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VegVault dataset: linking global paleo-, and neo-vegetation data with functional traits and abiotic drivers

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Understanding the dynamics and persistence of biodiversity patterns over short (contemporary) and long (thousands of years) time scales is crucial for predicting ecosystem changes under global climate and land-use changes. A key challenge is integrating currently scattered ecological data to assess complex vegetation dynamics over time. Here, we present VegVault, an interdisciplinary SQLite database that uniquely integrates paleo- and neo-ecological plot-based vegetation data on a global and millennial scale, directly linking them with functional traits, soil, and climate information. VegVault currently comprises data from *BIEN*, *sPlotOpen*, *TRY*, *Neotoma*, *CHELSA*, and *WoSIS*, providing a comprehensive and ready-to-use resource for researchers across various fields to address questions about past and contemporary biodiversity patterns and their abiotic drivers. To further support the usability of the data, VegVault is complemented by the {*vaultkeepr*} R package, enabling streamlined data access, extraction, and manipulation. This study introduces the structure, content, and diverse applications of VegVault, emphasizing its potential role in advancing ecological research to improve predictions of biodiversity responses to global climate change.

Background & Summary

Biodiversity and ecosystem dynamics are currently profoundly influenced by global climate change, creating an urgent need for robust predictive models capable of anticipating these impacts. Such models are crucial in guiding conservation efforts during this global crisis. However, many existing models rely on contemporary (present day) ecological data alone, which limits their ability to capture the long-term responses of species and ecosystems to environmental change. Incorporating paleoecological data—"ecology of the past" as opposed to neo-ecological, or "ecology of the present"—offers a vital temporal perspective that can enhance our understanding of biodiversity dynamics under shifting climate and land-use[1–3].

In recent years, an increasing number of large-scale ecological datasets have become available, providing unprecedented opportunities to investigate ecosystem dynamics across spatial and temporal scales. These datasets encompass contemporary vegetation data (e.g., *Global Biodiversity Information Facility*[4] ('*GBIF*' hereafter), *sPlot*[5], *Botanical Information and Ecology Network*[6] ('*BIEN*' hereafter), paleo-vegetation data (e.g., *Neotoma Paleoecology Database*[7] ('*Neotoma*' hereafter)), plant functional traits (e.g., *TRY plant trait database*[8] ('*TRY*' hereafter)), and abiotic drivers (e.g., *CHELSA*[9], *WorldClim*[10]), which are all critical for understanding the complex interactions that shape ecosystems. Yet, despite the growing availability of such datasets, efforts to integrate these diverse sources into a unified, open-access framework remain limited. An integrated database, built with reproducible workflows, is a crucial step toward improving predictive models that estimate biodiversity dynamics under changing climatic conditions. Addressing this gap requires interdisciplinary solutions[11,12] and

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Database name	Contains contemporary vegetation data?	Contains paleoecological data?	Contains abundance information?	Contains link to abiotic data?	Contains link to functional traits?
VegVault	✓(Plot-based)	✓(Plot-based)	✓	✓	✓
BioDeepTime[13]	✓(Plot-based; limited)	✓(Plot-based)	✓	×	×
GIFT[14]	✓(Species lists)	×	×(Species lists)	×	✓
Botanical Information and Ecology Network (BIEN)[6]	✓(Plot-based)	×	✓	×	✓
sPlotOpen[15]	✓(Plot-based)	×	✓	×	×
Global Biodiversity Information Facility (GBIF)[4]	✓(Occurrences)	×	×(Occurrences)	×	✓
Neotoma Paleoecology Database (Neotoma)[7]	×	✓(Plot-based)	✓	×	×
TRY Plant Trait Database (TRY)[8]	×	×	×	×	✓

Table 1. Overview comparison of selected databases and VegVault to highlight the latter's novel contributions. Note that this comparison does not intend to be a comprehensive overview of all ecological databases. We specify the presence of "Plot-based" vegetation data and Species lists to flag the differences between stored data. The "Plot-based" databases contain a full survey of the vegetation at specific locations and, therefore, contain true negatives. Moreover, "Plot-based" databases contain some expression of species abundance.

a commitment to compiling, processing, and linking data in a systematic and transparent manner. Currently, no comprehensive framework exists to link global vegetation data across temporal scales with functional traits and abiotic drivers.

There have been previous attempts to integrate vegetation data across extensive time scales and link them with other data types. For example, *BioDeepTime*[13] compiles both contemporary and fossil biodiversity time series. However, it lacks coverage of contemporary vegetation plots and, more importantly, omits direct links to functional traits and abiotic data. GIFT[14] includes vegetation biodiversity linked with functional traits but only holds taxonomic lists for specific regions, without data on relative abundances. Additionally, the latter database lacks the long-term dimension of vegetation dynamics over time, derived from the currently existing large databases containing paleoecological records, such as the Neotoma database.

VegVault addresses these limitations by offering a unique resource that compiles extensive paleo- and neo-ecological vegetation data into a single, accessible SQLite database, accompanied by functional traits and abiotic information (i.e., climate and soil). Its design bridges paleo- and contemporary data, enabling the study of long-term processes, and linking them to today's patterns. Thereby, VegVault offers the possibility to specifically analyse the mechanisms of ecosystem responses to environmental change, which enhances our ability to study and ultimately predict future biodiversity trajectories. See Table 1 for the comparative table that summarises the strengths and weaknesses of existing databases versus VegVault. Specifically, VegVault advances analyses across spatial, temporal, and taxonomic scales in several ways:

- **Contemporary vegetation data**: VegVault incorporates plot-based data from *BIEN*[6] and *sPlotOpen*[15] (open-access version of sPlot), including essential "true negative" information about species' absence. These datasets are pre-cleaned for taxonomic and georeferencing errors, ensuring high reliability for subsequent analyses. The focus on plot-based data rather than occurrence data (e.g., *GBIF*) provides a closer match to paleoecological data formats, facilitating robust comparisons across temporal scales.
- **Paleo-vegetation data**: VegVault employs standardised fossil pollen data processed using the *FOSSILPOL* workflow[16] to integrate records globally from Neotoma. This workflow ensures quality control and creates "ready-for-analysis" data through a reproducible and detailed process for handling large fossil pollen dataset compilations (see **Methods** for details).
- **Interdisciplinary integration**: VegVault combines past and present vegetation data with functional traits and abiotic information to support comprehensive ecological analyses (see Table 2). The abiotic information includes soil data from the *WoSIS Soil Profile Database*[17] by *World Soil Information Service* ('*WoSIS*' hereafter), and global temperature and precipitation datasets from *CHELSA* and *CHELSA-TRACE21*[18,19], providing essential environmental context. Functional trait data from the *TRY* database and *BIEN* enrich the database by linking species characteristics to ecological roles and responses. This allows researchers to move beyond taxonomic diversity and explore functional dimensions, offering deeper insights into ecosystem processes.
- **Taxonomic classification**: VegVault ensures consistent and standardised taxonomic information by aligning all taxa present in vegetation data—both paleo and contemporary—with the GBIF backbone taxonomy[20]. This process, implemented via the {*taxospace*} R package[21], automates taxonomic classification by matching names to an existing taxonomy based on similarity (e.g., "Ulmus Type" will be classified as genus *Ulmus*). While original taxonomic names are preserved within the VegVault, users can access data at varying taxonomic resolutions (e.g., species, genus, family; if available) to suit specific analytical needs. The same standardisation approach is applied to vegetation and trait data, facilitating seamless integration between datasets. For instance, enabling the calculation of genus-level average trait values, when species-level identification is unavailable.
- **Accessibility**: VegVault is designed with user accessibility in mind. The SQLite database is supported by the {*vaultkeepr*} R package[22], which simplifies and streamlines the process of data extraction for project-specific needs. It ensures that researchers can efficiently retrieve and subsequently manipulate data in a reproducible and transparent manner.

Source	Type	Time period	Comment	References
Botanical Information and Ecology Network (BIEN)	Vegetation	contemporary data	Plot-based vegetation data	Botanical Information and Ecology Network (http://bien.nceas.ucsb.edu/bien/)[6]
sPlotOpen	Vegetation	contemporary data	The open-access version of sPlot[5]	Sabatini *et al.*[15]
Neotoma Paleoecological database and FOSSILPOL: Workflow for processing and standardizing global paleoecological pollen data	Vegetation	paleo data	We specifically state both FOSSILPOL and Neotoma Paleoecological database, which is the primary source of the data, as FOSSILPOL not only accesses the data but also applies several selection criteria and adds new information (e.g., new age-depth models)	Flantua *et al.*[16] Williams, J. W. *et al.*[7]
TRY Plant Trait Database (TRY)	Functional traits of vegetation	contemporary data		Kattge *et al.*[8]
CHELSA	Abiotic data – climate	contemporary data	global downscaled climate data at 1 km resolution	Karger *et al.*[9]
CHELSA-Trace21k	Abiotic data – climate	paleo data	global downscaled climate data at 1 km resolution since the Last Glacial Maximum (21,000 yr BP)	Karger *et al.*[18] Karger *et al.*[19]
World Soil Information Service (WoSIS)	Abiotic data – soil types	contemporary data	global downscaled climate data at 1 km resolution	Batjes *et al.*[17]

Table 2. Main sources of data presented in VegVault v1.0.0.

