminate growth and regeneration traits show strong correlation
425 (r=0.51; Fig. 5), which could influence each other's effects on vital rates. The same could be argued
426 for the correlation between volancy and reproductive strategy (r=0.28 with monogamy; Fig. 5).

427 The MOSAIC database can be used as a platform to showcase the lack of overlap between
428 trait and vital rate data for the same species. This picture calls for a more systematic way address
429 global biases in ecological data quantification/collection. Even where we have complete
430 information about species in the COMADRE, COMPADRE, and PADRINO databases, we are
431 subject to the constraints and biases of those datasets, such as spatial bias toward high-GDP
432 countries and the phylogenetic bias toward temperate regional perennial plants (Kendall et al.
433 2019; Römer et al. 2021). The compounding of error and density across datasets highlights the
434 need to prioritise stronger representation of functional traits linked with demography. The
435 standardised framework of MOSAIC is an ideal platform to work from to achieve this goal.

436 In view of potential biases introduced by low sampling density and the patchiness of cover
437 in traits, users of the database are advised to consult the literature about the representativeness and
438 congruency between MOSAIC data and related trait diversity within clades. Users need to be

439 mindful of the scope of the questions that they are setting out to answer and to be aware of the
440 influence of sample sizes and coherency or heterogeneity of traits across different taxonomic
441 levels.

442 **Discussion**

443 **From Databases to Data Networks**

444 Broad aperture digitisation efforts (*e.g.,* BIEN (Enquist et al., 2016; Maitner et al., 2018)
445 and TRY (Kattge et al., 2020)) have helped resolve many answers to demographic questions.
446 Examples include whether there are trait spectra and key trade-off patterns amongst functional
447 traits and whether these are correlated with particular environments and life history strategies
448 (Laughlin, 2018; Reich et al., 2003; Wilkes et al., 2020), Trait-based ecology and Trait Driver
449 Theory (Enquist et al., 2015) are indebted to such opportunity-driven research programmes. More
450 generally, however, the trait-based ecology paradigm has failed to support clear answers to many
451 research questions of central interest to demographers (Bellier, Kéry, & Schaub, 2018; Laughlin
452 et al., 2020). This limited reach of the functional trait programme coincides with a dearth of
453 species-specific overlap across the range of functional traits that are collected by the functional
454 trait databases.

455 The proliferation of databases and open data initiatives over the last two decades
456 (Cheruvelil & Soranno, 2018) evidences an interest in improving both data access and data
457 usability (Gallagher et al., 2020; Michener, 2006; Whitlock, 2011). While existing databases
458 standardise trait fields, collate records, and link associated metadata, existing databases often store
459 data for simple, quantitative traits. Relatively few ecological trait databases store diverse data types
460 (such as rate arrays, population time series, physiological rates at different structural levels, and
461 habitat shape files) that may be associated with multidimensional, ecological study systems (but

462 see CESTES (Jeliazkov et al., 2020), GFBio (Diepenbroek et al., 2014), DarwinCore (Wieczorek
463 et al., 2012)).

464 The digitisation and standardisation of *existing* data and their integration with
465 complementary, new data presents a growing set of challenges and opportunities in ecology
466 (Salguero-Gómez, Jackson, Gascoigne 2021). Efforts to gap-fill records can leverage the value of
467 existing datasets while expediting the schedule for specific research outcomes. As trait datasets
468 grow, the importance of targeted, gap-filling initiatives to address bias and to capitalise on existing
469 data will also increase (Conde et al., 2019). The value of existing records is further enhanced
470 through improvements in the interoperability of datasets. Much of this work is done manually, at
471 a high cost, and with little support from funding agencies (Salguero-Gómez, Jackson, Gascoigne
472 2021), and yet it has been effective at facilitating research and creating new value for old data. In
473 recent years, initiatives have sought to improve the interoperability of datasets by guiding
474 prospective data structure or retroactively harmonising existing datasets. These include
475 programmes that develop universal standards to improve global interoperability (such as
476 DarwinCore (Wieczorek et al., 2012) and Frictionless [https://frictionlessdata.io/]data standards)
477 or that contain guidelines for data metastructure (such as the FAIR principles (findability,
478 accessibility, interoperability, and reusability, *sensu* Wilkinson et al., 2016) and the OpenTraits
479 framework (Gallagher et al., 2020)). These initiatives address emerging and scaling challenges of
480 ecoinformatics, such as the protocols by which we share data, search data, and preserve provenance
481 within hierarchical data storage structures. These protocols will be essential in centralising datasets
482 as diverse as government monitoring datasets (*e.g.,* those stored in U.S. Data clearing houses
483 [https://www.data.gov; https://www.dataone.org/]; National Biodiversity Atlas
484 [https://nbnatlas.org/]); centralised monitoring and experimental networks (*e.g.,* LTER and

485 NEON), raw or reanalysed remote sensing datasets (*e.g.,* Landsat data, NASA EarthData datasets,
486 ERA-5 data), and private datasets (https://www.natureserve.org/) that will demand versatile and
487 navigationally efficient data structures.

488 Population ecology has benefitted from widespread open-access databases but requires
489 further dataset integration to answer its central questions. Understanding whether and how some
490 morphological or physiological traits predict demographic outcomes and why others fail to do so
491 is of central interest to questions in physiological, population, and community ecology (Adler et
492 al., 2014; Chalmandrier et al., 2021; Laughlin et al., 2020; Yang, Cao, & Swenson, 2018).
493 Population ecologists routinely use data that are distributed across a wide range of databases.
494 Comparative and macroecological researchers use phylogenies (*e.g.*, Daskalova, Myers-Smith, &
495 Godlee, 2020; Levin, Crandall, Pokoski, Stein, & Knight, 2020; Roper, Capdevila, & Salguero-
496 Gómez, 2021), adult bodymass (*e.g.*, Capdevila et al., 2020; Healy et al., 2014; Terry, O'Sullivan,
497 & Rossberg, 2022; Williams, McRae, Freeman, Capdevila, & Clements, 2021), and high-
498 resolution, global climate information (*e.g.*, Daskalova, Bowler, Myers-Smith, & Dornelas, 2021;
499 Paniw, Maag, Cozzi, Clutton-Brock, & Ozgul, 2019; Stenseth & Mysterud, 2002) to answer
500 relevant biological, evolutionary and ecological questions and to contextualise their findings.
501 Population ecologists frequently examine a subset of physiological, morphological, and
502 behavioural attributes associated with demographic outcomes ("functional traits", *sensu* Violle et
503 al., 2007). The trait-based research programme seeks to, among other aims (*e.g.*, Díaz et al., 2016),
504 identify the intrinsic and extrinsic regulators of vital rates and the causes of variation and
505 constraints on possible trait values (Buckley & Puy, 2022; Salguero-Gómez, Violle, Gimenez, &
506 Childs, 2018). Not all traits predict demographic outcomes and functional traits may exercise
507 influence on only a few demographic pathways (Pistón et al., 2019; Salguero-Gómez & Laughlin,

508 2021). The answers to these questions rely on the existence of vital rate and trait data, the overlap
509 of which has been limited in the absence of targeted attention. For instance, of the hundreds of
510 thousands of records available across thousands of plant species in TRY (Kattge et al., 2020) and
511 over 345 plant species in COMPADRE (Salguero-Gómez et al. 2015, COMPADRE Ver 1.0.0),
512 Adler et al. (2014) report functional trait-vital rate relationships for only 222 plant species due to
513 their limited data overlap.

514 Ecological data are complex and their structures will need consistent rules to link datasets
515 together. It will be important for future datasets to adopt hierarchical database designs that render
516 large, thematically, and structurally diverse data to be readily locatable and usable without expert
517 knowledge. Here, we show one such example in the scope of comparative research, using thematic
518 groups and a strategy of achieving adequate record breadth before revisiting depth of records for
519 specific species. The need for open access data, integrated workflows, and interoperable data
520 systems is increasing with the scaling of data collection through use of robotics and technologies.
521 The gaps in existing data systems, interoperability, and data acquisition can be filled strategically
522 for specific applications, offering targeted and efficient dataset development. With data
523 interoperability guiding the structure of new datasets, the modular development of area-specific
524 datasets will enable more generalised use over time and help meet the aims of existing database
525 initiatives.

526

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ORCID

Connor Bernard: 0000-0003-2175-5712

Gabriel Santos: 0000-0001-7991-8807

Jacques Deere: 0000-0001-6736-2223

Roberto Rodriguez-Caro: 0000-0003-2321-9497

Pol Capdevila: 0000-0002-2842-4302

Erik Kusch: 0000-0002-4984-7646

Samuel J L Gascoigne: 0000-0002-2984-1810

John Jackson: 0000-0002-1401-3035

Roberto Salguero-Gómez: 0000-0002-6085-4433

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10.1016/j.tree.2018.03.003

824 **Table 1**: Variable names and meaning contained in the MOSAIC Database, organised into seven
825 general trait domains. A more detailed description can be found in the MOSAIC user guide found
826 at: https://mosaicdatabase.web.ox.ac.uk/.

Aspect	Variable	Description	Units
Taxonomy (Parallels COM(P)ADRE)	1 *Species Author*	Taxonomic species name as used by the author(s) in the publication. When more than one study exists for the same species, these are given sequential numeric suffixes (e.g. Ursus_americanus, Ursus_americanus_2, etc.)	NA
	2 *Species Accepted*	Currently accepted taxonomic name according to the Catalogue of Life (www.catalogueoflife.org). See the Supplementary Online Material S3 for an R script to check accepted and synonym names from SpeciesAuthor above	NA
	3 *Common Name*	English common name of SpeciesAccepted	NA
	4 *Family*	Taxonomic family of study species	NA
	5 *Order*	Taxonomic order of study species	NA
	6 *Class*	Taxonomic class of study species	NA
	7 *Phylum*	Taxonomic phylum of study species	NA
	8 *Kingdom*	Taxonomic Kingdom of study species	NA
Species information General	9 *Organism type*	General plant/algae type, based mainly on architectural organisation. The species was assigned to one of these possible values using the description of plant growth type provided by the author and other external sources (e.g. other publications)	Categorical/ Factor
	10 *DicotMonocot*	Whether species is a dicot or monocot	Categorical/ Factor
	11 *AngioGymno*	Whether species is an angiosperm or a gymnosperm	Categorical/ Factor
Source information	12 *Authors*	Surname (family name) of all author	NA
	13 *Journal*	The document from which data were sourced.	NA
	14 *YearPublication*	Year of publication	NA
	15 *DOI*	Digital Object Identifier number	NA
Traits	01 *Biomass*	Mean mass of an individual/whole-organism. (Plants) Plant mass is measured as aboveground dry mass. See "Further information" for additional information on belowground biomass.	Grams
	02 Height	(Plants) Mean height of the whole organism/whole individual from surface (i.e. substrate) to tallest vertical extremity. (Animals) Mean ventro-dorsal length. (i.e. for terrestrial quadrupeds, vertical distance from the ground to the top of the shoulder. For marine bony fishes, from the top of the high point of the dorsal fin to the base of the ventral ridge or ventral fin, whichever is a longer distance perpendicular to the anterior-posterior axis.)	Centimetres
	03 Growth Determination	Whether a species exhibits growth determinacy or not.	Categorical/ Factorial
	04 Regeneration	Capacity for an individual to regenerate any substantial part of its body, including autotomy. Autotomy is defined as "The voluntary severance by an animal of a part of its body (commonly one of its own limbs), usually to escape capture	Categorical/ Factorial

		by a predator that has seized that part. The part then regrows."	
	05 Sexual Dimorphism	An indicator of whether sexual dimorphism is exhibited in the species. Sexual dimorphism is defined as "the occurrence of morphological differences (other than primary sexual characters) that distinguish males from females of a species of organism." (Oxford Dictionaries of Ecology and Zoology)	Categorical/ Factorial
	06 Mating System	System of mating; the organisation of sexual interactions of individuals within populations based on sex.	Categorical/ Factorial
	07 Hermaphrodism	Indicator of whether a species exhibits hermaphrodism or monoeicieosity. Hermaphrodism is defined as: "An individual that possesses both male and female sex organs; i.e. it is bisexual." (Oxford Dictionary of Zoology). Monoeciousness is defined as: "Applied to an organism in which separate male and female organs occur on the same individual (e.g. to a plant which bears male and female reproductive structures in the same flower or separate male and female flowers on the same plant, or to a hermaphrodite animal). Some authors restrict the term botanically to plants with separate male and female flowers; plants which bear male and female reproductive organs in the same flower are then called hermaphrodite."	Categorical/ Factorial
	08 Sequential Hermaphrodism	Indicator of whether a species is protogynous or protandrous.	Categorical/ Factorial
	09 Dispersal Capacity	An indicator for whether or not a species exhibits dispersal behaviour or at any stage in its life cycle. Where dispersing, a categorical description of whether dispersal is natal or breeding or otherwise. Dispersal is defined as "The tendency of an organism to move away, either from its birth site (natal dispersal) or breeding site (breeding dispersal): the opposite of philopatry." (Oxford Dictionary of Zoology).	Categorical/ Factorial
	10 Type of Dispersal	An indication of whether dispersal is a passive (requires assistance) or active (no assistance) event. See DispClasses for more information	Categorical/ Factorial
	11 Mode of Dispersal	An indicator of the mode of dispersal of the species (plant and animal specific terminology). (*e.g.,* phoretic dispersal in *Daphnia magna*).	Categorical/ Factorial
	12 Dispersal Classes	Age- or stage-classes of the species that are capable of dispersal.	Categorical/ Factorial
	13 Volancy	An indicator of whether a species is volant or non-volant (i.e., able to fly or not).	Categorical/ Factorial
	14 Aquatic Habitat Dependency	An indicator of whether a species is dependent on water or not. (e.g., limnic, lentic, lotic)	Categorical/ Factorial

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Figures

Figure 1. Structure of the MOSAIC database (v1.0.0). The MOSAIC database comprises a combination of existing trait records centralised from data servers, databases, and datasets and new records collected from the primary literature by the MOSAIC team. Existing records are labelled, MOSAIC-A, in the mosaic metadata attribute field and include provenance in the metadata. New data records that adhere to existing data standards and that fit into the remit of an existing database (*i.e.*, a data gap filled by the MOSAIC team) are labelled MOSAIC-B. New records that do not have an existing data standard or for which there is not an existing database are labelled MOSAIC-C.

Figure 2. Trait fields in the MOSAIC database (v1.0.0). The MOSAIC database contains a combination of continuous and discrete trait fields. Six of the 14 trait fields are illustrated here for animals, and organised by trait level (all discrete fields) and taxonomic classification. Trait distributions vary strongly by trait and taxonomy. Observed variation in trait values by taxonomic group is a prerequisite condition to their potential value toward explaining reported variation in vital rates and resulting demographic properties across the Tree of Life. Species included in the MOSAIC database are limited to those for which stage-structured population data exist in the COMADRE, COMPADRE, and PADRINO databases.

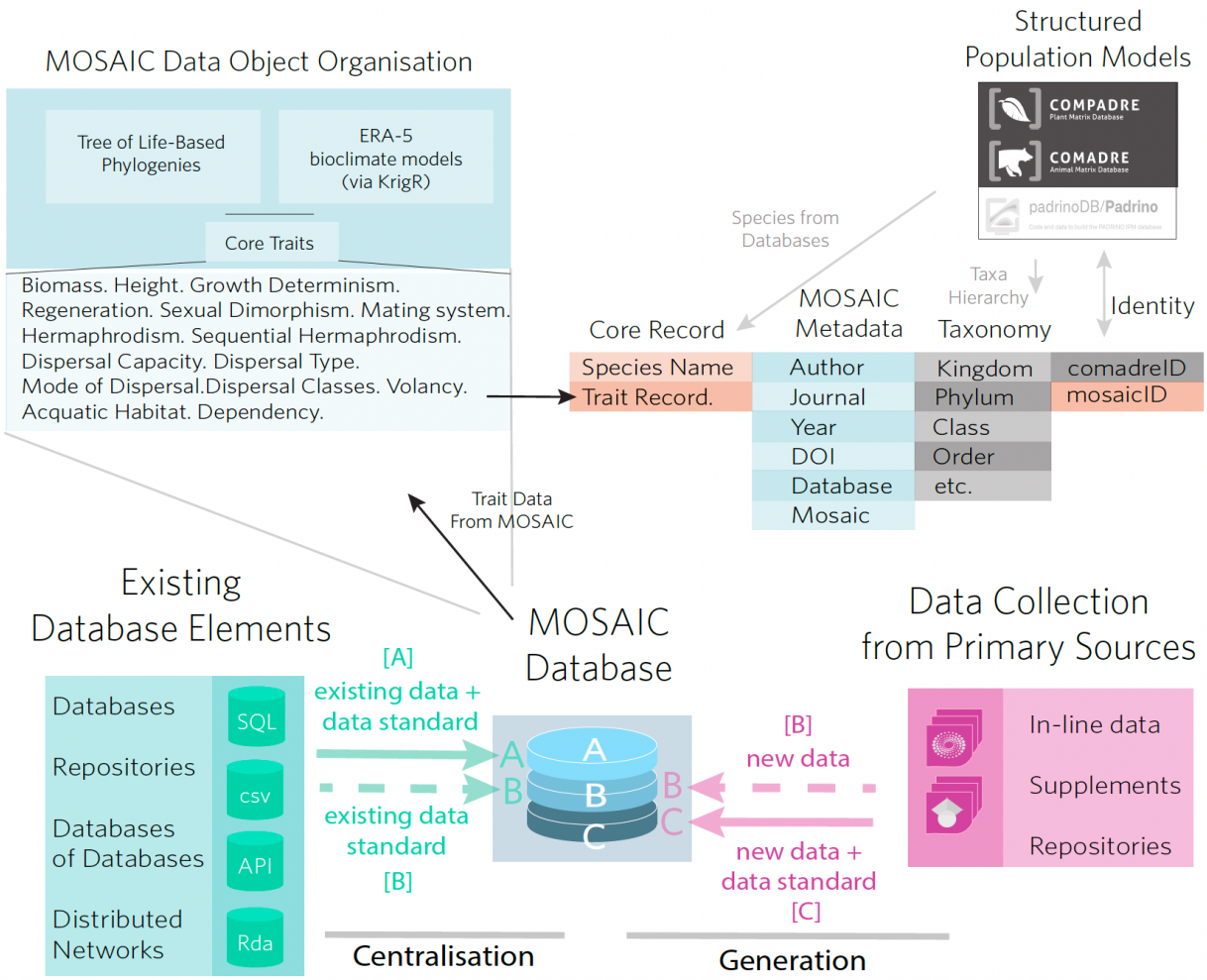
Figure 3. The spatial distribution of MOSAIC (v1.0.0) records relative to the (a) COMADRE and (b) COMPADRE databases. The COMADRE and COMPADRE dataset include animal and plant demographic data, respectively, on all continents except Antarctica, with a substantial bias to North America and Central Europe. MOSAIC introduces trait records that include models in all

major geographies of COMADRE and COMPADRE. The map shows the density of matrix population models globally (color graded by density per area in *ca.* 150 km^2 hexagonal cells). Cells bordered by white represent localities of population models for which there are trait records included in the first release of the MOSAIC trait database. Species prioritised in v1.0.0 of MOSAIC did not include the PADRINO dataset, so no distribution figure is shown for integral projection models.