The comprehensive nature of VegVault enables diverse applications across scientific disciplines. Its integration of fossil pollen data and functional traits allows researchers to investigate long-term vegetation dynamics and their responses to past climate variations. Such integration provides critical context for past ecological trends e.g.[23,24], including trait information, which is currently underrepresented in paleoecological analyses of vegetation dynamics[25]. While there are now studies showing the relationship between functional traits and climate for global contemporary data[26], VegVault allows testing the universality of such relationships across temporal scales. In addition, VegVault provides the needed data for advanced modelling approaches, such as comparing species distributions across temporal scales e.g.[27], and analysing biodiversity patterns using Joint Species Distribution Models[28]. VegVault also facilitates studies of functional ecology and biogeography by enabling assessments of shifts in ecosystem functioning and climatic drivers over time, and by identifying the taxonomic and functional novelty of communities undergoing climate-driven changes e.g.[29,30]. Furthermore, the detailed climate data (past and present) linked with vegetation records provide a robust foundation for examining the impacts of past and present climate change on ecosystems e.g.[31]. These capabilities make VegVault a valuable interdisciplinary resource for predicting biodiversity patterns and informing conservation strategies and policy decisions aimed at mitigating climate change effects. While this is not an exhaustive list of potential applications, VegVault offers a rich and accessible resource that can significantly advance ecological research and global biodiversity conservation.

Methods

VegVault workflow and reproducibility. VegVault integrates data from multiple well-established primary sources to provide a comprehensive view of vegetation dynamics. The current sources of data are summarised in Table 1.

The data processing and integration into VegVault follow a meticulous workflow to ensure consistency and reliability. Each data source is first accessed and processed individually using a specific pipeline. See Fig. 1 for the workflow process of accessing and processing all data sources (1 to 6 in Fig. 1).

Data extraction and pre-processing. To ensure the traceability of data, VegVault is designed as a versioned project. Each version (including the current v1.0.0) is created using the git Tags system[32]. Each Tag is a snapshot of code at certain points in time. Each of the individual data pipelines, coded in R programming language, is publicly available and stored in a separate GitHub repository with a specific git Tag and published with DOI (see legend of Fig. 1).

Fossil pollen record (Figure 1.7). Fossil pollen records have been downloaded from the *Neotoma Paleoecological Database*[7] using their API on 26th June 2023. All data acquisition and processing have been done using the *FOSSILPOL: Workflow for processing and standardizing global paleoecological pollen data*[16] (version 1.0.0). This includes the selection of depositional environments, ecological groups, chronology control point types, and a minimum number of chronology control points to construct age-depth models. Individual samples and records have been filtered by age limits, number of pollen grains, maximum age interpolation, and number of valid levels. In addition, the accuracy of fossil pollen data is increased by re-estimating all age-depth models using the Bayesian probabilistic approach[33] and including the information about individual age uncertainty. For field-specific terminology, see Flantua *et al.*[16] and for more information about *FOSSILPOL* workflow, see https://bit.ly/FOSSILPOL.

Individual steps in detail are as follows.

- Only records with type “pollen” have been requested with valid geological coordinates. Specifically, longitude between −180 and 180, and latitude between −90 and 90.
- Records have been filtered by their depositional environments, where in this case we only kept lakes, bogs, and mires. See Supplementary Table S1. for a list of selected depositional environments.

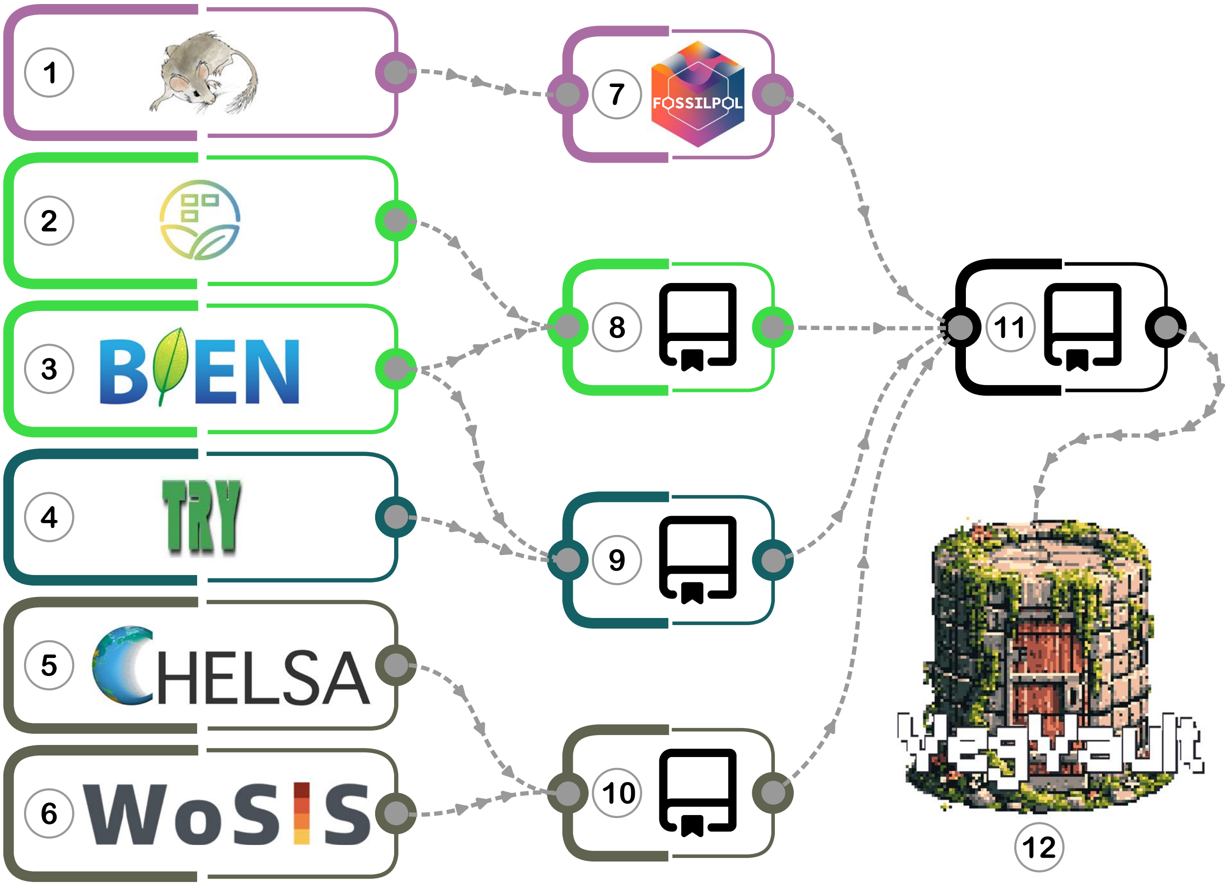


Fig. 1 Schematic workflow of accessing and processing all primary data sources into VegVault v1.0.0 database. (**1**) *Neotoma Paleoecological Database*[7]; (**2**) *sPlotOpen*[15]; (**3**) *Botanical Information and Ecology Network*[6]; (**4**) *TRY Plant Trait Database*[8]; (5) *CHELSA*[9] and *CHELSA-TRACE21*[18,19]; (**6**) *World Soil Information Service*[17]; (**7**) *FOSSILPOL: Workflow for processing and standardizing global paleoecological pollen data*. A project-specific version with all the settings used for VegVault is stored as GitHub repository *VegVault-FOSSILPOL* (can be accessed as https://doi.org/10.5281/zenodo.14745060); (**8**) The GitHub repository *VegVault-Vegetation_data* used to processes data for contemporary vegetation plots (can be accessed as https://doi.org/10.5281/zenodo.16729978); (**9**) A GitHub repository *VegVault-Trait_data* used to processes data for plant vegetation traits (can be accessed as https://doi.org/10.5281/zenodo.16729756); (**10**) The GitHub repository *VegVault-abiotic_data* used to process climate and soil abiotic data (can be accessed as https://doi.org/10.5281/zenodo.14745293); (**11**) The GitHub repository *VegVault* used to integrate all data together and migrate them into SQLite database (can be accessed as https://doi.org/10.5281/zenodo.16987345). Additional steps such as the creation of *gridpoints*, grouping of *Traits* into *Trait Domains*, and classification of taxa are also present (for more details see **Methods**); (**12**) VegVault - SQLite database (v1.0.0; https://doi.org/10.48700/datst.t21cz-2nq07); For details about primary data sources, see Table 1.

- Only taxa in specific ecological groups have been accepted. See Supplementary Table S2. for a list of selected ecological groups.
- All age-depth models have been recalculated using the {*Bchron*} package[33]. Only records with at least 5 chronology control points of specific types have been retained. See Supplementary Table S3. for a list of valid control types.
- To ensure the highest possible data quality and facilitate numerical comparisons across multiple records, several filtering criteria were carefully chosen and applied:
    - Exclusion of samples with a total pollen count below a specified threshold. While the preferred minimum number of pollen grains was initially set at 150, this threshold resulted in a significant loss of records, particularly in regions with limited data coverage. To balance data retention and quality, the threshold was adjusted to 125, with the condition that less than 75% of the samples would have a low pollen sum (i.e., lower than 125 pollen grains).
    - Exclusion of samples older than 3,000 years of the last chronology control point.
    - Exclusion of samples beyond 20,000 cal yr BP.
    - Exclusion of records if the total number of samples was fewer than 5.

The VegVault-specific version of FOSSILPOL with all the individual R scripts and tables is stored as a GitHub repository titled *VegVault-FOSSILPOL* (https://github.com/OndrejMottl/VegVault-FOSSILPOL/tree/v1.0.0) and can be accessed as https://doi.org/10.5281/zenodo.14745060.

Contemporary vegetation plots (Figure 1.8). The primary sources of contemporary plot-based vegetation data are *BIEN*[6] (Botanical Information and Ecology Network) and *sPlotOpen*[15] (the open-access version of sPlot[15]).

The GitHub repository titled *VegVault-Vegetation_data (*https://github.com/OndrejMottl/VegVault-Vegetation_data/tree/v1.1.0*)*, used to process data for contemporary vegetation plots, can be accessed as https://doi.org/10.5281/zenodo.16729978.

BIEN. The plot-based data have been downloaded using the {*RBIEN*} R package[34] (version 1.2.7) on 2nd August 2023 by using the function '*BIEN::BIEN_plot_datasource()*'. The following columns have been retained: "datasource_id", "datasource", "plot_name", "sampling_protocol", "methodology_reference", "methodology_description", "longitude", "latitude", "plot_area_ha", "subplot", "individual_count", "family_matched", "name_matched", "name_matched_author", "verbatim_family", "verbatim_scientific_name", "scrubbed_species_binomial", "scrubbed_taxonomic_status", scrubbed_family", "scrubbed_author". All columns have been renamed using the "snake case". Finally, rows containing NA values in "datasource_id, "datasource", "plot_name", "longitude", "latitude", and/or "plot_area_ha" have been filtered out.

sPlotOpen. The sPlotOpen dataset[35] (version 2.0) has been downloaded on 26th September 2023. Tables "DT2.oa" and "header.oa" have been linked via the "PlotObservationID" column, and rows containing NA values in "PlotObservationID", "GIVD_ID", "Longitude", "Latitude", and/or "Releve_area" have been filtered out. All columns have been renamed using the "snake case".

Functional traits of vegetation (Figure 1.9). The primary sources of vegetation functional traits are *TRY Plant Trait Database*[8] and *BIEN*[6].

We followed Diaz *et al.*[36] and selected traits representing Stem specific density, Leaf nitrogen content per unit mass, Diaspore mass, Plant height, Leaf area, and Leaf mass per area.

A GitHub repository titled *VegVault-Trait_data* (https://github.com/OndrejMottl/VegVault-Trait_data/tree/v1.2.0), used to process data for plant vegetation traits, can be accessed as https://doi.org/10.5281/zenodo.16729756.

TRY. We made a data request from the *TRY Plant Trait Database* on the 29th of August 2023 (ID of the request is 28498), requesting all values for traits with codes 3106, 4, 3108, 3110, 3112, 3114, 3116, 3117, 14, and 26 (as they are the closest to the Diaz *et al.*[36] description). Next, we used the {*rtry*} R package[37] (version 1.1.0) to import the data into R.

For each trait ("TraitID"), we extracted all relevant observations ("ObservationID"), ensuring that only observations unique to each trait are considered (i.e., filtering out overlapping observations with other traits). Next, we identified all unique data ("DataID") associated with each trait. Certain data were excluded ("DataID": 2221, 2222, 2223, 2224, 2225, 3646, 3647, 3698, 3699, 3727, 3728, 3730, 3731, 3849, 3850, 4029, and 4030) as not meaningful variation of the trait, e.g. *height at 15 days*. We filtered the observations and extracted the actual trait values, ensuring that only non-missing values were kept. Third, we extracted covariate information (additional data associated with each observation but not directly a trait value stored in the "DataName" column). Finally, all columns were renamed using the "snake case".

As there are differences in trait names across sources of data (e.g., "*Leaf nitrogen (N) content per leaf dry mass*" and "*leaf nitrogen content per leaf dry mass*"), we added a new variable *Trait Domain* that groups traits together following the trait selection by Diaz *et al.*[36]. For example, the traits "*Leaf area (in case of compound leaves: leaf, petiole excluded)*" and "*Leaf area (in case of compound leaves: leaf, petiole included)*" are grouped under the "Leaf area" *Trait Domain*. See Table 3 for the full list of traits and their *Trait Domain*. Such grouping is also aimed to serve as an efficient extraction of traits across both *TRY* and *BIEN*.

BIEN. The trait data have been downloaded using the {*RBIEN*} R package[34] (version 1.2.7) on 15th December 2023 by using the function '*BIEN::BIEN_trait_trait()*'. Specifically, we requested data for traits "*whole plant height*", "*stem wood density*", "*leaf area*", "*leaf area per leaf dry mass*", "*leaf nitrogen content per leaf dry mass*", and "*seed mass*". The following columns have been retained: "trait_name", "trait_value", "unit", "id", "longitude", "latitude", "method", "url_source", "source_citation", "project_pi", "scrubbed_species_binomial", and "access".

Abiotic data (Figure 1.10). The primary sources of abiotic data are *CHELSA*[9], *CHELSA-TRACE21*[18,19], and *WoSIS Soil Profile Database*[17]. The first two data sources provide high-resolution downscaled climatic data, while the latter offers detailed soil information (only available for contemporary data). The abiotic variables included in VegVault are summarised in Table 4.

The GitHub repository titled *VegVault-abiotic_data (*https://github.com/OndrejMottl/VegVault-abiotic_data/tree/v1.1.0*)*, used to process climate and soil abiotic data, can be accessed as https://doi.org/10.5281/zenodo.14745293.

CHELSA. Climate data have been downloaded from *CHELSA*[9] (version 2.1) using the {*ClimDatDownloadR*} R package[38] on the 8th of September 2023 with the function '*ClimDatDownloadR::Chelsa.Clim.download()*'. The specific bio-variables selected are 1, 4, 6, 12, 15, 18, and 19. Next, we used the {*terra*} R package[39] to spatially aggregate the values using the function '*terra::aggregate(factor = 25, fun = "median")*'.

Trait Domain	*Trait name*	*Trait units*	Source of *Datasets*	Number of *Datasets*
Stem specific density	*Stem specific density (SSD, stem dry mass per stem fresh volume) or wood density*	g/cm^3	TRY	8058
Stem specific density	*stem wood density*	g/cm^3	BIEN	348
Leaf nitrogen content per unit mass	*Leaf nitrogen (N) content per leaf dry mass*	mg/g	TRY	11464
Leaf nitrogen content per unit mass	*leaf nitrogen content per leaf dry mass*	mg/g	BIEN	707
Diaspore mass	*Seed dry mass*	mg	TRY	1635
Diaspore mass	*Seed mass*	mg	BIEN	48
Plant height	*Plant height vegetative*	m	TRY	11476
Plant height	*whole plant height*	m	BIEN	193492
Leaf area	*Leaf area (in case of compound leaves: leaf, petiole excluded)*	mm^2	TRY	1415
Leaf area	*Leaf area (in case of compound leaves: leaf, petiole included)*	mm^2	TRY	1374
Leaf area	*Leaf area (in case of compound leaves: leaf, undefined if petiole in- or excluded)*	mm^2	TRY	897
Leaf area	*Leaf area (in case of compound leaves undefined if leaf or leaflet, undefined if petiole is in- or excluded)*	mm^2	TRY	2202
Leaf area	*Leaf area*	mm^2	BIEN	902
Leaf mass per area	*Leaf area per leaf dry mass (specific leaf area, SLA or 1/LMA): petiole included*	mg/mm^2	TRY	1935
Leaf mass per area	*Leaf area per leaf dry mass (specific leaf area, SLA or 1/LMA): undefined if petiole is in- or excluded)*	mg/mm^2	TRY	8777
Leaf mass per area	*Leaf mass per area*	mg/mm^2	BIEN	835

Table 3. Selected *Traits* presented in the VegVault v1.0.0. The *Traits* were selected based on similarity to Diaz *et al.*[36] and grouped into six main *Trait Domains* to simplify the navigation between different data sources.