Figure 4. Phylogenetic mapping of traits included in MOSAIC (v1.0.0). (a) Phylogenetic distribution of seven major traits for animals: (1) growth determination; (2) sexual dimorphism; (3) monogamy; (4) gonochory; (5) volancy; (6) dispersal; and (7) biomass. (b) Phylogenetic distribution of four traits in plants: (1) dispersal capability; (2) dispersal type; (3) dispersal mode; and (4) dispersal class. Figures developed in R using the ggtree package.

Figure 5. Trait covariance in the MOSAIC database (v1.0.0). Some traits exhibit high correlation in the MOSAIC database, such as between growth determination and between growth regeneration. Trait associations are expected to occur in the MOSAIC dataset and may reflect widespread constraints or statistical anomalies, particularly when dealing with small samples or specific taxonomic subgroups. Trait covariation can be symptomatic of biomechanical constraints (*e.g.*, flight and biomass), major growth characteristics (*e.g.*, modularity and growth determination), or other past or presently compelled associations (*e.g.*, height and vessel density).

872 **Figure 1**



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874 **Figure 2**

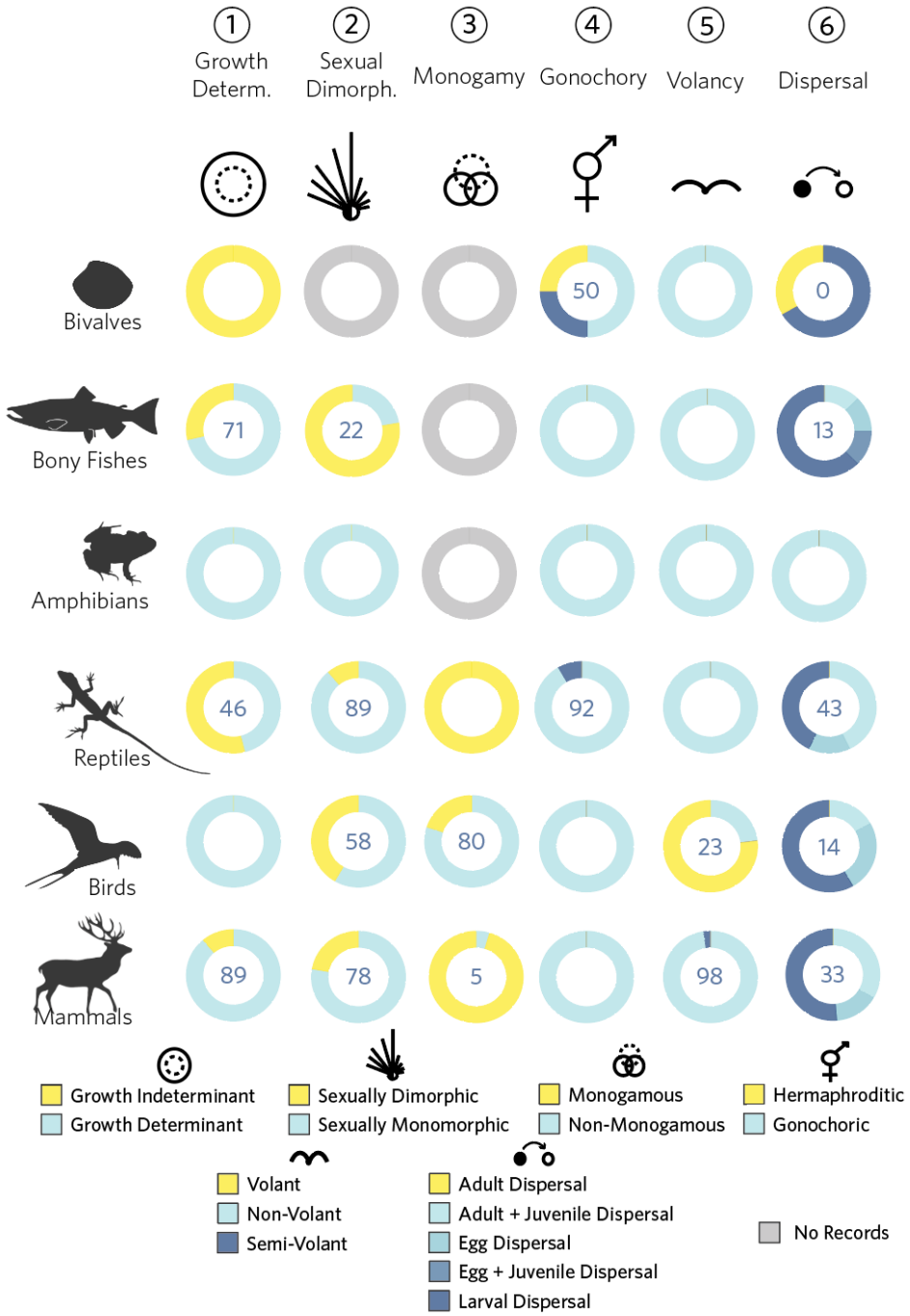

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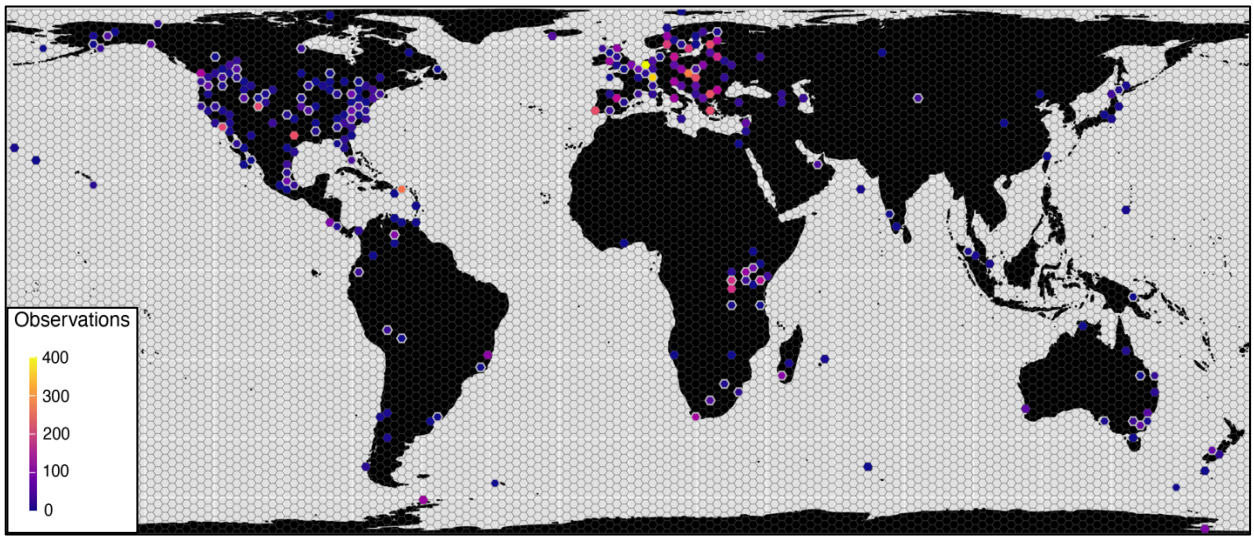
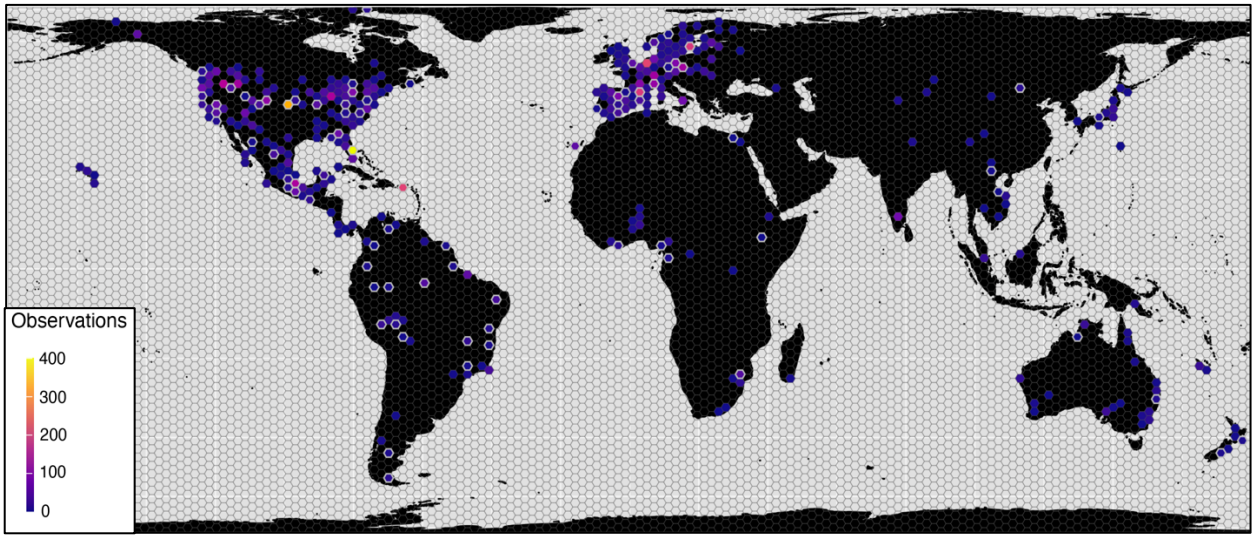
Figure 3

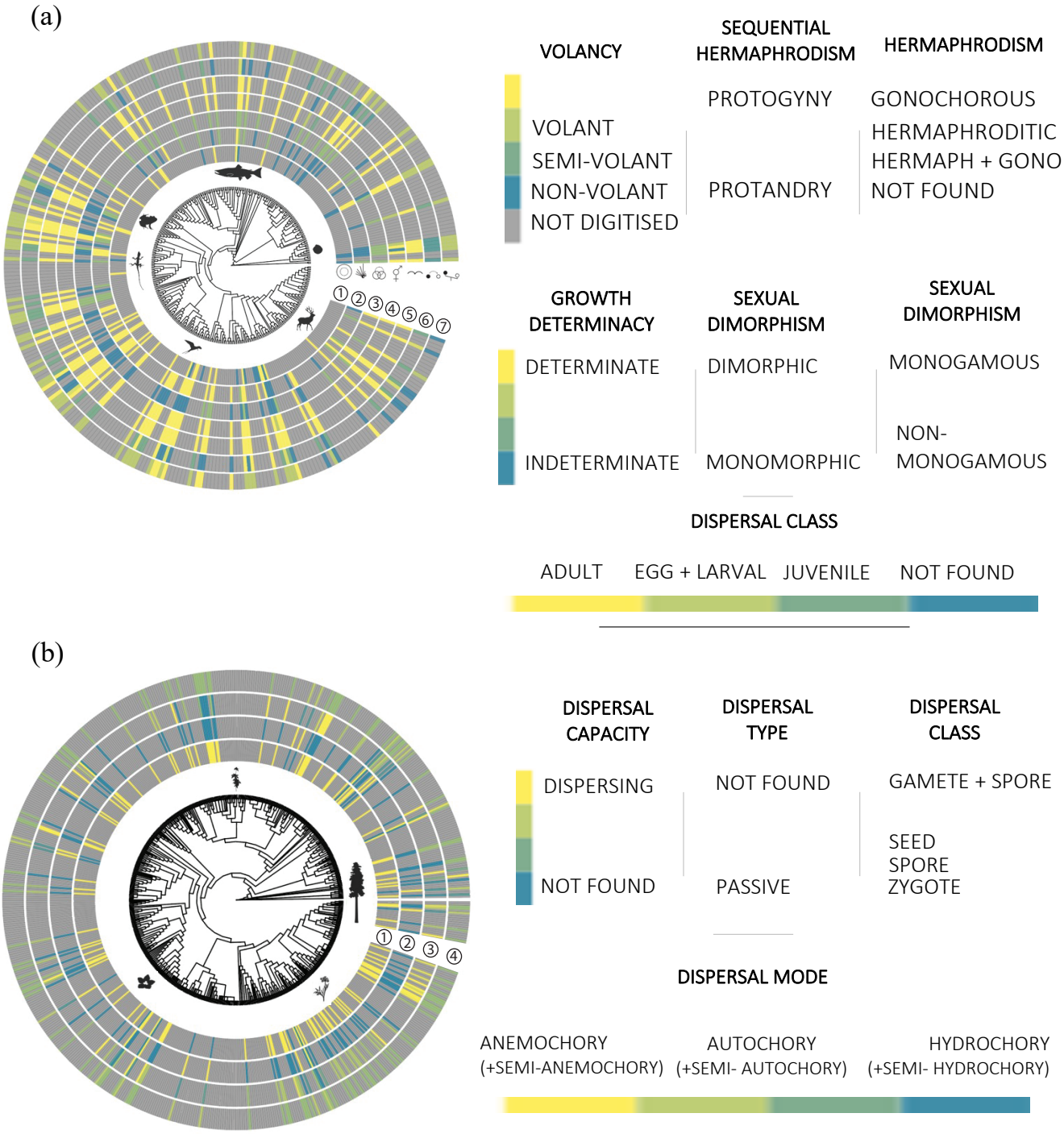
(a) COMADRE



(b) COMPADRE

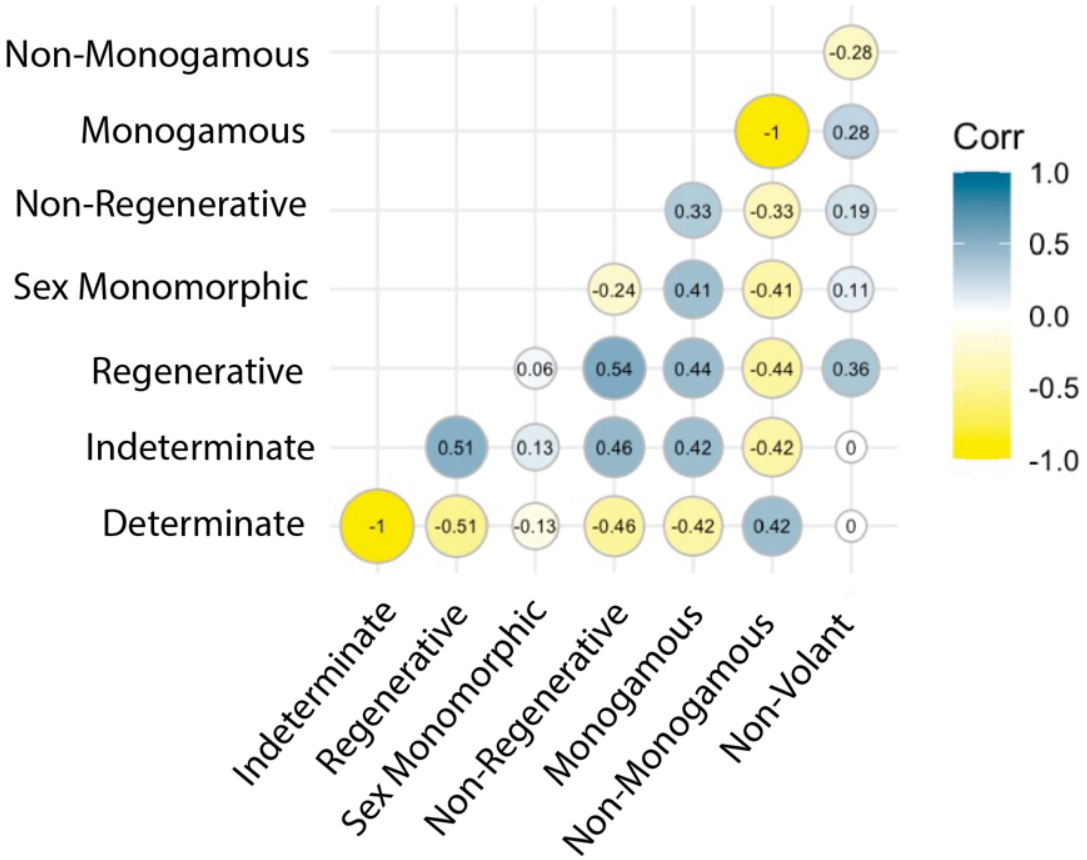


878 **Figure 4**



879

880 **Figure 5**



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MOSAIC: A Unified Trait Database to Complement Structured Population Models

Connor Bernard, Gabriel Silva Santos, Jacques Deere, Roberto Rodriguez-Caro, Pol Capdevila, Erik Kusch, Samuel J L Gascoigne, John Jackson, & Roberto Salguero-Gómez

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S1: MOSAIC User Guide

USER GUIDE TO THE MOSAIC LIFE HISTORY DATABASE

A Companion to COM(P)ADRE and PADRINO/A demographic databases

Working document – 06 February 2022

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Metadata

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2. **A2** Kingdom Page 11

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Primary User Guide/Variables

* Applicable to plants

** Applicable to animals

A. Morphometry & Growth

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User guide version information

Version 1.0.0

Release date: 6 February 2021

Contact: mosaicdatabase@biology.ox.ac.uk

General Instructions

Database Organization

The data associated with MOSAIC are provided in a single R data (extension.Rdata) and as a comma separated value (.csv) file format. The code for downloading the data can be located from the mosaic portal (https://mosaicdatabase.web.ox.ac.uk/download-database) In addition, these files are accompanied by R scripts and a nexus phylogeny available in the Supplementary Information of the manuscript introducing MOSAIC, and in our GitHub repository (https://github.com/mosaicdatabase/mosaicdatabase)

MOSAIC_v_1_0_0.RData: Contains basic information regarding the source of publication, as well as ecological, biogeographic, and taxonomic details of the demographic study for each study species, the demographic information (i.e., the matrix population model) and metadata.

Database Design

In developing the MOSAIC database, we balance level of detail with accessibility. A highly detailed, comprehensive profile of life history traits for species in COM(P)ADRE and PADRINO/A, if possible to collect, would be difficult to navigate. So rather than collating a wealth of information in many different formats, we designed this dataset to highlight a smaller collection of traits in a single format which is of most interest, and expressed, by COM(P)ADRE and PADRINO/A users. In MOSAIC's future updates, we plan to add additional detail and additional fields, but we initially took a limited approach and plan to keep the design minimal. If there are life history traits, alternative formats for existing variables, or other features you would like to see added to MOSAIC, please suggest them to us at: mosaicdatabase@biology.ox.ac.uk

Understanding the diverse needs of users, we include in this guidance document additional direction on obtaining information on the variables we report in more detail. In this guide, we also highlight the scope of use, and caution against the most foreseeable abuses of data. We ask that all users approach this dataset with a caution and pay close attention to what variables and their statistical expression reflect.

The Meanings of NA and NDY in MOSAIC

NA in the MOSAIC data generally means that the data are not applicable. An example of where the data are not applicable is volancy within plants, as this trait does not occur in plants. NDY in the MOSAIC data means that the data have not yet been digitized. NF in the MOSAIC data means that the data are not available to date as no affirmative records were found upon review.