Abiotic variable name	Abiotic variable description	Abiotic variable unit	Time period	Source of data	Original spatial resolution	Original temporal resolution
bio1	Annual Mean Temperature	°C	contemporary and paleo data	CHELSA & CHELSA-TRACE21	1 km (30 arc-second)	100 years for paleo records
bio4	Temperature Seasonality	°C	contemporary and paleo data	CHELSA & CHELSA-TRACE21	1 km (30 arc-second)	100 years for paleo records
bio6	Min Temperature of Coldest Month	°C	contemporary and paleo data	CHELSA & CHELSA-TRACE21	1 km (30 arc-second)	100 years for paleo records
bio12	Annual Precipitation	kg m-2 year-1	contemporary and paleo data	CHELSA & CHELSA-TRACE21	1 km (30 arc-second)	100 years for paleo records
bio15	Precipitation Seasonality	Unitless	contemporary and paleo data	CHELSA & CHELSA-TRACE21	1 km (30 arc-second)	100 years for paleo records
bio18	Precipitation of Warmest Quarter	kg m-2 quarter-1	contemporary and paleo data	CHELSA & CHELSA-TRACE21	1 km (30 arc-second)	100 years for paleo records
bio19	Precipitation of Coldest Quarter	kg m-2 quarter-1	contemporary and paleo data	CHELSA & CHELSA-TRACE21	1 km (30 arc-second)	100 years for paleo records
HWSD2	Soil type	Unitless	contemporary data	WoSIS	1 km (30 arc-second)	N/A

Table 4. Overview of abiotic variables present in VegVault v1.0.0.

CHELSA-TRACE21. Paleoclimate data have been downloaded from *CHELSA-TRACE21*[18,19] (version 1.0) on the 31st December 2023. We only downloaded values for each 500-year time-slice between 0 and 18,000 years before present (BP) for the selected bio-variables (1, 4, 6, 12, 15, 18, and 19). For each time slice, we also used the function '*terra::aggregate(factor = 25, fun = "median")*' to spatially aggregate the values.

WoSIS Soil Profile Database. As soil information has been previously confirmed as important predictors for vegetation distribution[40–42], we opted for including such data, though only representing the present day. We downloaded the soil data from the *WoSIS Soil Profile Database*[17] on the 11th of September 2023 (both HWSD2_RASTER.zip and HWSD2_DB.zip). We extracted the soil type names (column "HWSD2_SMU_ID") by combining tables "HWSD2_SMU" and "D_WRB4", and added this information to the raster. Finally, we resampled the raster using the '*terra::resample(method = "near")*' function to match the resolution of the climate data.

Data integration (Figure 1.11). All processing pipelines with their corresponding Tags are then migrated into an SQLite database using the GitHub repository titled *VegVault* (https://github.com/

OndrejMottl/VegVault/tree/v1.0.0-website_rewiev), which can be accessed as https://doi.org/10.5281/zenodo.16987345).

Migrating sPlotOpen vegetation data. The Dataset name ("dataset_name") has been created from "plot_observation_id" as "splot_[plot_observation_id]". The original data source (e.g., sub-databases) from column "givd_id" has been stored in the *DatasetSourcesID* table.

The Sample name ("sample_name") has been created using column "plot_observation_id" as "splot_[plot_observation_id]". The Sample Size ("sample_size") has been created from the "releve_area" column. All samples are automatically assigned an age of 0.

Taxonomic names have been extracted from column "Species" and the abundances from "Original_abundance".

Migrating BIEN vegetation data. The Dataset name ("dataset_name") has been created as "bien_[row number]". The original data source (e.g., sub-databases) from column "datasource" has been stored in the *DatasetSourcesID* table. The Sampling method has been extracted from the "methodology_description" column, and its reference has been extracted from the "methodology_description" column.

The Sample name ("sample_name") has been created as "bien_[row number]". The Sample Size ("sample_size") has been created from the "plot_area_ha" column, and multiplied by 10,000 to be stored in square meters. All samples are automatically assigned an age of 0.

Taxonomic names have been extracted from column "name_matched" and the abundances from "taxon_name".

Migrating fossil pollen data. The Dataset name ("dataset_name") has been created from "dataset_id" (fossilpol_[dataset_id]). Note that the column "dataset_id" is from the primary source and does not match the "dataset_id" in VegVault. The original data source from column "source_of_data" has been stored in the *DatasetSourcesID* table. The Sampling method has been extracted from the "depositionalenvironment" column. The individual Dataset Reference have been extracted from the column "doi".

The Sample name ("sample_name") has been created using columns "dataset_id" and "sample_id" as "fossilpol_[dataset_id]_[sample_id]". Ages have been extracted from column "levels".

Age uncertainties from age-depth models have been extracted from "age_uncertainty" column.

Taxonomic names and their abundances have been extracted from the column "counts_harmonised".

Migrating TRY functional traits. The Dataset name ("dataset_name") has been created as "try_[row number]". The original data source (e.g., sub-databases) from column "dataset" has been stored in the *DatasetSourcesID* table. The individual Dataset Reference have been extracted from the column "reference_source".

The Sample name ("sample_name") has been created as "try_[row number]". The individual Sample reference has been extracted from "dataset_reference_citation". All samples are automatically assigned an age of 0.

Trait names have been extracted from "trait_full_name", taxonomic names from the column "acc_species_name", and trait values from "trait_value".

Migrating BIEN functional traits. The Dataset name ("dataset_name") has been created as "bien_traits_[row number]". The original data source (e.g., sub-databases) from column "project_pi" has been stored in the *DatasetSourcesID* table. The individual Dataset Reference have been extracted from the column "source_citation".

The Sample name ("sample_name") has been created using column "id" as "bien_traits_[id]". All samples are automatically assigned an age of 0.

Trait names have been extracted from "trait_name", taxonomic names from the column "scrubbed_species_binomial", and trait values from "trait_value". Trait "leaf mass per area" is calculated from "leaf area per leaf dry mass" as 1/value.

Creation of gridpoints of abiotic data. We developed a data structure that provides readily available environmental context for each vegetation (and trait) record by creating spatio-temporal links between these records and abiotic information. As the rasters are not suitable to be stored in an SQLite database, we created artificial points, called '*gridpoints*', located in the middle of each raster cell. This resulted in a uniform spatio-temporal matrix of gridpoints holding the abiotic information (see Fig. 2B for an example area).

Gridpoints Dataset names ("dataset_name") have been created as "geo_[longitude]_[latitude]" and gridpoints Sample names ("sample_name") have been created as "geo_[longitude]_[latitude]_[age]". Next, we linked *gridpoints* and other non-*gridpoint Samples*, namely *vegetation_plot*, *fossil_pollen_archive*, and *traits* (see **Internal Dataset Structure** section), and calculated the spatial and temporal distances between them. We kept any *gridpoint Sample* within 50 km and/or 5,000 years from any other non-*gridpoint Sample* and discarded the rest. See Fig. 2C for an example of linking abiotic information at *gridpoints* and vegetation data. In VegVault, users can select the information for each non-*gridpoint Sample* from the closest spatio-temporal abiotic data or get the average from all surrounding *gridpoints*. We hope that by providing such a comprehensive and well-linked structure between vegetation and abiotic data, VegVault enhances the ability to study the interactions between vegetation and their environment, facilitating the workflow for advanced ecological research and modelling efforts.

Taxon classification. As VegVault consists of data on taxa from various sources, the {*taxospace*} R package[21] has been used to classify the diverse taxa into a unifying backbone in the VegVault. The {*taxospace*} tool

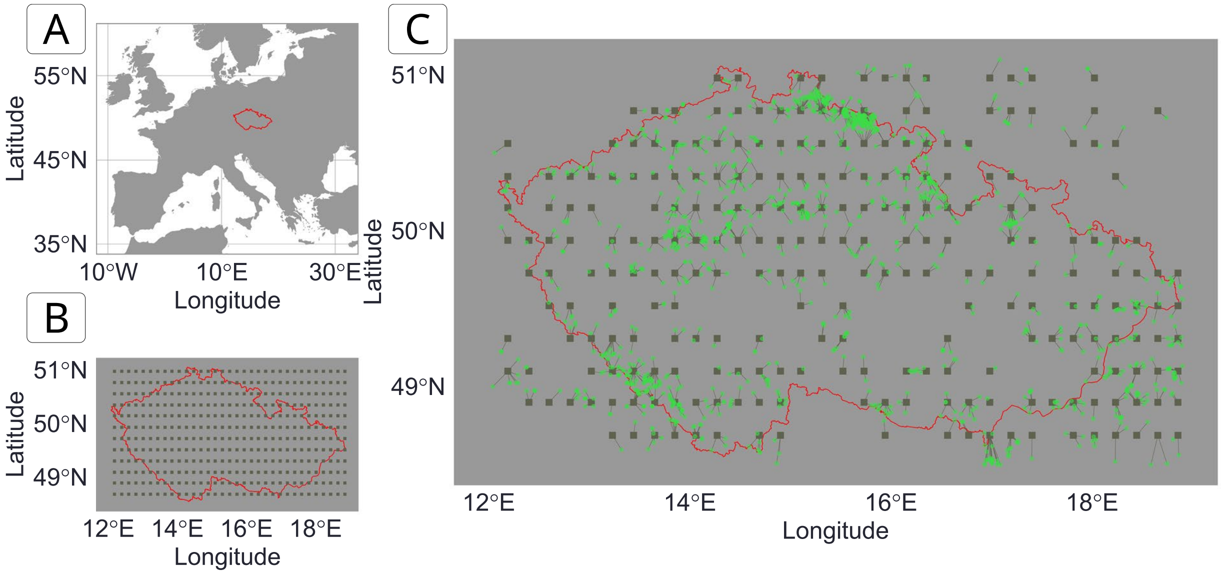


Fig. 2 Example of the resolution of the *gridpoint Datasets* extracting abiotic information. (**A**) Map of Europe. The red line indicates country borders with the Czech Republic as the focus of the map. (**B**) Distribution of the individual *gridpoints* (grey squares) within the Czech Republic (red). (**C**) Linking vegetation plots and *gridpoints*. The green circles represent the contemporary vegetation plots. The grey lines connect the vegetation points to their closest *gridpoint*. Note that the abiotic data is provided to each vegetation plot from their closest *gridpoint* (i.e., the vegetation plots connected to the same gridpoint will have the same abiotic data). *Gridpoints* without vegetation plots in their spatio-temporal vicinity (here contemporary data) were excluded from the VegVault to reduce the database size. See **Methods** section for more details.

automatically aligns taxon names with the taxonomical backbone of the *GBIF*[20]. Specifically, we find the best match of the raw names of taxa using the *Global Names Resolver*[43], which is then aligned with *GBIF*. The resulting information of taxonomic classification, detailed up to the family level, is stored for each taxon, ensuring consistency and facilitating comparative analyses across different datasets. However, note that taxonomic classification down to the species level is not available for each taxon (e.g., some fossil pollen types can only be identified to the genus or family level). For several taxa, we were unable to find a matching classification. Note that the taxon classification is additional information; the original taxon name is always present and returned by default. Finally, we would like to stress to the user that this classification is an automated process and may contain errors.