Disclaimer

The MOSAIC digitization team does its best to ensure data accuracy, and every piece of information goes through multiple error-checks prior to its release in www. mosaicdatabase.web.ox.ac.uk. However, we claim no responsibility for any damage that may arise from using MOSAIC. A list of error checks and potential issues in the use and

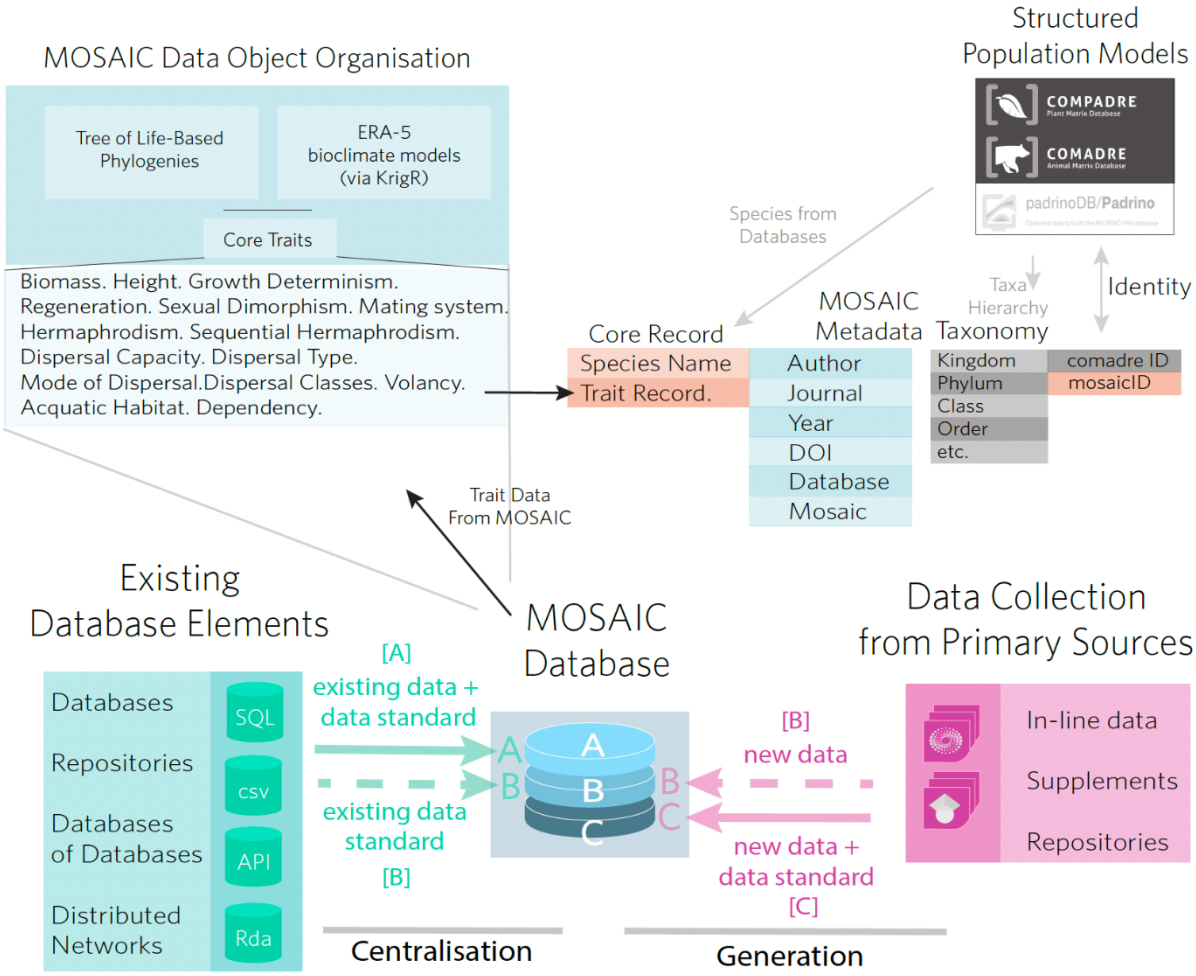
interpretation of the database are described in the main manuscript. The end user is ultimately responsible for his/her interpretations of the data.

What is new in this version?

Version 1.0.0

- The first version of the database. No updates.

DIAGRAM OF THE MOSAIC DATABASE ARCHITECTURE



Variables in MOSAIC

The MOSAIC database is constructed of objects containing life history information across variables and organized into themes to aid in navigation. The metadata object is the object containing information about every study for which data is stored in the MOSAIC database. Every variable containing a value in the MOSAIC database will have corresponding metadata.

Associated with every data record is a value and its corresponding metadata. The metadata details data providence and relationships to existing databases. The fields within metadata are detailed below:

Format Guide

[Index] *Variable Name*

Definition: [Definition of the variable]

Possible values, [cat. = categorical/discrete; cont. = continuous], [r variable class: character, numeric, integer, complex, or logical.]

- <XX> [variable with two digits]
  XXX –XXX [discrete variable name] – [discrete variable definition]
  <...>XXX<...> [discrete variable with additional content on either side]
- Units: [unit of measure (integer, percent, ratio, mm, km^2, g, etc.)]
- Precision: [for continuous variables: scientific notation of the precision of the measure - e.g., $1e^1$ for km = precise to the tens of km (3270 km), no decimal; $1e^{-1}$ for temperature = precise to the tenth of a degree (10.4 °C)]
- Error boundaries: [for continuous variables: boundaries beyond which values are errors]

Usage Notes: [Notes on boundaries of use – note that this is non-exhaustive and highlights major potential errors]

Additional Information: [Guidance on databases containing more detailed information]

Source Data: [Datasets from which information was gathered; note that this will not include individual papers unless the papers are associated with a larger dataset/database. This category reflects databases.]

Last updated: [Date that information was retrieved from other databases or searches]

A1 *Species Accepted*

Definition: Currently accepted latin name.

Possible values, cat., factor

- <Genus_species> - e.g., Taraxacum_officinale

Usage Notes: NA

Additional Information: NA

Source Data: This information is obtained from The Encyclopaedia of Life

Last updated: 24 January 2022

A2 *Kingdom*

Definition: Kingdom to which species belongs

Possible values, cat., factor

- <kingdom> - e.g., Plantae, Fungi, Rhodophyta, Chromista (yes, MOSAIC includes fungi and algae as well as plants)

Usage Notes: NA

Additional Information: NA

Source Data: The Encyclopaedia of Life

Last updated: 24 January 2022

B1 *Authors*

Definition: Surname (family name) of all authors

Possible values, NA, character

- <name(s)> - Separated with “;” e.g., “Smith; Jones”

Usage Notes: NA

Additional Information: NA

Source Data: NA

Last updated: 24 January 2022

B2 *Journal Name*

Definition: The document from which data were sourced.

Possible values, cat., factor

- <abbreviated journal name> - Where the data come from a scientific journal article, the abbreviated journal name is given. We use the standard abbreviation of the journal compliant with the ISO-4 standard.
- Book - Records are from a book, or book chapter
- PhD thesis - Records are from a doctoral thesis
- MSc thesis - Records are from a masters thesis
- Report - Records are from a report
- Conference talk - Records are from a conference talk
- Conference poster - Records are from a conference poster

Usage Notes: NA

Additional Information: NA

Source Data: NA

Last updated: 24 January 2022

B3 *Year Publication*

Definition: Year of publication

Possible values, cont., numerical

- <yyyy> - e.g., 2012

Usage Notes: NA

Additional Information: NA

Source Data: NA

Last updated: 24 January 2022

B4 *DOI/ISBN Number*

Definition: Digital Object Identifier number

Possible values, NA, character

- <XXXXXXXXXXXXXX> - e.g., doi.org/10.1073/pnas.1506215112

Usage Notes: NA

Additional Information: NA

Source Data: NA

Last updated: 24 January 2022

PRIMARY Variables

A1 *Biomass*

Definition: Maximum reported mass of adult individual/whole-organism. For plants, only aboveground dry mass is measured. See "Additional information" for additional information on belowground biomass.

Possible values, cont., numerical

- Units: Grams (g)
- Precision: 0.000
- Error Boundaries: 0-150,000,000g
- NF – Body mass reviewed and inconclusive (no affirmative records found upon review)
- NDY – Body mass not digitised yet (yet to be evaluated)
- NA – not applicable

Usage notes: When both male and female data were reported, only the maximum value was considered independently of the gender of the individuals.

Additional Information: Belowground biomass is not reported because information availability is appreciably more limited than for aboveground biomass. The BIEN database includes information on belowground biomass that can be referenced and utilized where of interest.

Source Data: Amniote, TRY database.

Last updated: 24 January 2022

A2 *Height*

Call: -Morph$Height

Definition: (Plants) Maximum height of the whole organism/whole individual from surface (i.e. substrate) to tallest vertical extremity.

Possible values, cont., numerical

- Units: centimeters (cm)
- Precision: 0.000
- Error Boundaries: 0-1000cm

Usage notes:

- Depending on the species group, height can have profoundly different meanings. Height corresponds with embolic risk in some woody plants and corresponds with size-based fitness in others.

Additional Information: NA

Source Data: TRY database.

Last updated: 24 January 2022

A3 *Growth Determination*

Call: -Morph$Growth$Determination

Definition: Growth indeterminacy is defined by continuous growth of individuals throughout their lifetimes (measured by mass, length, bone ossification, or other indicators). This field reflects a binary classification of whether an individual is growth (in)determinate.

Possible values, cat, factor

- Growth indeterminate – growth continues throughout an individual's lifespan
- Growth determinate – growth ceases or attenuates to negligibility before the end of an individual's lifespan
- NF - Growth determination reviewed and inconclusive (no affirmative records found upon review)
- NDY - Growth determination not digitised yet (yet to be evaluated)
- NA – Growth determination not applicable to the subject area

Usage notes: Additional classification systems for characterizing growth indeterminacy exist in the literature. Most well recognised is a six-type scheme describing growth and determination by Sebens (1987), which offers detailed characterization of growth patterns. Broad-scale information about growth and age for most species could not be located in the literature, and therefore a simplified schema is used. More resolved classifications might be incorporated into future versions of MOSAIC.

Additional Information: NA

Source Data: 24 January 2022

Last updated: NA

A4 *Regeneration*

Call: **-**Morphology$Growth$Regeneration

Definition: Capacity for an individual to regenerate any substantial part of its body, including autotomy. Autotomy is defined as "The voluntary severance by an animal of a part of its body (commonly one of its own limbs), usually to escape capture by a predator that has seized that part. The part then regrows."

Possible values, cat., factor

- Regenerative – individuals are capable of regenerating
- Non-regenerative – individuals do not exhibit the capacity to regenerate tissues
- NF - regenerative abilities reviewed and inconclusive (no affirmative records found upon review)
- NDY - regeneration information not digitised yet (yet to be evaluated)
- NA – regenerative abilities not applicable to the subject area

Usage notes: There are a number of more resolved schemes for detailing whether regenerating different parts of the body. For particular questions pertaining to the nature of injury, the level of recovery, the role of depredation, and the consequences for reproduction, more detail may be appropriate. This dataset covers the most general applications and initially screens for regenerative capability (from poor recovery of appendages to complete regeneration of limbs).

Additional Information: NA

Source Data: NA

Last updated: 24 January 2022

A5 *Sexual Dimorphism*

Call: -Morph$Dimorph

Definition: An indicator of whether sexual dimorphism is exhibited in the species. Sexual dimorphism is defined as "the occurrence of morphological differences (other than primary sexual characters) that distinguish males from females of a species of organism." (Oxford Dictionaries of Ecology and Zoology)

Possible values, cat., factor

- Sexually Dimorphic – species is sexually dimorphic
- Sexually Monomorphic – species is sexually monomorphic (i.e. non-dimorphic)
- NF - Sexual dimorphism reviewed and inconclusive (no affirmative records found upon review)
- NDY - Sexual dimorphism not digitised yet (yet to be evaluated)
- NA – Sexual dimorphism not applicable to the subject area

Usage Notes: NA

Additional Information:

Source Data: NA

Last updated: 24 January 2022

B1 *Mating system*

Call: **-**Reproduction$MatingSystem

Definition: System of mating; the organization of sexual interactions of individuals within populations based on sex.

Possible values, cat., factor

- Monogamy – exclusive mating between one male and one female
- Non-monogamy - Non-monogamy was assigned based on genetic or behavioural evidence
- NF - Mating system reviewed and inconclusive (no affirmative records found upon review)
- NDY - Mating system not digitised yet (yet to be evaluated)
- NA – Mating system not applicable to the subject area

Usage notes:

- Metric does not identify size of groups for plural mating systems
- Metric does not identify enforcement mechanisms for different mating systems

Additional Information: NA

Source Data: NA

Last updated: 24 January 2022

B2 *Sexual allocation*

Call: **-**Reproduction$Allocation

Definition: Indicator of whether a species exhibits hermaphroditism or monoeicieosity. Hermaphrodism is defined as: "An individual that possesses both male and female sex organs; i.e. it is bisexual." (Oxford Dictionary of Zoology). Monoeciousness is defined as: "Applied to an organism in which separate male and female organs occur on the same individual (e.g. to a plant which bears male and female reproductive structures in the same flower or separate male and female flowers on the same plant, or to a hermaphrodite animal). Some authors restrict the term botanically to plants with separate male and female flowers; plants which bear male and female reproductive organs in the same flower are then called hermaphrodite."

Possible values, cat., factor

- Hermaphroditic – species is hermaphroditic
- Monoecious – species is monoecious
- Dioecious or Gonochorous – species is dioecious (Gonochorous was adopted for animals)
- NF - Hermaphroditism reviewed and inconclusive (no affirmative records found upon review)
- NDY - Hermaphroditism not digitised yet (yet to be evaluated)
- NA – Hermaphroditism is not applicable to the subject area

Usage notes:

-

Additional Information: NA

Source Data: NA

Last updated: 24 January 2022

B3 *Sequesntial hermaphroditism*

Call: Reproduction$SeqHermaph

Definition: Indicator of whether there is a sex switch during the organism's lifespan.

Possible values, cat., factor

- Protogynous – species is protogynous: organisms that are female and at some point in their lifespan change sex to male.
- Protandrous – species is protandrous: organisms that are male and at some point in their lifespan change sex to male.
- NF - Protogyny/Protandry reviewed and inconclusive (no affirmative records found upon review)
- NDY - Protogyny/Protandry not digitised yet (yet to be evaluated)
- NA – Protogyny/Protandry is not applicable to the subject area.

Usage notes: NA

Additional Information: Note that is not rare flowers present protogyny/protandry but this was not considered in Mosaic so far

Source Data: NA

Last updated: 24 January 2022

C1 *Dispersal Capability*

Call: -Movement$Dispersal

Definition: An indicator for whether or not a species exhibits dispersal behaviour or at any stage in its life cycle. Where dispersing, a categorical description of whether dispersal is natal or breeding or otherwise. Dispersal is defined as "The tendency of an organism to move away, either from its birth site (natal dispersal) or breeding site (breeding dispersal): the opposite of philopatry." (Oxford Dictionary of Zoology).

Possible values: cat., factor

- Dispersing – Exhibits at least one age-/stage-class which disperses; natal or breeding components unknown.
- Natal Dispersal – Permanent dispersal of at least one age-/stage-class
- Breeding Dispersal – Dispersal of adults between breeding attempts in at least one age-/stage-class
- Multi-Dispersal – Both natal and breeding dispersal reported in the species; see DispClasses for more information
- Non-Dispersing – Species observed to have no dispersal traits/behaviour
- NF - dispersal capability reviewed and inconclusive (no affirmative records found upon review)
- NDY – dispersal capability unknown/not yet evaluated
- NA – not applicable

Usage Notes: NA

Additional Information: NA

Source Data: NA

Last updated: 24 January 2022

C2 *Type of Dispersal*

Call: -Movement$TypeDisp

Definition: An indication of whether dispersal is a passive (requires assistance) or active (no assistance) event. See DispClasses for more information.

Possible values: cat., factor

- Active – organism utilises its own morphology for the dispersal event
- Passive – organism is unable to disperse through their own means and require an external factor
- Active and Passive – organism is able to disperse with assistance but can also use external factors. Active and passive dispersal can occur within the same life stage or can occur in different life stages.
- NF – type of dispersal reviewed and inconclusive (no affirmative records found upon review)
- NDY – type of dispersal unknown/not yet evaluated
- NA – not applicable

Usage Notes: NA

Additional Information: NA

Source Data: NA

Last updated: 24 January 2022

C3 *Mode of Dispersal*

Call: -Movement$ModeDisp

Definition: An indicator of the mode of dispersal of the species (plant and animal specific terminology).

Possible values: cat., factor

- Motile – the dispersal of animal species without assistance
- Phoretic – the dispersal of animal species by attaching to another animal
- Water currents – the dispersal of animal species by water
- Motile and water currents – animal species that disperse without assistance and by water, both forms of dispersal can occur within the same life stage or can occur in different life stages
- Anemochory – the dispersal of plant seeds by wind
- Anthropochory – the dispersal of plant seeds by humans
- Autochory – the dispersal of plant seeds without assistance from an external vector (e.g., by gravity or ballistic dispersal)
- Hydrochory – the dispersal of plant seeds by water
- Zoochory – the dispersal of plant seeds by animals
- Anemochory and Anthropochory – plant seeds can be dispersed by wind and humans
- Anemochory and Autochory – plant seeds can be dispersed by wind and without the help of an external vector
- Anemochory and Hydrochory – plant seeds can be dispersed by wind and water
- Anemochory and Zoochory – plant seeds can be dispersed by wind and animals
- Autochory and Hydrochory – plant seeds can be dispersed without the help of an external vector and by water
- Autochory and Zoochory – plant seeds can be dispersed without the help of an external vector and by animals
- Hydrochory and Zoochory – plant seeds can be dispersed by water and animals
- Autochory, Anthropochory and Zoochory – plant seeds can be dispersed without the help of an external vector, by humans and by animals
- NF – mode of dispersal reviewed and inconclusive (no affirmative records found upon review)
- NDY – mode of dispersal unknown/not yet evaluated
- NA – not applicable

Usage Notes: Plant seed dispersal modes can be subdivided into further categories, however we collated lower order categories into the higher order categories identified here

Additional Information: NA

Source Data: NA

Last updated: 24 January 2022

1523
1524

C4 *Dispersal Class*

Call: -Movement$DispClass

Definition: Age- or stage-classes of the species that are capable of dispersal.

Possible values: cat., factor

- Adult – dispersal stage is an individual that has reached maturity, we include sub-adults into this category
- Egg – dispersal stage is a vessel within which an embryo develops and is expelled by an adult allowing for dispersal
- Fertile material – dispersal stage is a part of an individual, or in some cases a complete individual, that contains fertile material (e.g., the alga *Fucus vesiculosus*; detached floating material/individual that contains gametes)
- Gamete – dispersal stage is the reproductive cell not within a vessel
- Juvenile – dispersal stage is an individual that has not reached maturity
- Larval – dispersal in a specific juvenile stage restricted to non-mammal species, species can have multiple larval stages
- Seed – dispersal stage is fertilized, specific to plant species and, in our definition, references seeds and/or fruits that are dispersed
- Sperm – dispersal stage is the male gamete
- Spore – dispersal stage is a single cell that only contains half of the chromosome of the adult, can produce eggs or sperm
- Sporophyte – dispersal stage is a nonsexual phase of a species producing two diploid spores
- Zoospore – dispersal stage is a motile asexual spore
- Zygote – dispersal stage is a fused male and female gamete
- Adult and Juvenile – dispersal stage can be both the adult and juvenile stage
- Egg and Larval – dispersal stage can be both the egg and larval stage
- Gamete and Spore – dispersal stage can be both the gamete and spore
- Zoospore, Sperm and Sporophyte – dispersal stage can be a zoospore, sperm or sporophyte
- NF – dispersal class reviewed and inconclusive (no affirmative records found upon review)
- NDY – dispersal class unknown/not yet evaluated
- NA – not applicable

Usage Notes: Dispersal can occur in more than one age- or stage- class, where this occurs it is noted as such within the database

Additional Information: NA

Source Data: NA

Last updated: 24 January 2022

C5 *Volancy*

Call: -Movement$Volancy

Definition: An indicator of whether a species is volant or non-volant (i.e., able to fly or not).