Data Records

The VegVault v1.0.0 is available at the *National Repository*[44] (‘*REPO*’) under https://doi.org/10.48700/datst.t21cz-2nq07[45]. It is an SQLite database of a size of ~ 110 GB, which contains >480,000 *Datasets*, >13,000,000 *Samples*, >100,000 *Taxa*, 6 vegetation *Traits*, >11,000,000 *Trait* values, and 8 abiotic variables. The spatio-temporal overview of all vegetation data can be found in Fig. 3.

Internal dataset structure.

Currently, the dataset consists of 31 interconnected tables with 87 fields (variables), which are described in detail below. See Fig. 4 for the structure (schema) of the SQLite database. However, the internal structure of VegVault may not be of relevance to a user, as the {*vaultkeepr*} R package processes all the data to output only the most relevant information in a “ready-to-analyse” format (see **Usage Notes** section). We will describe all tables and their inter-relationships in the following sections.

Metadata tables.

There are currently several tables that are not directly linked to the data. First is the *Authors* table, which describes the authors and maintainers of VegVault, including the contact information. The next table is *version_control* table, which stores the information about database versions with a description of individual changes at a specific point in time. See Tables 5 and 6 for the description of individual columns, respectively. Finally, there are *sqlite_stat1* and *sqlite_stat4* tables, which hold descriptive information about database indexes, used for improving the performance of data extractions. See Tables 7 and 8 for the description of individual columns, respectively.

Datasets table.

The table contains one *Dataset* per row, with each *Dataset* may contain: a unique *Dataset ID* (“dataset_id”), *Dataset name* (“dataset_name”), geographic location (“coord_lat”, “coord_long”), *Dataset Type* (“dataset_type_id”), *Dataset Source* (“data_source_id”), *Dataset Source Type* (“dataset_source_type_id”), and *Sampling Method* (“sampling_method_id”). See Table 9 for the description of individual columns.

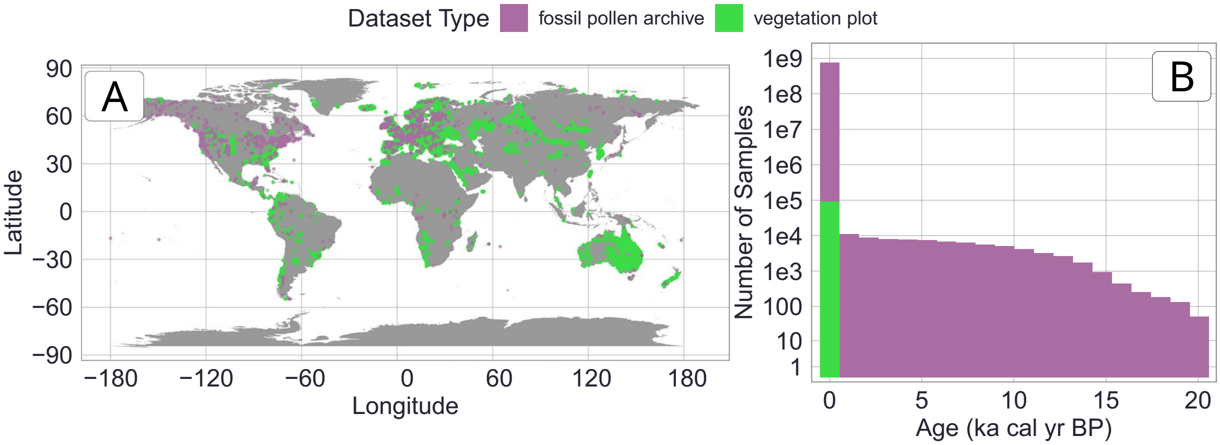


Fig. 3 Spatio-temporal distribution of vegetation Samples (for both vegetation plots and fossil pollen archives). Note that this is an overview of the current state of VegVault (v1.0.0.). (**A**) Spatial distribution with each point representing one plot. (**B**) Temporal distribution of individual Samples.

DatasetTypeID table. The table defines the most basic classification of each *Dataset*, ensuring that the vast amount of data is categorised systematically (see Table 10 for the description of individual columns). Currently, VegVault contains the following *Dataset Types*:

- ***'vegetation_plot'***: This type includes contemporary vegetation plot data, capturing contemporary vegetation characteristics and distributions.
- ***'fossil_pollen_archive'***: This type encompasses past vegetation plot data derived from fossil pollen records, providing insights into past vegetation and climate dynamics.
- ***'traits'***: This type contains functional trait data, detailing specific characteristics of plant species that influence their ecological roles.
- ***'gridpoints'***: This type holds artificially created *Datasets* to manage abiotic data, here climate and soil information (a dataset type created to hold abiotic data, see details in the **Methods** section).

See Fig. 5A for an overview of the number of *Datasets* in each *Dataset Type*.

DatasetSourceTypeID table. The table contains information about the primary data source (see Table 11 for the description of individual columns). Therefore, each *Dataset* is derived from a specific *Source-Type* including:

- ***BIEN***[6] (Botanical Information and Ecology Network).
- ***sPlotOpen***[15] (The open-access version of sPlot).
- ***TRY***[8] (TRY Plant Trait Database).
- ***Neotoma-FOSSILPOL*** (FOSSILPOL[16]: Workflow for processing and standardizing global paleoecological pollen data from *Neotoma*[7]) Note that we specifically state *Neotoma-FOSSILPOL* and not just *Neotoma*, as *FOSSILPOL* not only provides the data acquisition but also alters it (e.g., creating new age-depth models). It also addresses major challenges in paleoecological data integration, such as age uncertainty, by incorporating probabilistic age-depth models and their associated uncertainty matrices. This enables the propagation of temporal uncertainty in subsequent analyses, a critical advancement for robust macroecological studies, previously flagged as a major issue with paleo-data[46].
- ***gridpoints*** (artificially created *Datasets* for abiotic data). See details in the **Methods** section.

See Fig. 5B for an overview of the number of *Datasets* for each *Dataset Source-Type*.

DatasetSourceTypeReference table. The table links the *Dataset Source-Types* to their specific *Reference*. Note that one *Dataset Source-Type* may have several *References. See* Table 12 for the description of individual columns.

DatasetSourcesID table. The table contains information about the provider (*Dataset Source*) of the original data for the primary data source. The VegVault v1.0.0 currently includes 706 sources of *Datasets*, where each dataset can also have one or more direct references to specific data (see below), ensuring that users can accurately cite and verify the sources of their data. See Table 13 for the description of individual columns.

DatasetSourcesReference table. The table links the *Dataset Sources* to their specific *Reference*. Note that one *Dataset Source* may have several *References*. See Table 14 for the description of individual columns.

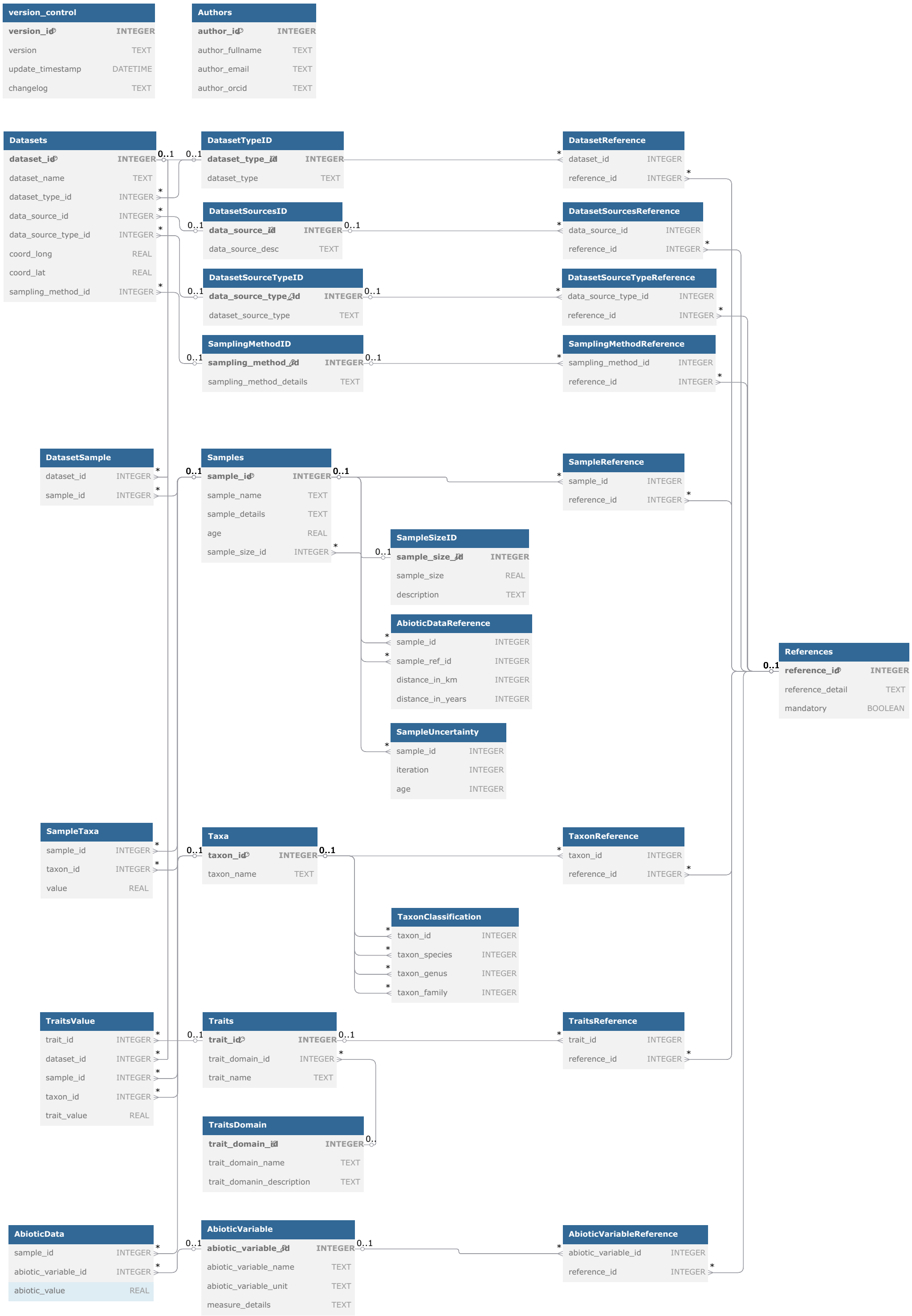


Fig. 4 Visualisation of database structure (schema) created using https://dbdiagram.io/. Each table contains its name, the names of individual columns, and the data type of each column. In addition, primary key columns are indicated using a small key icon. Individual lines indicate the connections.

SamplingMethodID table. The table contains information about the specific *Sampling Method* in the form of an abbreviated ID, which is only available for both *vegetation_plot* and *fossil_pollen_archive Datasets*, and varies substantially, reflecting the diverse nature of the data collected. Such information is crucial for understanding the context and limitations of each *Dataset Type*. For contemporary vegetation plots, sampling involves standardised plot inventories and surveys that capture detailed vegetation characteristics across various regions. Fossil pollen data are collected from sediment records from numerous different depositional environments[16] representing past vegetation and climate dynamics. See Table 15 for the description of individual columns.

Column name	Data type	Description
author_id	integer	ID of an Author (unique)
author_fullname	character	Full name of an *Author*
author_email	character	Contact email of an *Author*
author_orcid	character	ORCID ID of an *Author*

Table 5. Column names and types for table *Authors*.

Column name	Data type	Description
id	integer	ID a database version (unique)
version	character	Version number
update_date	character	Date of the creation of that version
changelog	character	Text description of main changes in the database

Table 6. Column names and types for table *version_control*.

Column name	Data type	Description
tbl	character	Name of a table
idx	character	Name of a database index
stat	character	Statistical information. Specifically, comma-separated list of numbers.

Table 7. Column names and types for table *sqlite_stat1*.

Column name	Data type	Description
tbl	character	Name of a table
idx	character	Name of a database index
neq	character	Number of entries in the index equal to the sample key
nlt	character	Number of entries less than the sample key
ndlt	character	Number of distinct values less than the sample key
sample	character	A sample value from the index (binary-encoded key values)

Table 8. Column names and types for table *sqlite_stat4*.

Column name	Data type	Description
dataset_id	integer	ID of a *Dataset* (unique)
dataset_name	character	Name of each *Dataset*
dataset_type_id	integer	ID of a *Dataset Type*
data_source_id	integer	ID of a *Dataset Source*
data_source_type_id	integer	ID of a *Dataset Source-Type*
coord_long	numeric	Geographical coordinates – longitude
coord_lat	numeric	Geographical coordinates – latitude
sampling_method_id	integer	ID of a *Sampling Method*

Table 9. Column names and types for table *Datasets*.

SamplingMethodReference table. The table links the *Dataset Sampling Methods* to their specific *Reference*. Note that one *Dataset Sampling Methods* may have several *References*. See Table 16 for the description of individual columns.

DatasetReference table. This table links individual *Datasets* to their specific *References* (see Table 17 for the description of individual columns). Note that one *Dataset* may have several *References*. To support robust and transparent scientific research, each *Dataset* in VegVault can have multiple *References* at different levels as the raw data was pooled from other databases that provide data from various authors. The *Dataset Source-Type*,

Column name	Data type	Description
dataset_type_id	integer	ID of a *Dataset Type* (unique)
dataset_type	character	Text description of individual *Dataset Types* (currently *vegetation_plot, fossil_pollen_archive, traits, gridpoints*)

Table 10. Column names and types for table *DatasetTypeID*.

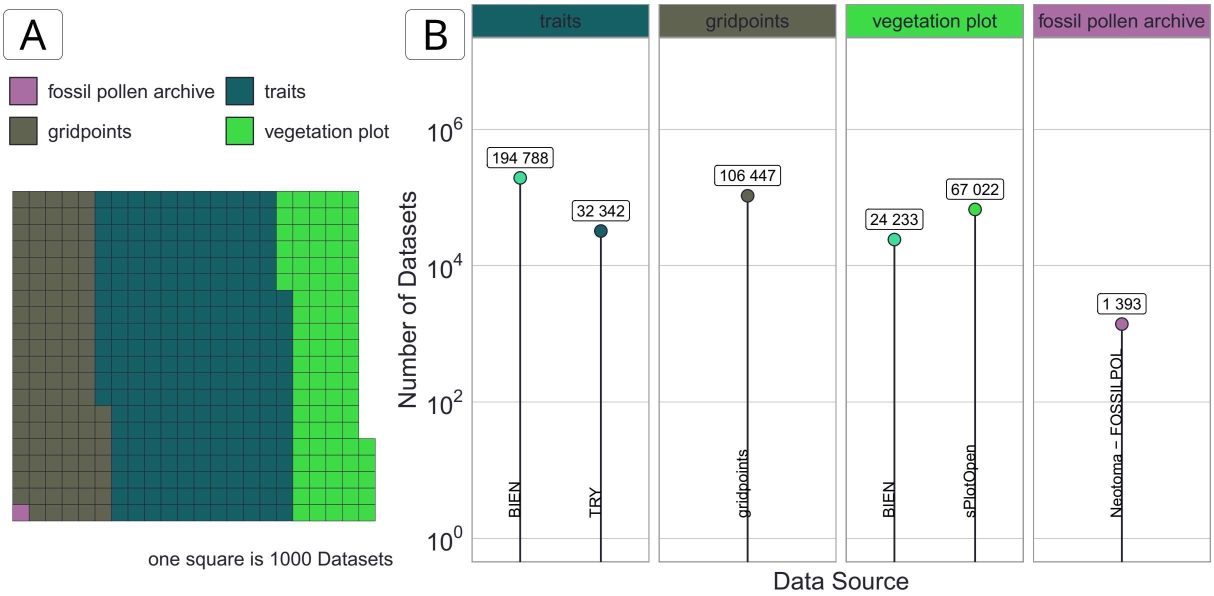


Fig. 5 Visualisation of the number of *Datasets*. (**A**) Waffle plot coloured by *Dataset Type* with each square representing ~1000 *Datasets*. (**B**) Number of *Datasets* by *Dataset Source-Type* grouped by *Dataset Type*. See **Internal Dataset Structure** section for more details.

Dataset Source, and *Sampling Method* can all have their own *References*, providing detailed provenance and citation information. This multi-level referencing system enhances the traceability and validation of the data.