Possible values, cat., factor

- Volant – the species is volant
  (Most Birds (Class Aves), all Bats (Order Chiroptera), and some invertebrate species)
- Non-volant – the species is non-volant
- Semi-volant – the species has gliding abilities
  (e.g., Gliding lizards (*Draco* spp.); flying squirrels such as the Northern flying squirrel (*Glaucomys sabrinus*); flying fish (Exocoetidae); gliding frogs such as Wallace's flying frog (*Rhacophorus nigropalmatus*); and gliding ants such as *Cephalotes atratus*).
- NF – volancy reviewed and inconclusive (no affirmative records found upon review)
- NDY – volancy unknown/not yet evaluated
- NA – not applicable

Usage Notes: NA

Additional Information: NA

Source Data: NA

Last updated: 24 January 2022

S2: MOSAIC Trait Primary Search Key Words

MOSAIC: Keywords used in primary literature search

Taxonomic names (binomial nomenclature) were used in connection with the field-specific terms in the search of primary literature in identifying the records of interest. The below include names that were searched in review of the primary literature.

Biomass—

NA (database only)

Height—

NA (database only)

Growth determination—

Sources: *Web of Science; Google Scholar; Scopus*

Terms: Growth determinat*, growth determination, growth determinate, growth indetermination, growth

Regeneration—

Sources: *Web of Science; Google Scholar; Scopus*

Terms: Regenerat*, regeneration, regenerate, rejuvenation

Sexual dimorphism—

Sources: *Web of Science; Google Scholar; Scopus*

Terms: Dimorphic

Mating system—

Sources: *Web of Science; Google Scholar; Scopus*

Terms: Monogamy, monogamous, polygyny, polygynous, polyandry, polyandrous, mating system

Hermaphrodism—

Mating system—

Sources: *Web of Science; Google Scholar; Scopus*

Terms: Hermaphrod*, hermaphroditic, hermaphrodism, hermaphrodite, gonochoric, gynochorous, monoecious, dioecious, sexual differentiation,

Sequential hermaphrodism—

Sources: *Web of Science; Google Scholar; Scopus*

Terms: Sequential hermaphrodism, protandry, protogyny, protogynous hermaphroditism, protandrous hermaphroditism

Dispersal capacity—

Sources: *Web of Science; Google Scholar; Scopus*
Terms: Dispers*, dispersal, dispersing, dispersal capacity, dispersal capability

Type of dispersal—
Sources: *Web of Science; Google Scholar; Scopus*
Terms: Dispers*, active, passive

Mode of dispersal—
Sources: *Web of Science; Google Scholar; Scopus*
Terms: Dispers*, motile, phoretic, currents, anemochory, anthropochory, autochory, hydrochory, zoochory, anthropochory

Dispersal classes—
Sources: *Web of Science; Google Scholar; Scopus*
Terms: Dispers*, adult, jouvenile, egg, fertile, seed, sperm, spore, sporophyte, zoospore, zygote, gamete

Volancy—
Sources: *Web of Science; Google Scholar; Scopus*
Terms: Volant, non-volant, flight, flying, flightless, non-flying, winged, glide, gliding, ground

Aquatic habitat dependency—
Sources: *Web of Science; Google Scholar; Scopus*
Terms: Anadromous, catandromous, estuarine, brackish, lotic, lentic, lemnitic, littoral, palagic, marine, freshwater, saltwater, sea, ocean.

S3. Databases Searched

MOSAIC: Databases Reviewed to Date for the MOSAIC Database

Type. Database Name. DOIs.

1. **Plants**. Botanical Information and Ecology Network (BIEN) (doi: 10.7287/peerj.preprints.2615v2)
2. **Plants**. TRY: Global Plant Trait Database (TRY) (doi: 10.1111/j.1365-2486.2011.02451.x)
3. **Phylogeny.** Open Tree of Life: A synthesis of phylogeny and taxonomy into a comprehensive tree of life (doi: 10.1073/pnas.1423041112)
4. **Vertebrates**. Amniote: An amniote life history database to perform comparative analysis with birds, mammals, and reptiles (doi: 10.1890/15-0846R.1)
5. **Amphibians**. AmphiBIO: a global database for amphibian ecological traits. (doi:L 10.1038/sdata.2017.123)
6. **Mammals**. PanTHERIA: a species-level database of life history, ecology, and geography of extant and recently extinct mammals (doi: 10.1890/08-1494.1)
7. **Animals**. AnAge Database of Animal Ageing and Longevity. (doi: 10.1111/j.1474-9726.2008.00442.x)
8. **General (Sex)**. Tree of Sex: A database of sexual systems (10.1038/sdata.2014.15)
9. **General (Variable)**. Open Trait Network Databases (https://opentraits.org/)

S4: Vignettes

Navigating MOSAIC

Vignette #1 - Navigating MOSAIC

Welcome to the **MOSAIC database**, a database of functional traits for comparative demography. The database, user, guide, and additional information can be found and http://mosaicdatabase.web.ox.ac.uk.

MOSAIC is a database that aggregates existing databases and adds new records for functional traits that currently do not have a database established. In this vignette, we will show you how to download the dataset, search records, and relate MOSAIC records with COMADRE, COMPADRE, and PADRINO databases.

Optional clearance of working space.

```
rm(list = ls()) # Clear your environment

if(!is.null(dev.list())) dev.off() # Clear plots/graphics

cat("\014") # Clear console
```

Downloading MOSAIC

MOSAIC can be downloaded as an S4 object by running the below code in R. S4 data objects in R are an object oriented system in the R language that allow control of constituent data fields Similar to S3 objects (which use the "$" operator). S4 are comprised of objects that can be searched with the "@" operator or slots, discussed in more detail below.

```
library(devtools) # Compulsory package to pull down packages from GitHub. Ins
tall if necessary.

install_github("mosaicdatabase/Rmosaic")

source_url("https://raw.githubusercontent.com/mosaicdatabase/mosaicdatabase/m
ain/mosaic_fetch.R") # Link to GitHub repo

mosaic <- mos_fetch("v1.0.0") # Download version 1.0.0 (active version Feb 20
22)

library(Rmosaic)
```

Basics of manually navigating MOSAIC

Mosaic traits can be searched using the "@" operator. Attribute names searched this way are analogous to the columns of a dataframe in a relational database structure.

Once downloaded, you should be able to type statements mosaicdatabase@[insertfield] (where [insertfield] is a particular trait). If you are working in Rstudio, after the "@" a drop-down of the slots (traits) should autopopulate.

```
# Three examples of querying traits (easiest for navigation)

mosaic@biomass

mosaic@height

mosaic@volancy
```

The species corresponding with each index can be queried by prompting:

```
# Three examples of querying traits (easiest for navigation)

mosaic@species
```

Data in mosaic can also be access using slots. Slots are the recommended mode of searching the database - though it has the disadvantage of not enabling the autopopulation of the attributes contained in the database (traits must be spelled out manually).

```
# You can also search these by slot (recommended)

slot(mosaic, "biomass")

slot(mosaic, "height")

slot(mosaic, "volancy")
```

Within each trait object, there are eight fields in mosaic. The first of field is called "values" and contains the data. Values are unitless values (either numeric or factorial) that are reported in units described in the **Mosaic User Guide** http://mosaicdatabase.web.ox.ac.uk/user-guide. The metadata is organised into additional attributes, reflecting the individual elements of the metadata for a given record, including the authors, journal, year of publication, databases from which data are sourced (if applicable)

mosaic@metaTaxa maps the complete taxanomic classification structure of a species - from Kingdom to species for taxonomic clustering.

The other six attributes - "author", "year", "journal,"doi","database", and"mosaic" - are metadata corresponding with each value record. For instance:

```
mosaic@species[[2]] # For this species, let us look at volancy (flight capaci
ty) value

mosaic@volancy@value[[2]] # or, equivalently:

slot(slot(mosaic, "volancy"), "value")[[2]]
```

Corresponds with the following metadata

```
mosaic@volancy@author[[2]] # for "Acinonyx jubatus"
```

```
slot(slot(mosaic, "volancy"), "author")[[2]] # Author of the source publicati
on

slot(slot(mosaic, "volancy"), "year")[[2]] # And year of the source publicati
on

slot(slot(mosaic, "volancy"), "journal")[[2]] # The journal of the source pub
lication

#etc.
```

Using MOSAIC functions to quickly access files

A series of convenience functions can be sourced from the MOSAIC GitHub page to facilitate navigating and working with the mosaic database that can be accessed by running the follwing script.

```
source_url("https://raw.githubusercontent.com/mosaicdatabase/mosaicdatabase/m
ain/navMosaic_46.R")
```

Below we highlight some of the basic queries for which the mosaic functions can assist.

Is a species included in Mosaic?

```
spp_check("Fritillaria biflora")

## [1] TRUE

spp_check("Pagophilus groenlandicus")

## [1] FALSE
```

Can I see all records for a given trait?

```
traitAllSpp("biomass") # Only the first five records are shown for space

## [1] "NDY"    "50578"  "ND"     "52500"  "351000" "62000"
```

Can I see an overview of all records for a given species?

```
singSppTraitSummary("Aepyceros melampus")

##   biomass height   growthdet regen   dimorph        matsyst     hermaph se
qherm

## 1   52500    NDY Determinate   NDY Dimorphic Non-monogamous Gonochorous
NDY

##           dispcap disptype modedisp dispclass    volancy

## 1 Natal Dispersal   Active   Motile     Adult Non-volant
```

```
##                                   aquadep
## 1 Terrestrial, Water Habitat Independent
```

Can I see all records for more than one species?

```
sppAllTrait(c("Acinonyx jubatus", # you can also pass lists or dataframes to
this command
               "Acropora downingi",
               "Aepyceros melampus",
               "Alces alces",
               "Alligator mississippiensis"))
##                      sppnames biomass height   growthdet        regen   dim
orph
## 1           Acinonyx jubatus   50578    NDY Determinate          NDY Dimor
phic
## 2          Acropora downingi      ND    NDY         NDY Regenerative
NDY
## 3         Aepyceros melampus   52500    NDY Determinate          NDY Dimor
phic
## 4                Alces alces  351000    NDY Determinate          NDY Dimor
phic
## 5 Alligator mississippiensis   62000    NDY Determinate Regenerative
NDY
##          matsyst        hermaph seqherm         dispcap disptype       mod
edisp
## 1 Non-monogamous    Gonochorous     NDY Natal Dispersal   Active         M
otile
## 2            NDY Hermaphroditic     NDY Natal Dispersal  Passive Water cur
rents
## 3 Non-monogamous    Gonochorous     NDY Natal Dispersal   Active         M
otile
## 4 Non-monogamous    Gonochorous     NDY Natal Dispersal   Active         M
otile
## 5 Non-monogamous    Gonochorous     NDY Natal Dispersal   Active         M
otile
##            dispclass    volancy                                      aqua
dep
## 1           Juvenile Non-volant        Terrestrial, Water Habitat Independ
ent
## 2           Juvenile Non-volant                                        Mar
ine
```

```
## 3              Adult Non-volant        Terrestrial, Water Habitat Independent
## 4           Juvenile Non-volant Terrestrial, Facultative Freshwater Dependent
## 5 Adult and Juvenile Non-volant  Terrestrial, Obligative Freshwater Dependent
```

Can I get a breakdown of counts/frequency of trait values?

```
traitFrequency("volancy")
##             counts  freq
## NDY           1329    NA
## Non-volant      82 0.882
## Semi-volant      1 0.011
## Volant          10 0.108
traitFrequency("growthdet")
##               counts  freq
## Determinate       31 0.596
## Indeterminate     21 0.404
## NDY             1370    NA
traitFrequency("hermaph")
##                              counts  freq
## Dioecious                        24 0.108
## Gonochorous                     106 0.475
## Hermaphroditic                   72 0.323
## Hermaphroditic & Gonochorous      1 0.004
## Monoecious                       20 0.090
## NDY                            1199    NA
```

Can I get all metadata for one or more traits?

```
metadata("volancy", 14)
##              author year                    journal database mosaic
## 1 Campos, Z. et al. 2006 The Herpetological Journal      NDY    NDY
multiMetaRecords("volancy", c(14:20))
##                                     author year
```

```
## 1                 Ekerna, L. S. & Cords, M. 2007
## 2                   Zimmerman, S. J. et al. 2019
## 3 Jack, K. M., Sheller, C. & Fedigan, L. M. 2012
## 4                                       DFO 2013
## 5                     Torres, R. T. et al. 2017
## 6                                       NDY  NDY
## 7                        Campos, Z. et al. 2006
##
journal
## 1                                                                    A
nimal Behaviour
## 2
The Condor
## 3                                                        American Journal
of Primatology
## 4 Canadian Science Advisory Secretariat Central and Arctic Region Science
Advisory Report
## 5
Oryx
## 6
NDY
## 7                                                           The Herpeto
logical Journal
##   database mosaic
## 1      NDY    NDY
## 2      NDY    NDY
## 3      NDY    NDY
## 4      NDY    NDY
## 5      NDY    NDY
## 6      NDY    NDY
## 7      NDY    NDY
```

Tidyverse + MOSAIC

http://mosaicdatabase.web.ox.ac.uk

Updated 14 March 2022

Vignette #2 - Tidyverse + MOSAIC

MOSAIC was built for use and integration with other datasets for comparative demography. Demographers are often interested in how traits scale across different taxonomic levels. The Tidyverse https://www.tidyverse.org/ collection of R packages (Dplyr in particular) are commonly used by ecologists to simplify workflows that subset and manipulate data. Here, we walk throught the basics of how Tidy tools can be use with the MOSAIC database to quickly isolate specific groups of organism or classes of records.

```
library(tidyverse)
```

Accessing MOSAIC

Download MOSAIC from the mosaic portal. For more information on the basics of downloading MOSAIC and navigating the data structure, see: Vignette #1:

```
remotes::install_github("mosaicdatabase/Rmosaic")
library(Rmosaic)
mosaic <- mos_fetch("v1.0.0")
```

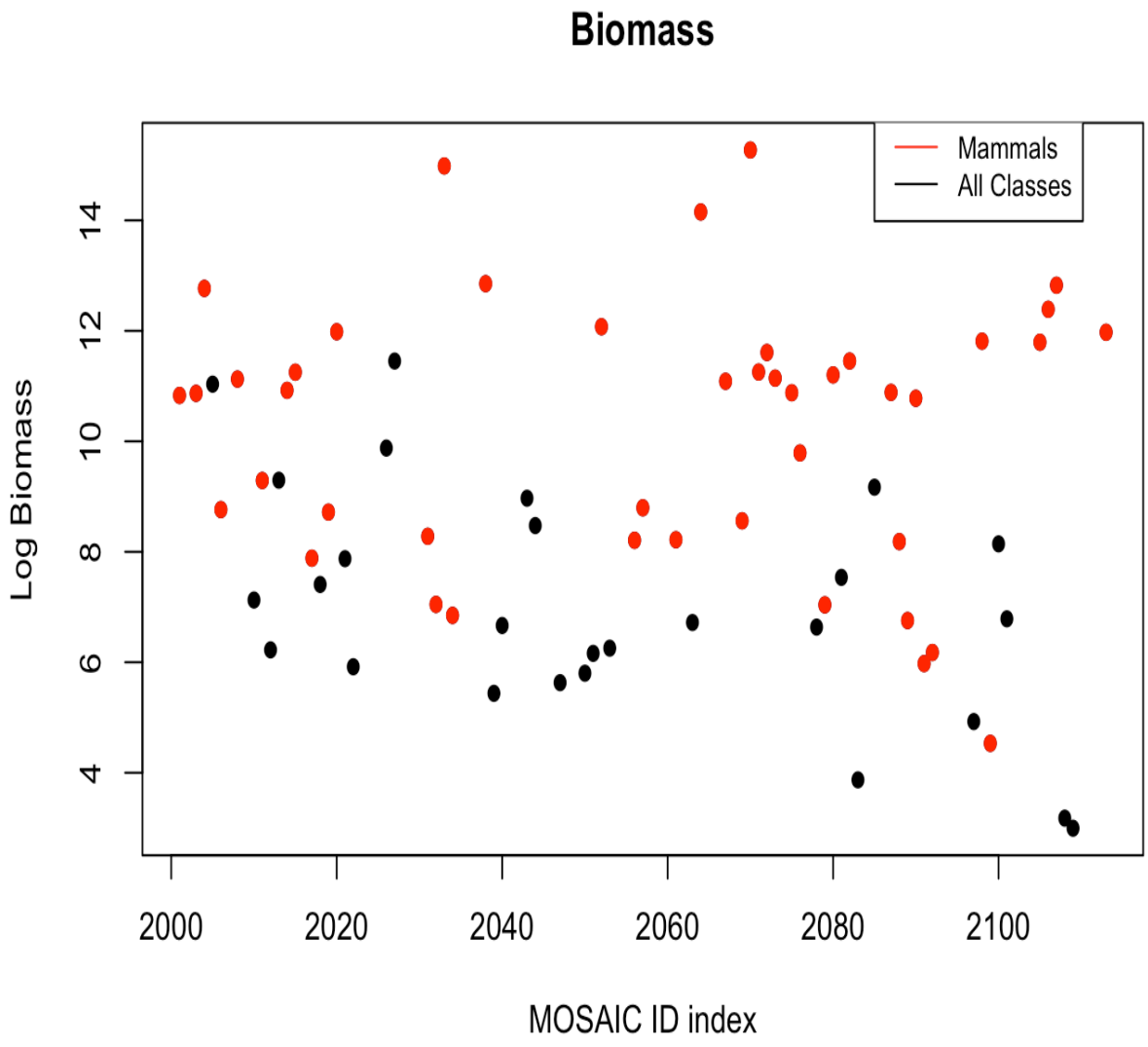
Using Tidyverse with MOSAIC

Tidyverse allows for the easily filtering of outliers and NAs, and the isolation of records to particular groups of taxa in MOSAIC. For example, one can isolate the differences in biomass between birds and mammals and see how the decomposition of variance in biomass between the groups informs the representation of biomass values in MOSAIC

```
# Bind the ID field, species, taxa, and biomass fields into a unified datafra
me

biomass_table <- cbind(mosaic@mosaicID,
                       mosaic@species,
                       mosaic@taxaMetadat,
```

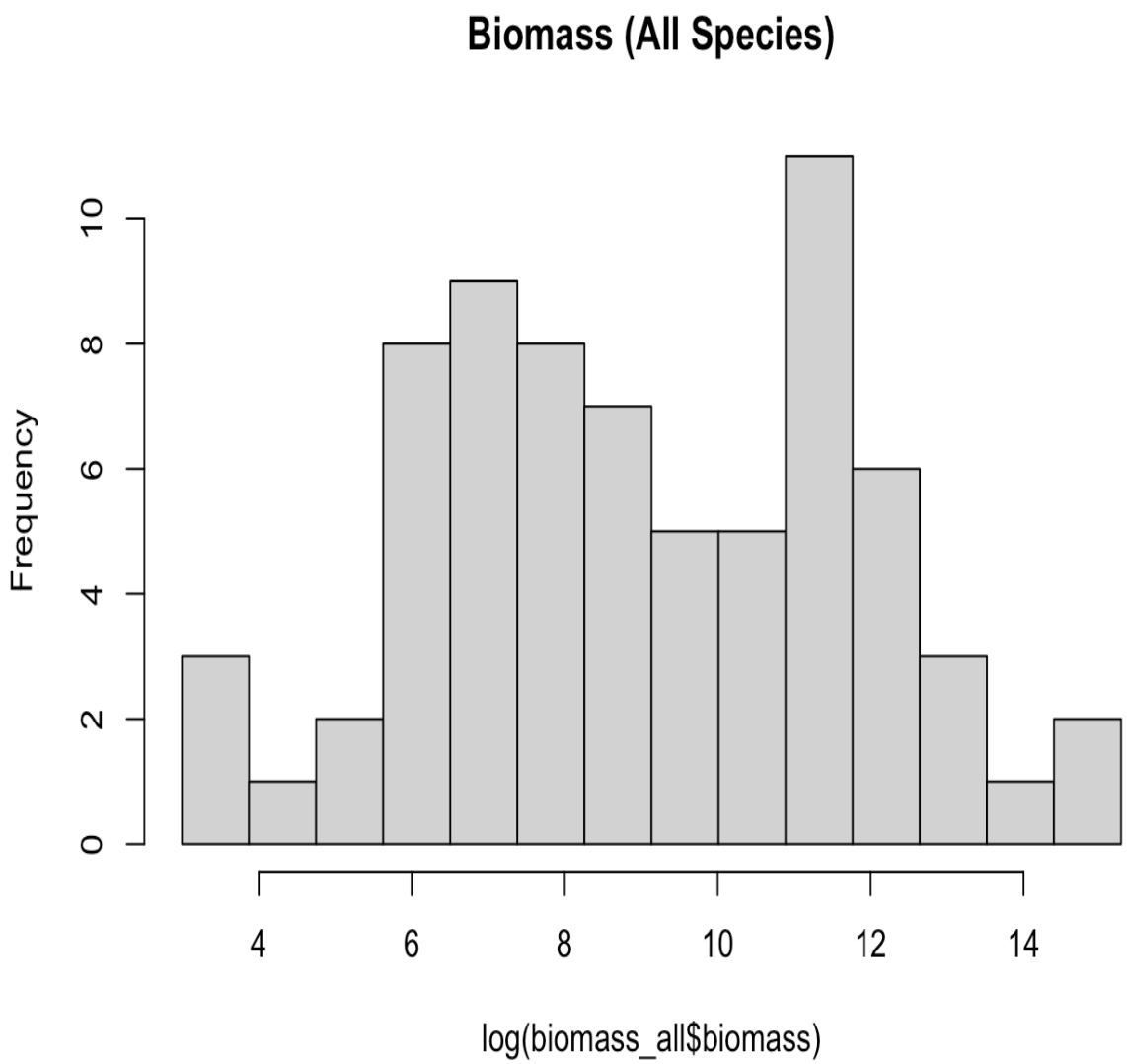
```
                        mosaic@biomass@value)

# Relabel the biomass field

names(biomass_table)[length(biomass_table)] <- "biomass"

# Coerce the field into a numeric values - transforms "NDY" into "NA"

biomass_table$biomass <- as.numeric(biomass_table$biomass)

# Removing an outlier and filtering out NAs

biomass_all <- biomass_table %>%
  drop_na(biomass) %>%
  filter(biomass < 12000000)

# Filter to mammals

biomass_mamm <- biomass_table %>%
  filter(Class == "Mammalia") %>%
  drop_na(biomass) # Remove results that are NA

# Filter to birds

biomass_aves <- biomass_table %>%
  filter(Class == "Aves") %>%
  drop_na(biomass)

# Plot all biomass

plot(biomass_all$`mosaic@mosaicID`, log(biomass_all$biomass), pch=16,
     xlab = "MOSAIC ID index", ylab = "Log Biomass", main = "Biomass")

# Highlight points for mammals
```

```
points(biomass_mamm$`mosaic@mosaicID`, log(biomass_mamm$biomass), pch=16, col
="red")


legend(2085, 16, legend=c("Mammals", "All Classes"),
       col=c("red", "black"), lty=1, cex=0.8)
```

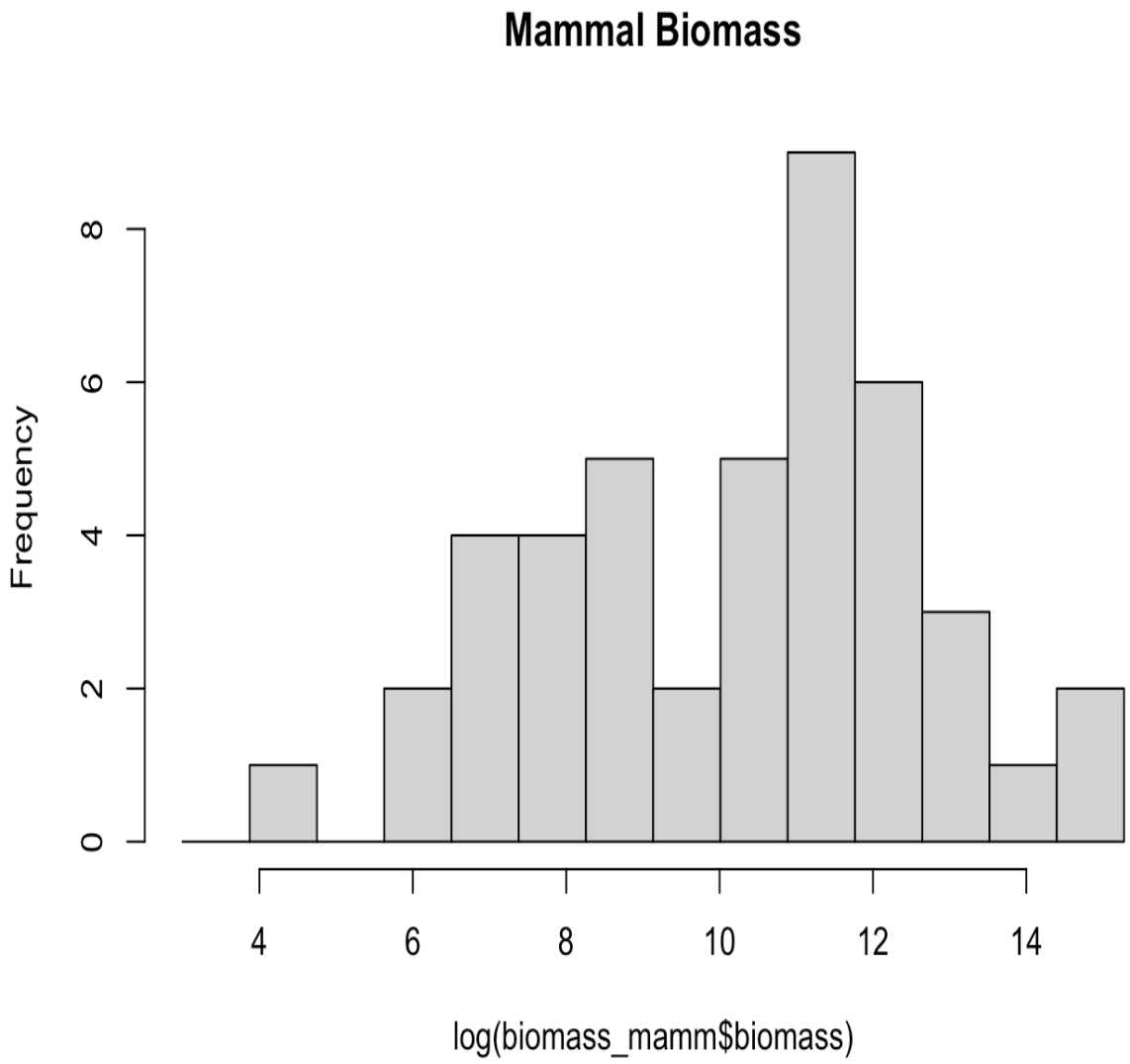



```
# Generate histograms for all species on the same binning scale


Bin_all <- hist(log(biomass_all$biomass),
```

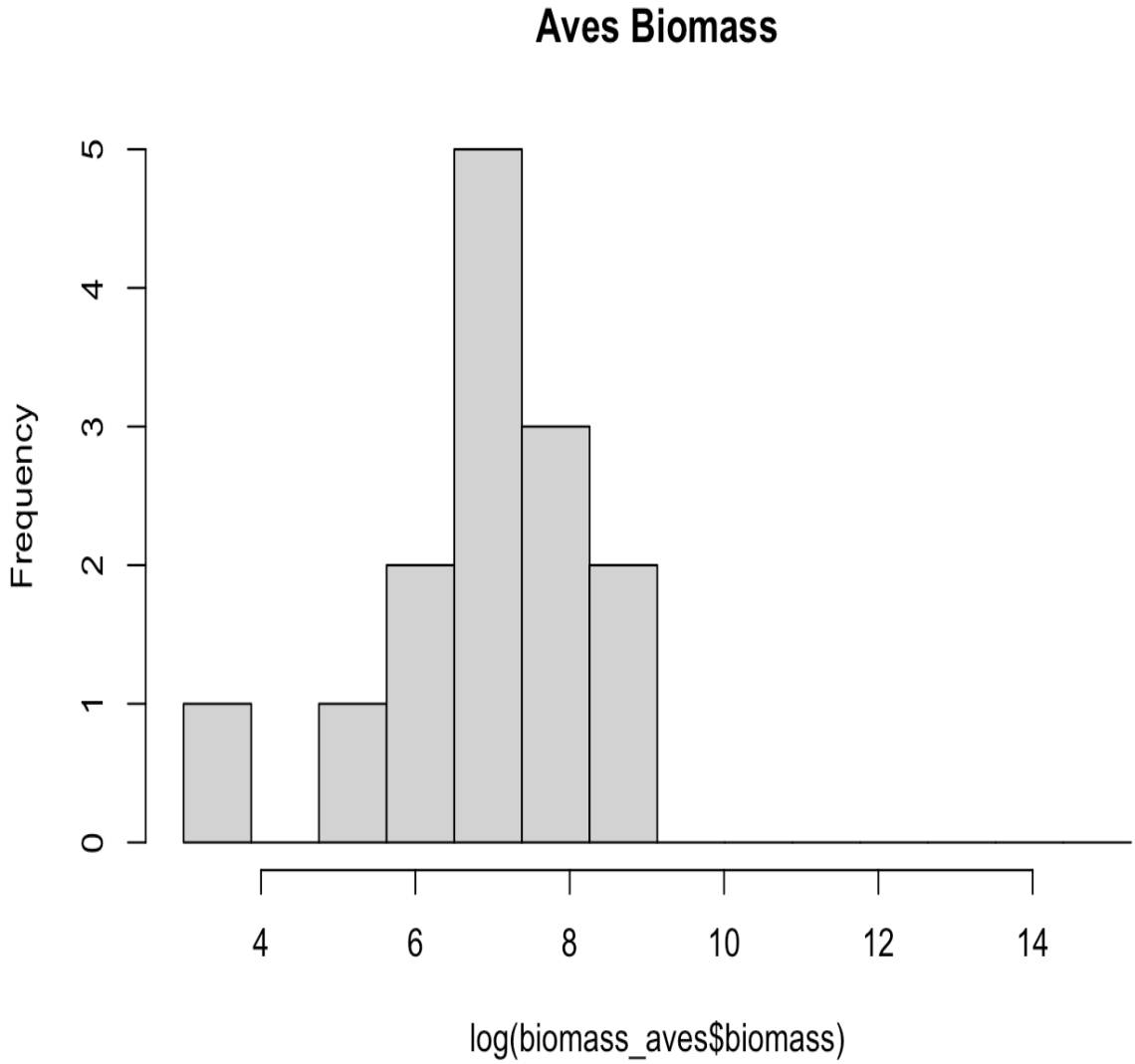
```
                 breaks=seq(min(log(biomass_all$biomass)), max(log(biomass_all
$biomass)),
                            length=15), main="Biomass (All Species)")
```




```
Bin_mamm <- hist(log(biomass_mamm$biomass),
                 breaks=seq(min(log(biomass_all$biomass)), max(log(biomass_all
$biomass)),
                            length=15), main = "Mammal Biomass")
```

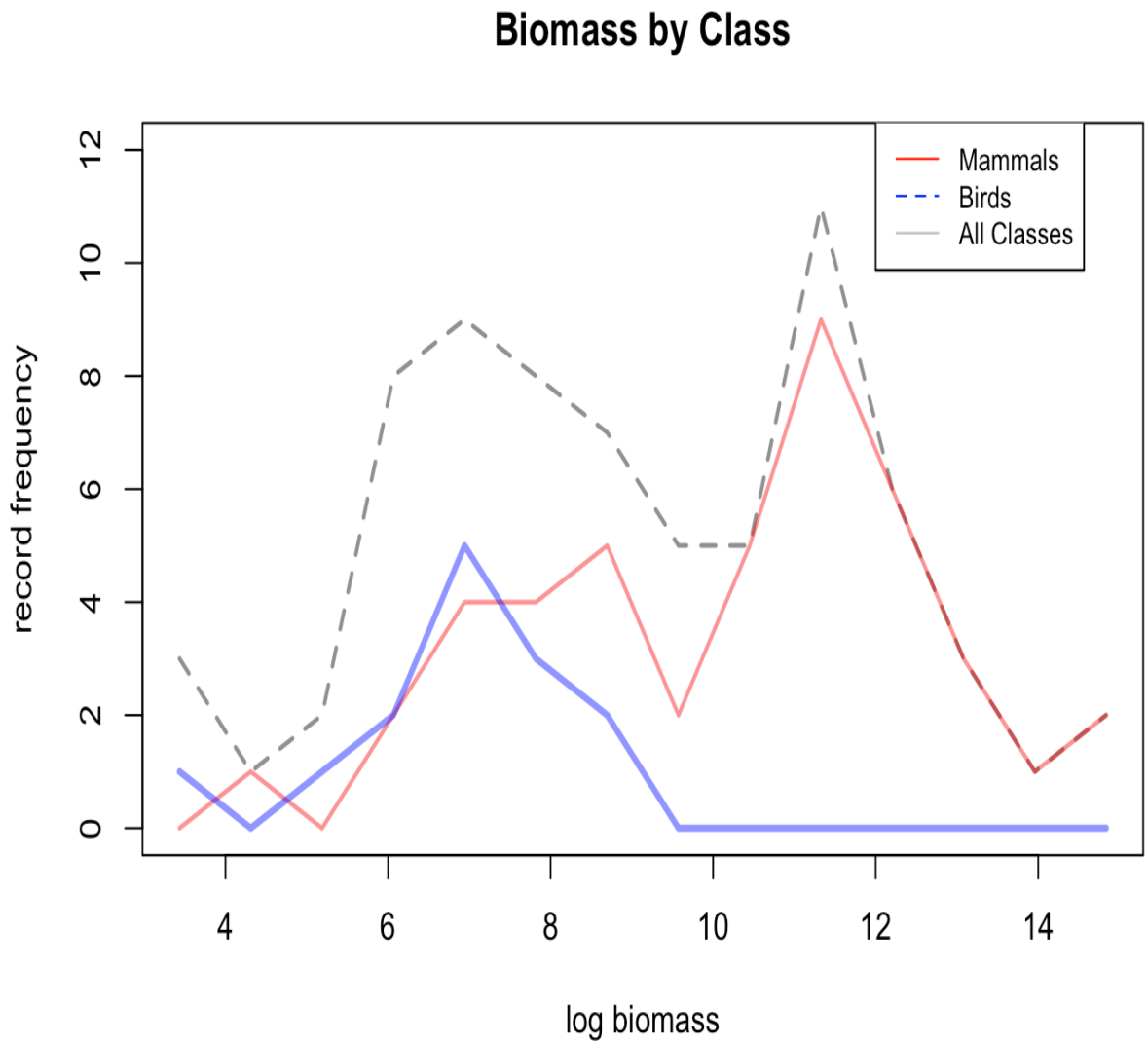



```
Bin_aves <- hist(log(biomass_aves$biomass),
                 breaks=seq(min(log(biomass_all$biomass)), max(log(biomass_al
l$biomass)),
                            length=15), main = "Aves Biomass")
```




```
# Ploting frequency-density curves for species


plot(Bin_all$mids, Bin_all$counts, pch=16, type="l", col=alpha("black", 0.5),
lwd=2, lty=2,

     ylim=c(0,12), ylab="record frequency", xlab="log biomass", main="Biomass
by Class")

points(Bin_mamm$mids, Bin_mamm$counts, pch=16, type="l", col=alpha("red", 0.5
), lwd=2)

points(Bin_aves$mids, Bin_aves$counts, pch=16, type="l", col=alpha("blue", 0.
5), lwd=3)

legend(12, 12.5, legend=c("Mammals", "Birds", "All Classes"),
```

```
        col=c("red", "blue", "gray"), lty=1:2, cex=0.8)
```