***Samples* table.** *Samples* represent the main unit of data in the *VegVault*, serving as the fundamental building blocks for all analyses. There are currently over 13 million *Samples* in the VegVault v1.0.0 (of which ~ 1.6 million are *gridpoints* of abiotic data, see **Methods** section). For contemporary and fossil pollen records, each Sample is a representation of vegetation community at a specific location and time. The *Samples* table contains one *Sample* per row, with each *Sample* may contain: a unique *Sample ID* ("sample_id"), *Sample name* ("sample_name"), temporal information about *Sample* ("age"), *Sample size* (size of the plot if available; "sample_size_id"*)*, and additional information about *Sample* ("sample_details"; this is currently not being used in v1.0.0.). As VegVault encompasses both contemporary and paleo-data, accurate age information for each *Sample* is needed. Contemporary *Samples* are assigned an age of 0, while *Samples* from fossil pollen records are in calibrated years before the present (cal yr BP). The 'present' is here specified as 1950 AD. *See* Table 18 for the description of individual columns.

DatasetSample table. Each *Sample* is linked to a specific *Dataset* via the *DatasetSample* table, which ensures that every *Sample* is correctly associated with its corresponding *Dataset Type* (whether it is *vegetation_plot*, *fossil_pollen_archive*, *traits*, or *gridpoint*) and other *Dataset* properties (e.g., geographic location). One *Dataset* contains several *Samples* only in cases where *Samples* differ in time ("age"). See Table 19 for the description of individual columns.

SampleSizeID table. The size of vegetation plots can vary substantially. This detail is crucial for ecological studies where plot size can influence species diversity and abundance metrics, thus impacting follow-up analyses and interpretations[47]. To account for this variability, information about the plot size is recorded separately for each contemporary *Sample*. See Fig. 6 for an overview of the number of *Samples* in each size category and Table 20 for the description of individual columns.

SampleUncertainty table. Each *Sample* from the *fossil_pollen_archive Dataset* is also associated with an uncertainty matrix generated during the re-estimation of ages using FOSSILPOL workflow[16]. This matrix provides a range of potential ages derived from age-depth modelling, reflecting the inherent uncertainty in dating paleoecological records. See an example of detailed age uncertainty information for one fossil pollen record in Fig. 7, and the Table 21 for the description of individual columns

Column name	Data type	Description
data_source_type_id	integer	ID of a *Dataset Source-Type* (unique)
dataset_source_type	character	Text description of individual *Dataset Source-Type* (currently, *BIEN*, *sPlotOpen*, *TRY*, *Neotoma-FOSSILPOL*, *gridpoints*)

Table 11. Column names and types for table *DatasetSourceTypeID*.

Column name	Data type	Description
data_source_type_id	integer	ID of a *Dataset Source-Type*
reference_id	integer	ID of a *Reference*

Table 12. Column names and types for table *DatasetSourceTypeReference*.

Column name	Data type	Description
data_source_id	integer	ID of a *Dataset Source* (unique)
data_source_desc	character	Text description of individual *Dataset Sources* (e.g., name of the sub-database from the primary source)

Table 13. Column names and types for table *DatasetSourcesID*.

Column name	Data type	Description
data_source_id	integer	ID of a *Dataset Source*
reference_id	integer	ID of a *Reference*

Table 14. Column names and types for table *DatasetSourcesReference*.

Column name	Data type	Description
sampling_method_id	integer	ID of a *Dataset Sampling Method* (unique)
sampling_method_details	character	Text description of individual *Dataset Sampling Method* (e.g., name of the sub-database from the primary source)

Table 15. Column names and types for table *SamplingMethodID*.

Column name	Data type	Description
sampling_method_id	integer	ID of a *Dataset Sampling Method*
reference_id	integer	ID of a *Reference*

Table 16. Column names and types for table *SamplingMethodReference*.

Column name	Data type	Description
dataset_id	integer	ID of a *Dataset*
reference_id	integer	ID of a *Reference*

Table 17. Column names and types for table *DatasetReferences*.

Column name	Data type	Description
sample_id	integer	ID of a *Sample* (unique)
sample_name	character	Name of a *Sample*
sample_details	character	Specific description of a *Sample*. Currently not being used.
age	numeric	Age of a *Sample*. Mainly used for *fossil_pollen_archives*, where the age of a *Sample* is specified in calibrated years before present. Note that all contemporary *Samples*, have age of 0.
sample_size_id	integer	ID of a *Sample Size*

Table 18. Column names and types for table *Samples*.

Column name	Data type	Description
dataset_id	integer	ID of a *Dataset*
sample_id	integer	ID of a *Sample*

Table 19. Column names and types for table *DatasetSample*.

SampleReference table. Each *Sample* in VegVault can have specific *References* in addition to those at the *Dataset*-level. These individual *Sample References* provide detailed provenance and citation information, ensuring that users can trace the origin and validation of each data point. Note that a single *Sample* can have several *References*. This level of referencing enhances the transparency and reliability of the data, especially when the dataset continues to be updated in the future. See Table 22 for the description of individual columns.

Taxa table. The VegVault database records the original taxonomic names derived directly from the primary data sources, and currently, it holds over 100 thousand taxonomic names. See **Methods** for the names of columns used from the primary sources. See Table 23 for the description of individual columns.

SampleTaxa table. Each individual *Taxon* is linked to corresponding *Samples* through the *SampleTaxa* table, ensuring accurate and systematic association between species and their ecological data. Note that the abundance information varies across the primary data sources (see **Methods** for the names of columns used as abundance). Therefore, users have to be careful while processing data from various sources. See Table 24 for the description of individual columns.

TaxonClassification table. Each taxonomic name undergoes an automated classification (see **Methods** section), and results are stored in the *TaxonClassification* table. Taxonomic classification for some *Taxa* might be only available down to the genus or family level, while most of the data is classified to species level. See Fig. 8 for an overview of the number of species, genus and family classification. However, 1,312 (1.2%) of all *Taxa* currently do not contain classification, and only their name from the primary source is available. The best possible name is returned for each request, which means that *Taxa* without classification will return the name from the primary source. See Table 25 for the description of individual columns.

TaxonReference table. Each *Taxon* might get a *Reference*. Currently, this is used to track the origin of the *Taxon* name (i.e., which primary source was used first with this *Taxon*). Note that *Taxa*, generated from taxonomic classification (see **Methods**), are associated with "taxospace" *Reference*. See Table 26 for the description of individual columns.

Traits table. The *Traits* table contains the list of functional traits currently contained in VegVault. The table contains one *Trait* per row, with each *Trait* may contain: a unique *Trait* ID ("trait_id"), original *Trait name* from primary source ("trait_name"*;* see **Methods** for the details about the specific columns used from primary sources), and *Trait Domain* ("trait_domain_id"). See Table 27 for the description of individual columns.

TraitsDomain table. Traits are grouped into *Trait Domains* to allow for easier aggregation of *Traits* across data sources (see **Methods** section). In total, six *Trait Domains* are present: "Stem specific density", "Leaf nitrogen content per unit mass", "Diaspore mass", "Plant height", "Leaf area", "Leaf mass per area", following Diaz *et al.*[36]. See Table 3 for an overview of *Traits* in various *Trait Domains* and the number of *Trait* values. Yet, it is up to the user to decide how to further aggregate trait values if multiple trait samples of one *Trait Domain* are available for the same environmental or taxonomic entity. See Table 28 for the description of individual columns.

TraitsValue table. In general, data of functional traits of vegetation taxa follow the same structure of the *Dataset* and *Samples* obtained directly from the *Dataset Source-Types*. Therefore, the *TraitsValue* table contains not only the actual measured value of *Trait* observation but also information about linking information across *Datasets*, *Samples*, and *Taxa*. This comprehensive linkage ensures that each *Trait* value is accurately associated with its relevant ecological, environmental and taxonomic context. See Table 29 for the description of individual columns.

TraitsReference table. To ensure clarity and reproducibility, each *Trait* in the VegVault can have additional *References* beyond the general *Dataset* and *Sample References*. These *Trait*-specific *References* provide detailed provenance and citation information, supporting rigorous scientific research and enabling users to trace the origins and validation of each trait value. See Table 30 for the description of individual columns.

AbioticVariable table. As the VegVault contains abiotic variables from several primary sources, the *AbioticVariable* table contains descriptions of abiotic variables ("abiotic_variable_name"), their units ("abiotic_variable_unit"), and measurement details ("measure_details"). See Table 4 for the overview of abiotic variables and their primary source, and Table 31 for the description of individual columns.

AbioticData table. The table holds the actual values of abiotic variables (the units are the same for each *Abiotic Variable*). See Table 32 for the description of individual columns.

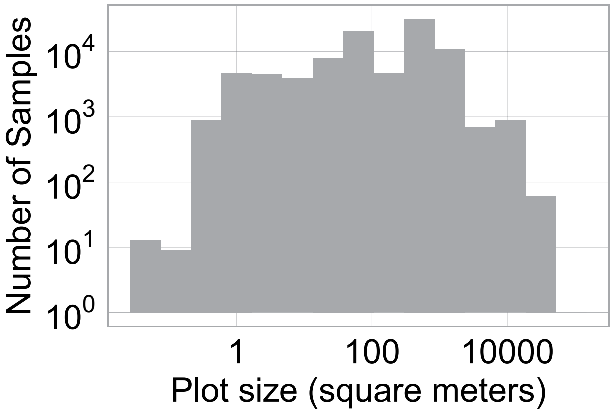


Fig. 6 Distribution of *Samples* by vegetation plot sizes. In VegVault, only *vegetation_plot Samples* and *Datasets* have such information. See **Internal Dataset Structure** section for more details.