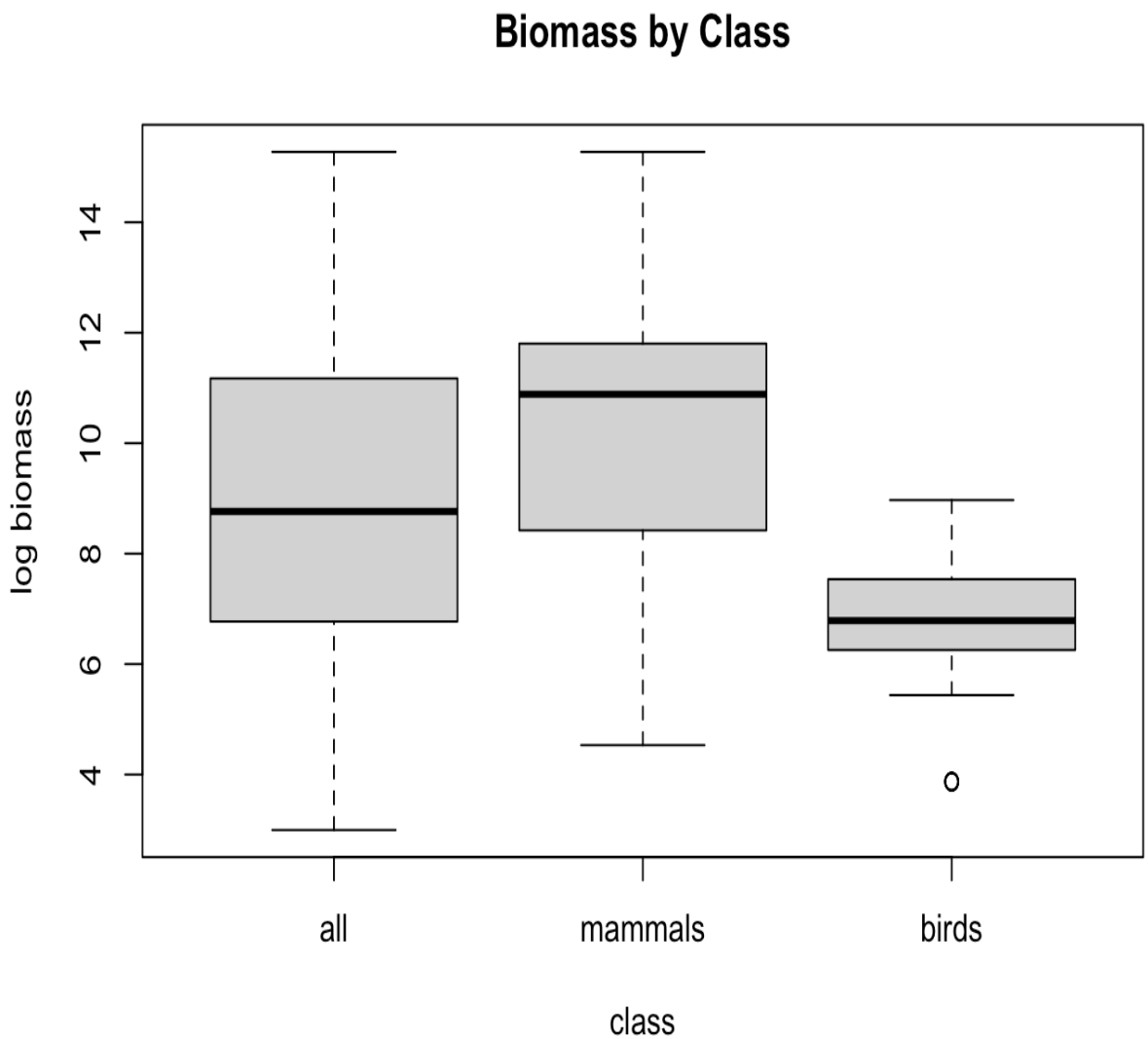



```
# Note how the peak in records of large mammals is driven by mammals, whereas
the high record count in smaller values is sustained on the aves records. Ind
ividually, the biomass distributions are semi-normal, whereas the joint distr
ibution is more complex.
```

Alternatively, the same data could be plotted by group with boxplots, illustrating the same sotry.

```
bio_mamm.aves <- cbind(log(biomass_all$biomass), log(biomass_mamm$biomass), l
og(biomass_aves$biomass))

colnames(bio_mamm.aves) <- c("all", "mammals", "birds")
```

```
boxplot(bio_mamm.aves, ylab="log biomass", xlab="class", main="Biomass by Cla
ss")
```

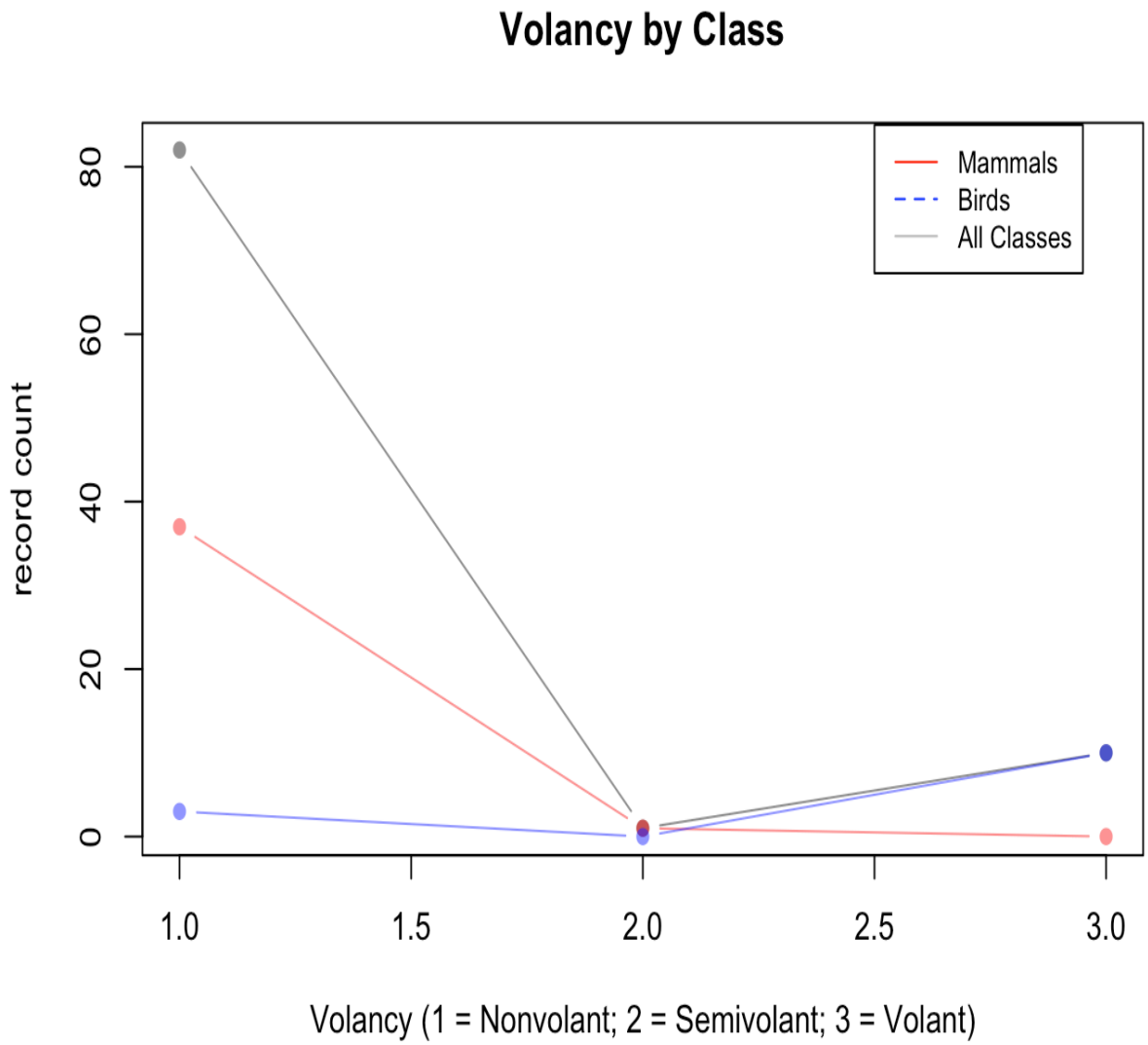


Factor variables can similarly be parsed by class.

```
# Bind the ID field, species, taxa, and volancy fields into a unified datafra
me


bio_vol <- cbind(mosaic@mosaicID,
                 mosaic@species,
                 mosaic@taxaMetadat,
                 mosaic@volancy@value)
```

```
# Relabel the volancy field

names(bio_vol)[length(bio_vol)] <- "volancy"

# Assign into a factor class

bio_vol$volancy <- as.factor(bio_vol$volancy)

# Filter out NDYs

vol_all <- bio_vol %>%
  filter(!volancy == "NDY")

# Filter to Mammals

vol_mamm <- bio_vol %>%
  filter(Class == "Mammalia") %>%
  filter(!volancy == "NDY")

# Filter to birds

vol_aves <- bio_vol %>%
  filter(Class == "Aves") %>%
  filter(!volancy == "NDY")

# Look at the summary of factors to counts

summary(vol_mamm$volancy)
##         NDY  Non-volant Semi-volant      Volant
##           0          37           1           0
summary(vol_aves$volancy)
##         NDY  Non-volant Semi-volant      Volant
##           0           3           0          10
```

```r
# Store summaries

vol_all_summary <- summary(vol_all$volancy)
vol_mamm_summary <- summary(vol_mamm$volancy)
vol_aves_summary <- summary(vol_aves$volancy)

# Plot the points

plot(vol_all_summary[2:4],  type="b", pch=16, col=alpha("black", 0.5),
     ylab="record count", xlab="Volancy (1 = Nonvolant; 2 = Semivolant; 3 = V
olant)", main="Volancy by Class")
points(vol_mamm_summary[2:4], type="b", pch=16, col=alpha("red", 0.5))
points(vol_aves_summary[2:4], type="b", pch=16, col=alpha("blue", 0.5))
legend(2.5, 85, legend=c("Mammals", "Birds", "All Classes"),
       col=c("red", "blue", "gray"), lty=1:2, cex=0.8)
```



If one is more generally interested in the class breakdown of factors across a trait field without a priori interest in a specific variable, one can take advantage of the tools.

```
# Evaluating the variance breakdown within a given class

Volant_sum <- bio_vol %>%
  filter(volancy=="Volant")%>%
  group_by(Class, volancy)%>%
  count()

Semivolant_sum <- bio_vol %>%
```

```
  filter(volancy=="Semi-volant")%>%
  group_by(Class, volancy)%>%
  count()

Nonvolant_sum <- bio_vol %>%
  filter(volancy=="Non-volant")%>%
  group_by(Class, volancy)%>%
  count()

volTable <- Nonvolant_sum # Generating DF

volTable <- volTable[,-2]
colnames(volTable)[2] <- "Nonvolant"
volTable[,3] <- rep(0, length(Nonvolant_sum$Class))
volTable[,4] <- rep(0, length(Nonvolant_sum$Class))
colnames(volTable)[3] <- "Volant"
colnames(volTable)[4] <- "Semivolant"
volTable[match(Volant_sum$Class, Nonvolant_sum$Class),3] <- Volant_sum$n
volTable[match(Semivolant_sum$Class, Nonvolant_sum$Class),4] <- Semivolant_su
m$n

volTable
## # A tibble: 13 × 4
## # Groups:   Class [13]
##    Class          Nonvolant Volant Semivolant
##    <chr>              <int>  <dbl>      <dbl>
##  1 Actinopterygii         9      0          0
##  2 Amphibia               1      0          0
##  3 Anthozoa               5      0          0
##  4 Aves                   3     10          0
##  5 Bivalvia               3      0          0
##  6 Branchiopoda           2      0          0
##  7 Demospongiae           1      0          0
##  8 Elasmobranchii         1      0          0
##  9 Gastropoda             3      0          0
```

```
## 10 Insecta                 2      0          0
## 11 Mammalia               37      0          1
## 12 Reptilia                8      0          0
## 13 <NA>                    7      0          0
```

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Basic Regression using MOSAIC

http://mosaicdatabase.web.ox.ac.uk

Updated 22 February 2022

Vignette #3 - Basic Regression Using MOSAIC & COMPADRE

MOSAIC was built with the intention of its use in comparative biodemography - to strengthen the map of which functional traits predict vital rates and which do not. Traits in the MOSAIC database (factorial and numeric variables) are formatted to be easily accessed and used for regression-based analyses, among other types of analysis. MOSAIC was also designed for quick integration with the COMADRE, COMPADRE, and PADRINO structural population model databases, as outlined in the model exercise below.

```
library(devtools)

library(tidyverse)

library(Rcompadre) # package to access matrix population models

library(Rage) # package to perform life-history calculations
```

Accessing MOSAIC

Download MOSAIC from the mosaic portal. For more information on the basics of downloading MOSAIC and navigating the data structure, see: Vignette #1:

```
library(devtools) # Compulsory package to pull down packages from GitHub. Ins
tall if necessary.

install_github("mosaicdatabase/Rmosaic") # library of navigation-aiding funct
ions

source_url("https://raw.githubusercontent.com/mosaicdatabase/mosaicdatabase/m
ain/mosaic_fetch.R") # Link to GitHub repo

mosaic <- mos_fetch("v1.0.0") # Download version 1.0.0 (active version Feb 20
22)

library(Rmosaic)
```

Regressing Biomass on Generation Time

In this exercise, the simple bivariate relationship of biomass on generation time is explored through basic regression. Bare in mind, that the below offer the building blocks for more complex multiple regression exercises and other forms of analysis – such as geospatial interpolation and ordination-based practices (see Vignette #4 for a brief vignette of PVA using mosaic).

#1: Extract biomass data for mammals

Extract the biomass values for mammals in the MOSAIC dataset.

```
# Extracting all biomass data

mosaic_dataframe <- data.frame(mosaic@taxaMetadat,
                               Biomass = as.numeric(mosaic@biomass@value),
                               MOSAIC_index = 1:length(mosaic@index))

# Restrict mammal data with non NA biomass data

mosaic_mammal <- subset(mosaic_dataframe,
                        Class == "Mammalia" & is.na(Biomass) == F)

# Extracting the first COMPADRE matrix id for each entry

matrix_ids_full <- mosaic@index[mosaic_mammal$MOSAIC_index]

# Extract just the first matrix id using sapply

mammal_matrix_ids <- sapply(matrix_ids_full, `[[`, 1)

# Add matrix id to the mammal data

mosaic_mammal$MatrixID <- mammal_matrix_ids

# Add full species names

mosaic_mammal$Binomial <- paste0(mosaic_mammal$Genus, " ", mosaic_mammal$Spec
ies)
```

#2: Download COMADRE matrix population models

A cdb_fetch() function is used to clone the Comadre database <www.compadre-db.org> - which is an s3 copy of a SQL-based relational database - into an S4 data object locally manipulable in R.

Using ids associated with each matrix population model, we will subset the Comadre database of matrix population models for the animals. First we use the Rcompadre package to 'fetch' the Comadre database.

```
# Download the most recent database

comadre <- cdb_fetch("comadre")

# Rcompadre function flags potential issues with matrices, including NAs and ergodicity

comadre_flag <- cdb_flag(comadre)

# Remove matrices with NAs and those that are non-ergodic (which throw errors in generation time)

comadre_correct <- subset(comadre_flag,
                          check_NA_A == FALSE &
                          check_ergodic == TRUE)
```

The subsets of mosaic and Compadre can be overlapped in one line of code.

```
# Subset to mammal matrices

comadre_biomass <- subset(comadre_correct,
                          MatrixID %in% mammal_matrix_ids)
```

3. Calculating generation time

Rcompadre enables sub-setting of a matrix population model (life table) into constituent matrices representing the survival and fecundity/reproductive components (U and F matrices, respectively). Functions in the Rage package often require the specification of both the U and the F matrix, not the combined A matrix. The Rage package contains a suite of common demographic calculations - including GENERATION TIME - which are used to simplify this exercise. Note that other common demographic derivations, including transient indices can be extracted using the identical procedure.

```
# Calculate Generation Time

comadre_biomass$Generation_Time <- mapply(Rage::gen_time,
                                          matU(comadre_biomass),
```

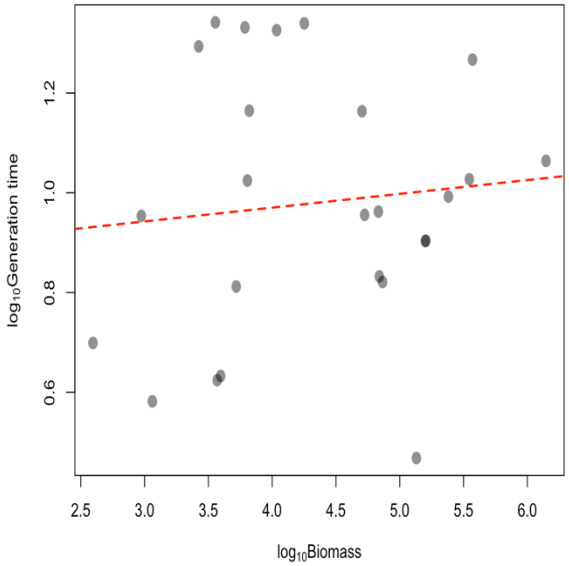
```
                                                matF(comadre_biomass))
```

4. Explore the relationship of generation time data and biomass data

Matrix IDs can be used to bridge generation time from comaadre with mosaic records.

```
# Extract matrix ID and generation time columns (excluding other matrix metad
ata)

comadre_biomass <- as.data.frame(comadre_biomass)

comadre_biomass <- comadre_biomass[,c("MatrixID", "Generation_Time")]

# Join the datasets, using Matrix IDs to crosswalk the data

mosaic_biomass <- merge(mosaic_mammal, comadre_biomass,
                        by = "MatrixID", all.x = TRUE)
# Remove infinity values or NA

mosaic_biomass <- mosaic_biomass[!(is.infinite(mosaic_biomass$Generation_Time
) |
                                   is.na(mosaic_biomass$Generation_Time)),]

# Log biomass and generation time

mosaic_biomass$log10_biomass <- log10(mosaic_biomass$Biomass)
mosaic_biomass$log10_gent <- log10(mosaic_biomass$Generation_Time)




# The plot

plot(mosaic_biomass$log10_biomass, mosaic_biomass$log10_gent,
     pch=16, cex=1.5, col=alpha("black", 0.5),
     xlab=expression(paste(log[10], "Biomass")),
     ylab=expression(paste(log[10], "Generation time"))
```

```
)



# Simple linear regression (note that we are skipping model fitting in this b
rief vignette)

lmBioGenT = lm(log10_gent~log10_biomass, data = mosaic_biomass)

summary(lmBioGenT)
##
## Call:
## lm(formula = log10_gent ~ log10_biomass, data = mosaic_biomass)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.53325 -0.16107 -0.01597  0.19936  0.38382
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.85966    0.25372   3.388  0.00253 **
## log10_biomass  0.02762    0.05728   0.482  0.63418
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2623 on 23 degrees of freedom
## Multiple R-squared:  0.01001,    Adjusted R-squared:  -0.03303
## F-statistic: 0.2326 on 1 and 23 DF,  p-value: 0.6342
abline(lmBioGenT, col="red", lty=2, lwd=2)
```


log10Generation time
0.6
0.8
1.0
1.2
2.5
3.0
3.5
4.0
4.5
5.0
5.5
6.0
log10Biomass

Dimension Reduction + MOSAIC

http://mosaicdatabase.web.ox.ac.uk

Updated 14 March 2022

Vignette #4 - Dimension Reduction + MOSAIC

MOSAIC was built for integrated analyses across trait fields. Whether the data are continuous (e.g., biomass) or categorical (e.g., dispersal class), MOSAIC allows researchers to explore these dimensions to identify the primary axes of variation across functional traits. Here, we will use a Multiple Factor Analysis (MFA) to explore the primary axes of variation between: biomass, dispersal capacity, growth determination, habitat type and mating system.

Note: These traits are picked solely to illustrate the analysis method that can be scaled for other traits in MOSAIC, demographic rates in COMADRE, COMPADRE and PADRINO and climate data from ERA5-Land.

```
library(devtools)
library(tidyverse)
library(FactoMineR) # Required for MFA.
library(factoextra) # Required for visualizing MFA.
```

Accessing MOSAIC

Download MOSAIC from the mosaic portal. For more information on the basics of downloading MOSAIC and navigating the data structure, see: Vignette #1:

```
remotes::install_github("mosaicdatabase/Rmosaic")
library(Rmosaic2.0)
mosaic <- mos_fetch("v1.0.0")
```

```
##
## Phylogenetic tree with 1359 tips and 1358 internal nodes.
##
## Tip labels:
##   Oxalis_acetosella, Rourea_induta, Euphorbia_telephioides, Euphorbia_font
queriana, Triadica_sebifera, Actinostemon_concolor, ...
## Node labels:
##   Node1, Node2, Node3, Node4, Node5, Node6, ...
##
```

```
## Rooted; includes branch lengths.
```

Generating Dataframe

```
# Create a dataframe storing the values of the traits of interest.

mosaic_dataframe <- data.frame(mosaic@taxaMetadat,
                               Biomass = as.numeric(mosaic@biomass@value),
                               Growth_Determination = as.factor(mosaic@growth
det@value),
                               Mating_System = as.factor(mosaic@matsyst@value
),
                               Dispersal_Capacity = as.factor(mosaic@dispcap@
value),
                               Habitat_Type = as.factor(mosaic@aquadep@value)
)

# Create a dataframe that only contains data for MFA.
# This step makes all dimension reduction functions easier.

mosaic_dataframe_subset <-  mosaic_dataframe[,c(8:12)] %>%
  drop_na() %>%
  filter(Growth_Determination != "NDY") %>%
  filter(Mating_System != "NDY") %>%
  filter(Dispersal_Capacity != "NDY") %>%
  filter(Habitat_Type != "NDY")
```

Perform MFA

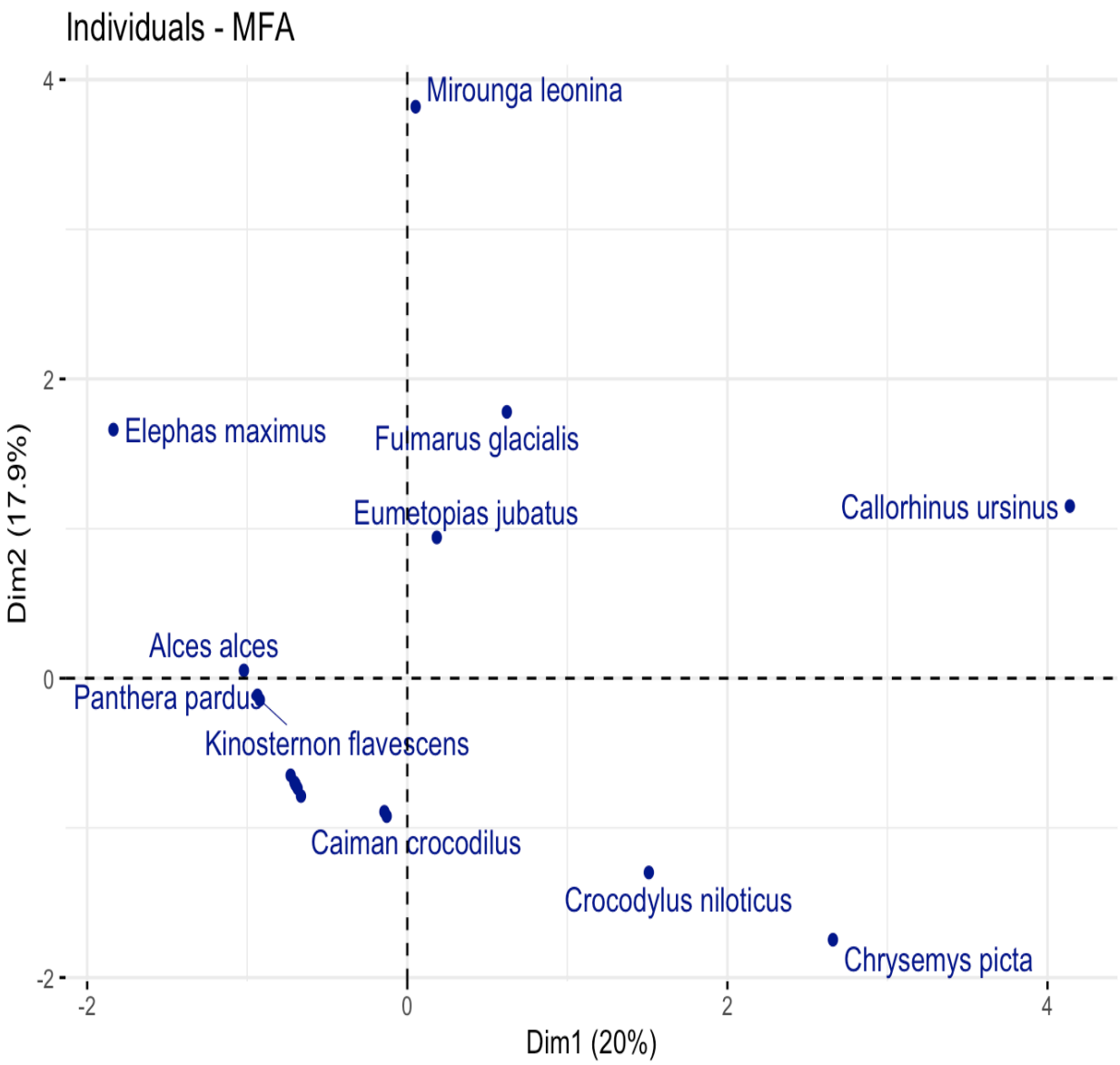
```
# Run the multiple factor analysis using the MFA() function from FactoMineR.

mfa_mosaic <- MFA(mosaic_dataframe_subset, group = c(1, 1, 1, 1, 1),
    type = c("s", rep("n", 4)),
    name.group=c("Biomass","Growth_Determination","Mating_System","Dispersal_
Capacity", "Habitat_Type"),
    graph = FALSE)

```

```
# Note: Changing the graph argument to TRUE will return some diagnostic graph
s of the MFA.
```

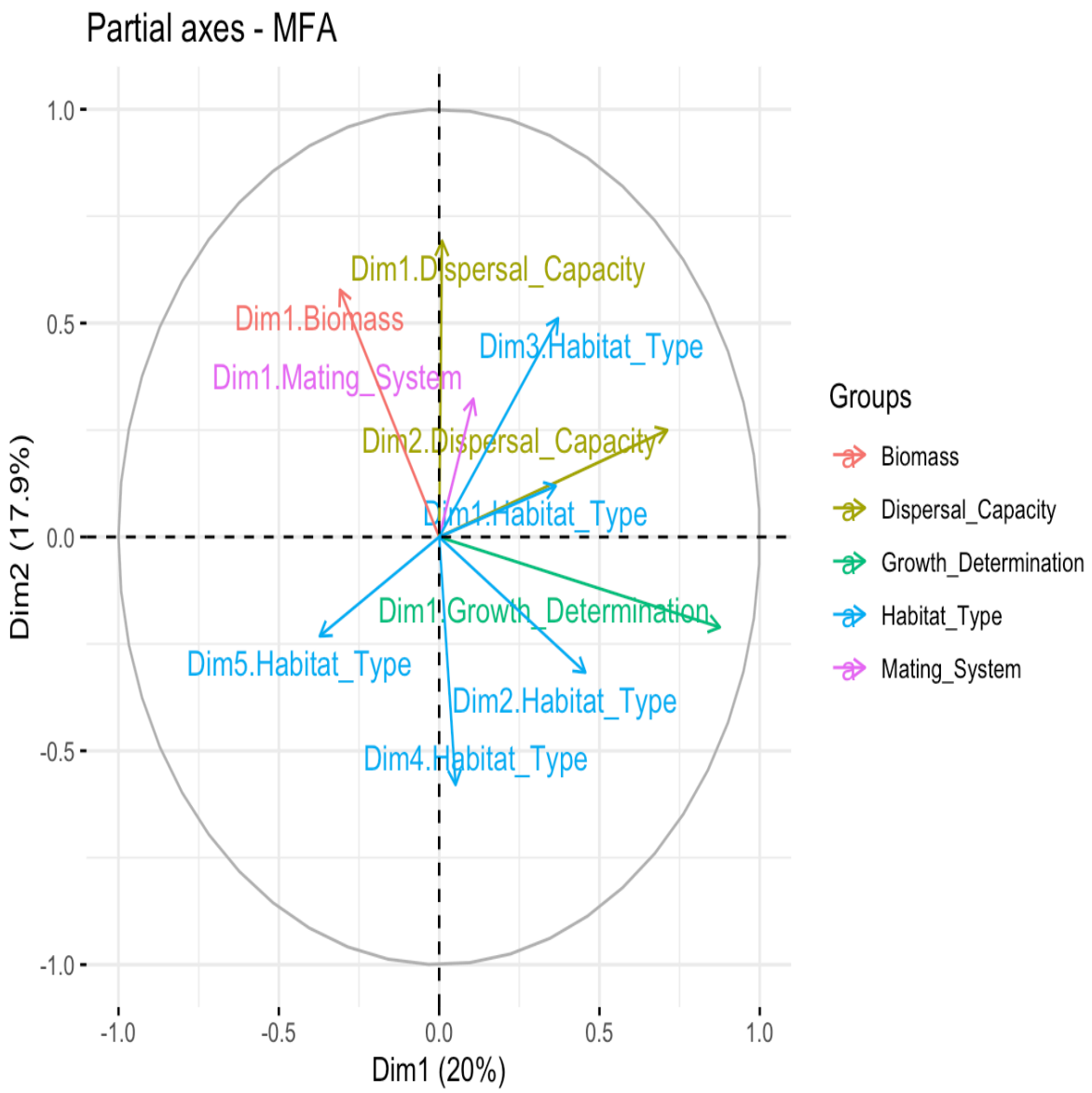
Explore MFA

In this hypothetical example, we are interested in what traits covary with the primary axes of variation in the MFA (i.e., Dim1 and Dim2). To visualize these relationships, we can use the in-built fviz functions in the factoextra package to illustrate (1) position of individuals, (2) average effect of trait level (i.e. monogamous) on individual position within the 2 dimensions and (3) average effect of trait type (i.e. mating system).

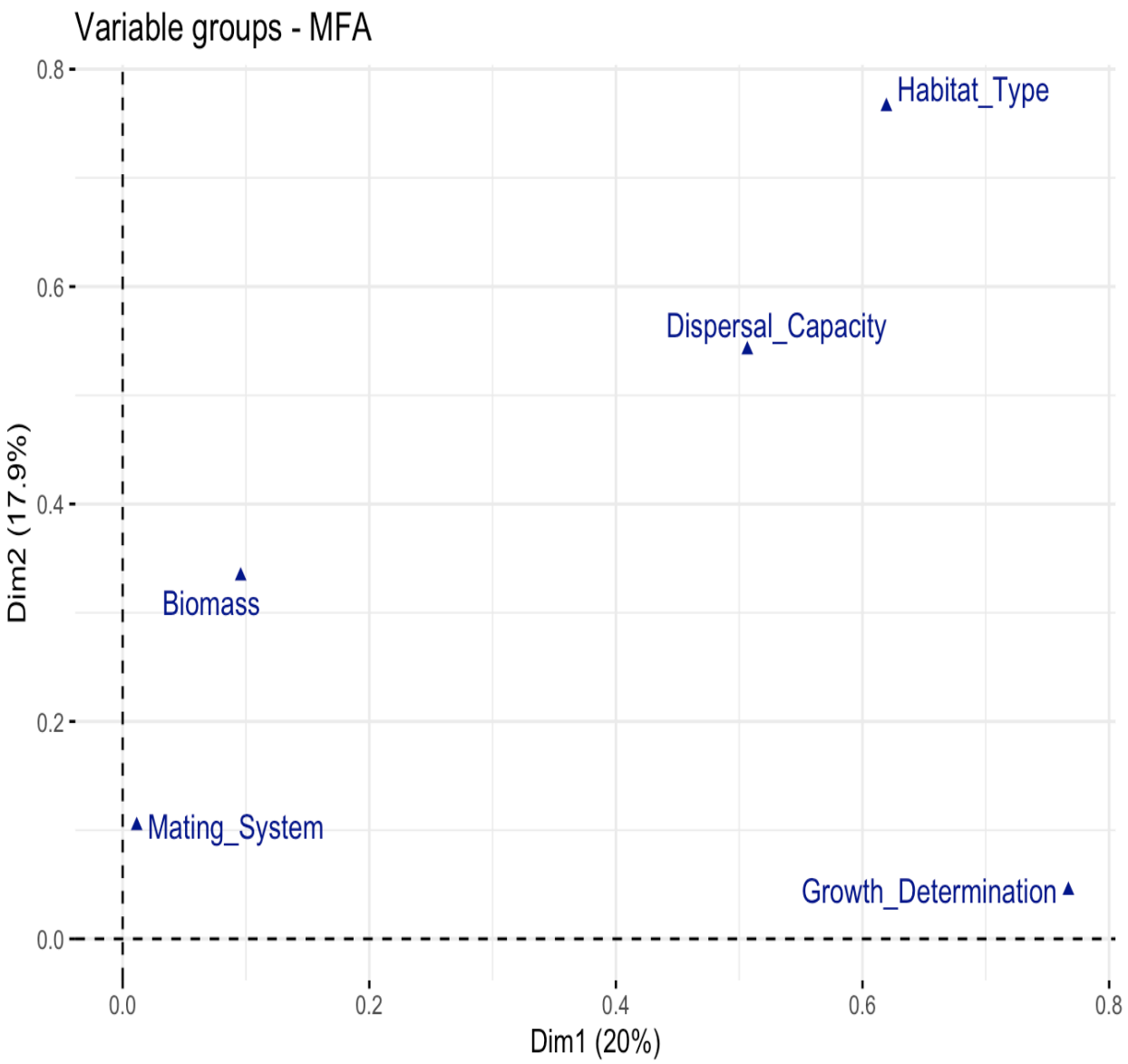
```
fviz_mfa_ind(mfa_mosaic,
             repel = TRUE,
             col.ind = "dark blue")
```




```
fviz_mfa_axes(mfa_mosaic,
              repel = TRUE)
```




```
fviz_hmfa_var(mfa_mosaic,
              repel = TRUE,
              choice = "group",
              col.var = "dark blue")
```


Variable groups - MFA
Habitat_Type
Dispersal_Capacity
Biomass
Mating_System
Growth_Determination
Dim2 (17.9%)
Dim1 (20%)
0.0
0.2
0.4
0.6
0.8

2380

2381

Climate Data + MOSAIC

http://mosaicdatabase.web.ox.ac.uk

Updated 14 March 2022

Vignette #5 - Climate Data + MOSAIC

MOSAIC was built with the intention of its use in comparative biodemography - to strengthen the map of which functional traits predict vital rates and which do not. Traits in the MOSAIC database (factorial and numeric variables) are formatted to be easily accessed and used for regression-based analyses, among other types of analysis. MOSAIC was also designed with the analysis of demographic metrics and traits in their environmental contexts. To this end, MOSAIC includes a separate object (climate) which we will access and make use of in the following exercise.

```
library(devtools)
library(tidyverse)
library(leaflet)
```

Accessing MOSAIC

Download MOSAIC from the mosaic portal. For more information on the basics of downloading MOSAIC and navigating the data structure, see: Vignette #1:

```
remotes::install_github("mosaicdatabase/Rmosaic")
library(Rmosaic2.0)
mosaic <- mos_fetch("v1.0.0")
```

```
##
## Phylogenetic tree with 1359 tips and 1358 internal nodes.
##
## Tip labels:
##   Oxalis_acetosella, Rourea_induta, Euphorbia_telephioides, Euphorbia_font
queriana, Triadica_sebifera, Actinostemon_concolor, ...
## Node labels:
##   Node1, Node2, Node3, Node4, Node5, Node6, ...
##
## Rooted; includes branch lengths.
```

Selecting Target Matrices

To get this exercise started, we first need to select which part of MOSAIC we are interested in. For simplicity, we are here focusing on mammal biomass as was done in Vignette #2:

```
# Extracting all biomass data
mosaic_dataframe <- data.frame(mosaic@taxaMetadat,
                               Biomass = as.numeric(mosaic@biomass@value),
                               MOSAIC_index = 1:length(mosaic@index))

# Restrict mammal data with non NA biomass data
mosaic_mammal <- subset(mosaic_dataframe,
                        Class == "Mammalia" & is.na(Biomass) == FALSE)

# Extracting the first COMPADRE matrix id for each entry
matrix_ids_full <- mosaic@index[mosaic_mammal$MOSAIC_index]

# Extract just the first matrix id using sapply
mammal_matrix_ids <- sapply(matrix_ids_full, `[[`, 1)

# Add matrix id to the mammal data
mosaic_mammal$MatrixID <- mammal_matrix_ids

# Add full species names
mosaic_mammal$Binomial <- paste0(mosaic_mammal$Genus, " ", mosaic_mammal$Spec
ies)
```

We now have a data frame containing MOSAIC IDs, taxonomic information, and biomass values for all mammals within MOSAIC. The corresponding matrix IDs are:

```
mammal_matrix_ids
##  [1] 249092 249094 240296 240307 249126 240331 249159 240358 240362 249214
## [11] 249248 240402 249269 249273 249275 249286 240470 249399 249409 249455
## [21] 249504 240502 249524 249526 249597 249598 240504 249671 249674 249723
## [31] 249726 240674 249753 249759 249787 240511 249817 249821 249866 240565
## [41] 249878 240677 249909 240645
```

Accessing the Climate Data

With our matrix IDs at hand for analysis, we are now ready to tap into the climate data pool contained within MOSAIC. The climate data hereafter, has been obtained using the R-package KrigR and climate data is reported as mean and standard deviation of monthly time-series belonging to the location and study duration for each matrix contained within MOSAIC.

Climate Data in MOSAIC

The climate data within MOSAIC is stored in the climate object:

```
head(mosaic@climate)
```

```
##   X.1 X MatrixID      Lat       Lon StudyStart StudyEnd     GenTime      d
b
## 1   1 1   240296 61.79944 -150.3694       1976     1986 10.64398229 comadr
e
## 2   2 2   240297 61.79944 -150.3694       1976     1986        <NA> comadr
e
## 3   3 3   240298 61.79944 -150.3694       1976     1986        <NA> comadr
e
## 4   4 4   240299 61.79944 -150.3694       1976     1986        <NA> comadr
e
## 5   5 5   240300 61.79944 -150.3694       1976     1986  8.16781721 comadr
e
## 6   6 6   240301 61.79944 -150.3694       1976     1986  12.2931104 comadr
e
##   Download air_temperature air_temperature_SD total_precipitation
## 1        1        273.7485           9.862699          0.06464312
## 2        1        273.7485           9.862699          0.06464312
## 3        1        273.7485           9.862699          0.06464312
## 4        1        273.7485           9.862699          0.06464312
## 5        1        273.7485           9.862699          0.06464312
## 6        1        273.7485           9.862699          0.06464312
##   total_precipitation_SD volumetric_soil_water_layer_1
## 1              0.0420547                     0.3704328
## 2              0.0420547                     0.3704328
## 3              0.0420547                     0.3704328
## 4              0.0420547                     0.3704328
## 5              0.0420547                     0.3704328
## 6              0.0420547                     0.3704328
##   volumetric_soil_water_layer_1_SD volumetric_soil_water_layer_2
## 1                       0.02808088                     0.3684833
```

```
## 2                       0.02808088                     0.3684833
## 3                       0.02808088                     0.3684833
## 4                       0.02808088                     0.3684833
## 5                       0.02808088                     0.3684833
## 6                       0.02808088                     0.3684833
##   volumetric_soil_water_layer_2_SD volumetric_soil_water_layer_3
## 1                       0.02796726                       0.36928
## 2                       0.02796726                       0.36928
## 3                       0.02796726                       0.36928
## 4                       0.02796726                       0.36928
## 5                       0.02796726                       0.36928
## 6                       0.02796726                       0.36928
##   volumetric_soil_water_layer_3_SD volumetric_soil_water_layer_4
## 1                       0.02442513                     0.3888525
## 2                       0.02442513                     0.3888525
## 3                       0.02442513                     0.3888525
## 4                       0.02442513                     0.3888525
## 5                       0.02442513                     0.3888525
## 6                       0.02442513                     0.3888525
##   volumetric_soil_water_layer_4_SD     runoff  runoff_SD total_evaporation
## 1                       0.01339378 0.03377308 0.02755258       -0.02956482
## 2                       0.01339378 0.03377308 0.02755258       -0.02956482
## 3                       0.01339378 0.03377308 0.02755258       -0.02956482
## 4                       0.01339378 0.03377308 0.02755258       -0.02956482
## 5                       0.01339378 0.03377308 0.02755258       -0.02956482
## 6                       0.01339378 0.03377308 0.02755258       -0.02956482
##   total_evaporation_SD
## 1           0.03250795
## 2           0.03250795
## 3           0.03250795
## 4           0.03250795
## 5           0.03250795
## 6           0.03250795
```

As you can see, there are NA values for some matrix IDs in the above output. This results from either (1) missing geolocations of the underlying matrix models making extraction of environmental parameters impossible, (2) study durations of matrix models pre-dating climate data availability at monthly scale within ERA5-Land, or (3) geolocation of matrix models falling outside of land masses.

Extracting Climate Data

Since we are only interested in a subset of matrix models, we do not require the full climate data object and so we can refer to only the relevant subset of the climate object by matching MatrixID values:

```
clim_df <- mosaic@climate[mosaic@climate$MatrixID %in% mammal_matrix_ids, ]
```

With the subsetted climate data, we can now create a data frame holding all necessary data for some exploratory analyses:

```
analysis_df <- merge(mosaic_mammal, clim_df, by = "MatrixID")

analysis_df <- na.omit(analysis_df[analysis_df$Biomass < 1e6, ]) # we set a c
utoff on biomass here, to avoid influence of outliers. This is just a procedu
re for simplicity of this exercise
```

Let's plot the remaining data out in their geospatial context:

```
cols <- rainbow(n = length(unique(analysis_df$Order)))

names(cols) <- unique(analysis_df$Order)

analysis_df$Col <- cols[match(analysis_df$Order, names(cols))]


Map <- leaflet(analysis_df, width = "100%")

Map <- addProviderTiles(Map, providers$Esri.WorldTopoMap)

Map <- addCircleMarkers(map = Map, lng = ~Lon, lat = ~Lat,

                        label = ~Order,

                        col = ~Col,

                        labelOptions = labelOptions(textsize = "12px")

)

Map
```

Regression & Analysis

Now we are ready to run analyses. The ones we are focussing on here are rudimentary at best and should simply serve as a demonstration of how easily one can make use of state-of-the-art ERA5-Land climate data with the MOSAIC data base.

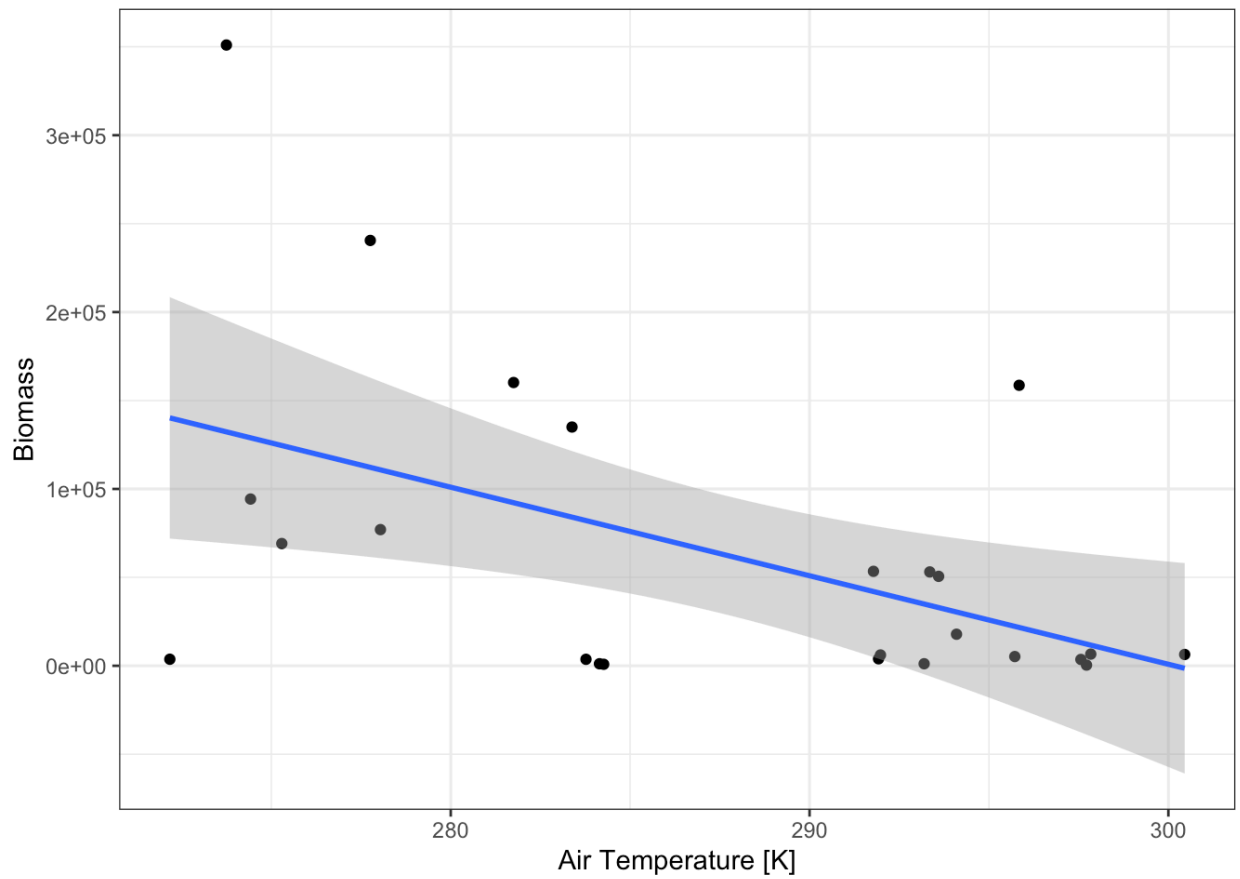
All Mammals

First, let's assess the effect of temperature on biomass of all mammals:

```
summary(lm(data = analysis_df, Biomass ~ air_temperature))
##
## Call:
## lm(formula = Biomass ~ air_temperature, data = analysis_df)
##
## Residuals
##     Min      1Q  Median      3Q     Max
## -136457  -35516  -12225   17982  218728
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1502659     532349   2.823  0.00991 **
## air_temperature    -5006       1850  -2.706  0.01290 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 79270 on 22 degrees of freedom
## Multiple R-squared:  0.2498, Adjusted R-squared:  0.2157
## F-statistic: 7.324 on 1 and 22 DF,  p-value: 0.0129
```

According to this, mammals in colder regions are heavier. This is in support of Bergmann's rule.

```
ggplot(data = analysis_df, aes(x = air_temperature, y = Biomass)) +
  geom_point() +
  stat_smooth(method = "lm") +
  labs(x = "Air Temperature [K]", y = "Biomass") +
  theme_bw()
```



Mammals by Order

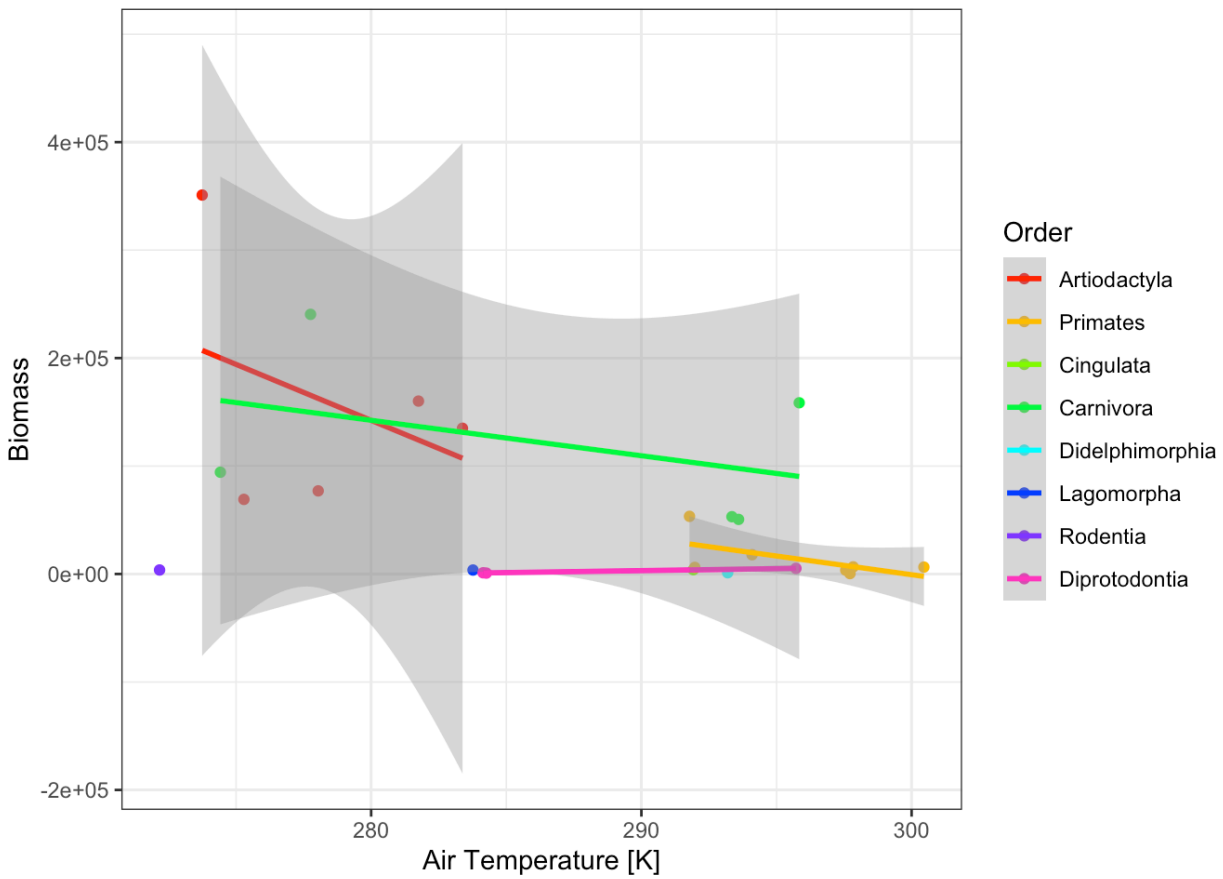
Now let's make use of the higher-resolution taxonomic information available in MOSAIC and assess the impact of air temperature on biomass by order of mammals:

```
summary(lm(data = analysis_df, Biomass ~ air_temperature * Order))
##
## Call:
## lm(formula = Biomass ~ air_temperature * Order, data = analysis_df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -122023  -10392       0   12873  143838
##
## Coefficients: (4 not defined because of singularities)
##                                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)                           3047458    2548979   1.196    0.255
```

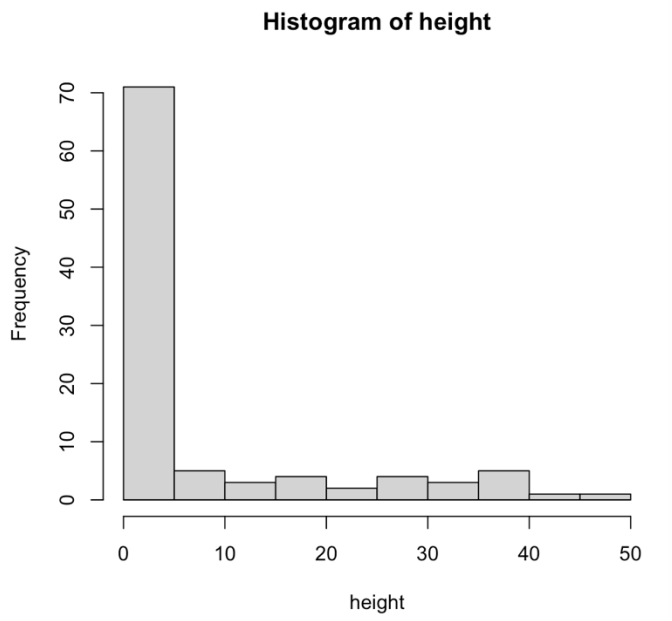
```
## air_temperature                        -10376       9154  -1.133    0.279
## OrderCarnivora                       -1985731    2765125  -0.718    0.486
## OrderCingulata                         -14654     148341  -0.099    0.923
## OrderDidelphimorphia                    -4262     158154  -0.027    0.979
## OrderDiprotodontia                   -3150686    3435359  -0.917    0.377
## OrderLagomorpha                        -99518      95702  -1.040    0.319
## OrderPrimates                        -2008837    3738418  -0.537    0.601
## OrderRodentia                         -219816     100383  -2.190    0.049
*
## air_temperature:OrderCarnivora           7092       9885   0.717    0.487
## air_temperature:OrderCingulata             NA         NA      NA       NA
## air_temperature:OrderDidelphimorphia       NA         NA      NA       NA
## air_temperature:OrderDiprotodontia      10742      12153   0.884    0.394
## air_temperature:OrderLagomorpha            NA         NA      NA       NA
## air_temperature:OrderPrimates            6911      13007   0.531    0.605
## air_temperature:OrderRodentia              NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 75170 on 12 degrees of freedom
## Multiple R-squared:  0.6319, Adjusted R-squared:  0.2945
## F-statistic: 1.873 on 11 and 12 DF,  p-value: 0.148
```

Well, this is just a mess, but should serve to illustrate how many different analyses can easily be performed with MOSAIC and the in-built climate parameters.

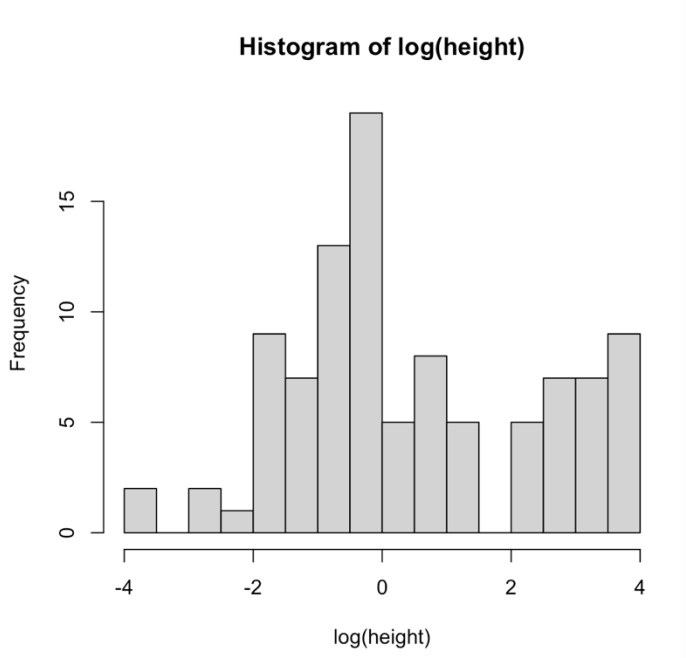
```
ggplot(data = analysis_df, aes(x = air_temperature, y = Biomass, col = Order)
) +
  geom_point() +
  stat_smooth(method = "lm") +
  labs(x = "Air Temperature [K]", y = "Biomass") +
  theme_bw() + scale_color_manual(values = cols)
```


Biomass
4e+05
2e+05
0e+00
-2e+05
280
290
300
Air Temperature [K]
Order
Artiodactyla
Primates
Cingulata
Carnivora
Didelphimorphia
Lagomorpha
Rodentia
Diprotodontia

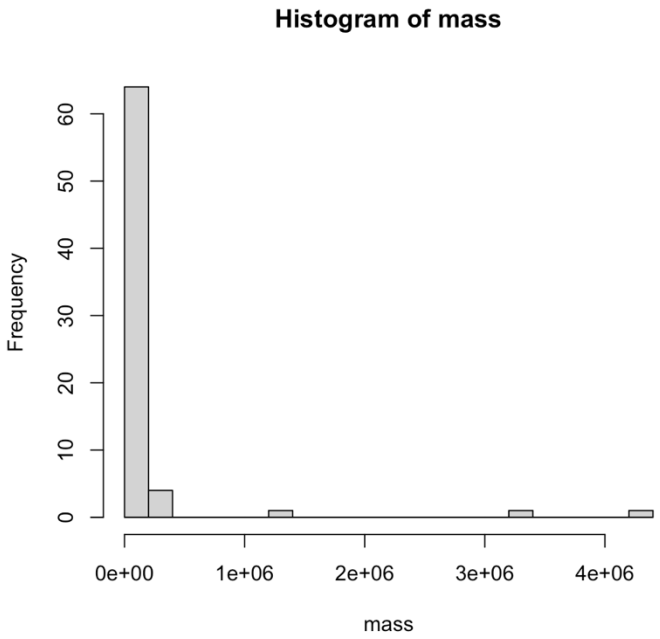
S5: LogNormal Distribution of Mass and Height



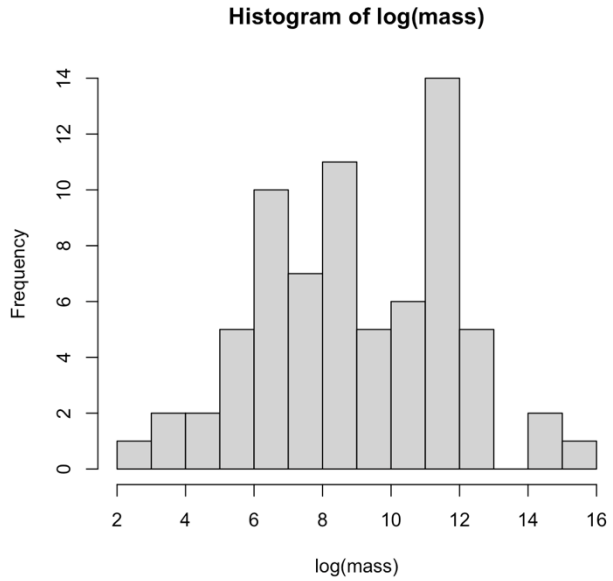
Raw heights from MOSAIC v1.0.0



Log Heights from MOSAIC v.1.0.0



Raw mass from MOSAIV v1.0.0



Log mass from MOSAIC v1.0.0