Column name	Data type	Description
sample_size_id	integer	ID of a size category (unique)
sample_size	numeric	Numeric expression of size
description	character	Mostly description of units in which the values are stored

Table 20. Column names and types for table *SampleSizeID*.

AbioticVariableReference table. Each *Abiotic Variable* can have a separate *Reference*, in addition to a *Dataset* and *Sample*. See Table 33 for the description of individual columns.

AbioticDataReference table. As abiotic data is stored in a special *Dataset Type—gridpoints*, we have also pre-calculated the spatio-temporal distance of *gridpoints* to other *Datasets*. See **Methods** for details about the creation of *gridpoints*. There, the *AbioticDataReference* table contains information about specific distances among *Samples* for both temporal (age in years) and geographic (distance in km). See Table 34 for the description of individual columns.

***References* table.** This table contains all *References*, independent of the source of the reference and the type of data. Each row contains a single *Reference* that is then linked to the type of data which is being referenced. This allows to have a single *Reference* to be used across data types, but also one data point having many different references.

Moreover, most primary sources of the data have a license, which requires correct attribution. Therefore, each *Reference* has information on whether such a *Reference* needs to be cited while using the specific data ("mandatory" column). See Table 35 for more details about column names.

Technical Validation

The data validity of VegVault is driven by the completeness, accuracy, and reliability of the source data. Several steps have been undertaken to ensure that VegVault provides high-quality data for research applications. For the fossil pollen records, strict data-quality rules have been applied by using the *FOSSILPOL* workflow[16]. The data preparation and execution are backed up by open-source publicly available code versioned and controlled by a git Tag system.

Usage Notes

Guidelines for data reuse and update. Due to the version system of VegVault, the dataset is expected to be updated using new data and/or changing the process of data migration and processing. Therefore, we recommend citing the latest VegVault version with the corresponding DOI, see bit.ly/VegVault for the latest release of the dataset (v1.0.0 can be found here: https://doi.org/10.48700/datst.t21cz-2nq07).

As the primary data sources are held under various licences, VegVault has a *CC BY 4.0* Licence (https://creativecommons.org/licenses/by/4.0/), allowing the copying and redistribution of the material as long as correct attribution is given. We recommend that users carefully review the restrictions associated with data usage. In addition, when citing the usage of VegVault, users should always cite the primary sources of the data, as well as any individual datasets. For those purposes, we created a function '*vaultkeepr::get_references()*' within the {*vaultkeepr*} R package (see below) that will output a list of recommended references for the specific data compilation created by the user.

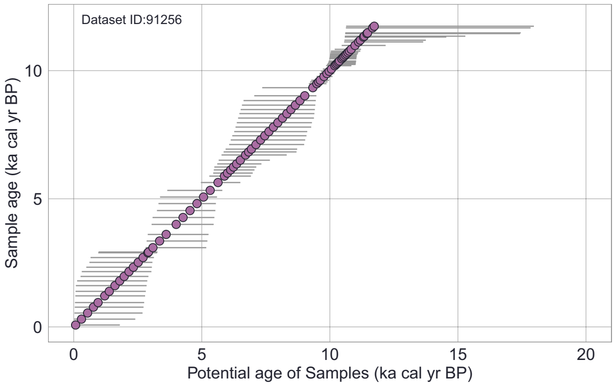


Fig. 7 Example of age uncertainty of *Samples* for selected fossil pollen *Dataset* (ID: 91256). Each point represents one *Sample*. Each horizontal line represents a range of all potential ages associated with that *Sample*. Potential ages are gathered from age-depth models and stored in the *SampleUncertainty* table. See **Internal Dataset Structure** section for more details about the data structure and *FOSSILPOL* workflow[16] for more details about age uncertainty from age-depth models.

Column name	Data type	Description
sample_id	integer	ID of a *Sample*
iteration	integer	ID of a iteration from age depth model. Currently, the is 1000 iteration per each *Sample*.
age	integer	Potential age of a *Sample*

Table 21. Column names and types for table *SampleUncertainty*.

Column name	Data type	Description
sample_id	integer	ID of a *Sample*
reference_id	integer	ID of a *Reference*

Table 22. Column names and types for table *SampleReference*.

Column name	Data type	Description
taxon_id	integer	ID of a *Taxon* (unique)
taxon_name	character	Name of a *Taxon* from primary source.

Table 23. Column names and types for table *Taxa*.

Column name	Data type	Description
sample_id	integer	ID of a *Sample*
taxon_id	integer	ID of a *Taxon*
value	numeric	Abundance representation of a *Taxon* (the units may differ among primary sources, i.e., *Dataset Source-Types*)

Table 24. Column names and types for table *SampleTaxa*.

Limitations and considerations for future research. Potential limitation lies in the completeness, accuracy, and reliability of the primary data sources. For example, it has been suggested that improper data practices erode the quality of global ecological databases such as *TRY*[48], which have been used in VegVault. We do not attempt to solve these problems as VegVault's main purpose is the re-usability of the data.

Next, as VegVault database contains more than 100GB of data, we advise the users to make sure that their machine has enough space on their drives, as downloads can be challenging on certain machines (e.g., a laptop).

Finally, to increase the accessibility of the data, we have also deposited the flat version of the database (i.e. individual tables saved as CSV files), accessible under https://doi.org/10.48700/datst.thktf-5rr35[49]. However, note that many of those files are larger than 1GB and some machines do not have enough memory (RAM) to fully load them.

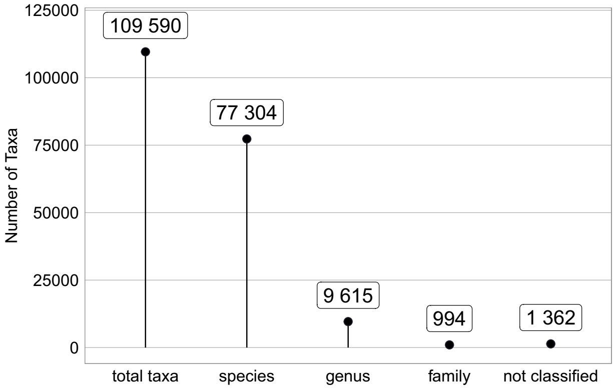


Fig. 8 Total number of *Taxa* and their classification present in VegVault. See **Methods** section for more information about the classification process.

Column name	Data type	Description
taxon_id	integer	ID of a *Taxon* (unique)
taxon_species	integer	ID of a *Taxon*, which was assigned as species level
taxon_genus	integer	ID of a *Taxon*, which was assigned as genus level
taxon_family	integer	ID of a *Taxon*, which was assigned as family level

Table 25. Column names and types for table *TaxonClassification*.

Column name	Data type	Description
taxon_id	integer	ID of a *Taxon*
reference_id	integer	ID of a *Reference*

Table 26. Column names and types for table *TaxonReference*.

Column name	Data type	Description
trait_id	integer	ID of a *Trait* (unique)
trait_domain_id	integer	ID of a *Trait Domain*
trait_name	character	Name of the trait from the primary source. See **Methods** for the details about the specific columns used from primary sources.

Table 27. Column names and types for table *Traits*.

Column name	Data type	Description
trait_domain_id	integer	ID of a *Trait Domain* (unique)
trait_domain_name	character	Name of the *Trait Domain* from Diaz *et al.*[36]
trait_domanin_description	character	Additional information about the *Trait Domain*

Table 28. Column names and types for table *TraitsDomain*.

Column name	Data type	Description
trait_id	integer	ID of a *Trait*
dataset_id	integer	ID of a *Dataset*
sample_id	integer	ID of a *Sample*
taxon_id	integer	ID of a *Taxon*
trait_value	numeric	Value of specific measured observation of *Trait*. See **Methods** for the details about the specific columns used from primary sources.

Table 29. Column names and types for table *TraitsValue*.

Column name	Data type	Description
trait_id	integer	ID of a *Trait*
reference_id	integer	ID of a *Reference*

Table 30. Column names and types for table *TraitsReference*.

Column name	Data type	Description
abiotic_variable_id	integer	ID of a *Abiotic Variable*
abiotic_variable_name	character	Name of a *Abiotic Variable* from primary source
abiotic_variable_unit	character	Unit of a *Abiotic Variable*
measure_details	character	Additonal details about *Abiotic Variable*

Table 31. Column names and types for table *AbioticVariable*.

Column name	Data type	Description
sample_id	integer	ID of a *Sample*
abiotic_variable_id	integer	ID of an *Abiotic Variable*
abiotic_value	numeric	The actual value of abiotic data

Table 32. Column names and types for table *AbioticData*.

Column name	Data type	Description
abiotic_variable_id	integer	ID of an *Abiotic Variable*
reference_id	integer	ID of a *Reference*

Table 33. Column names and types for table *AbioticVariableReference*.

Column name	Data type	Description
sample_id	integer	ID of non-*gridpoint Sample*
sample_ref_id	integer	ID of *gridpoint Sample*
distance_in_km	integer	Distance among samples expressed in kilometres
distance_in_years	integer	Distance among samples expressed in years

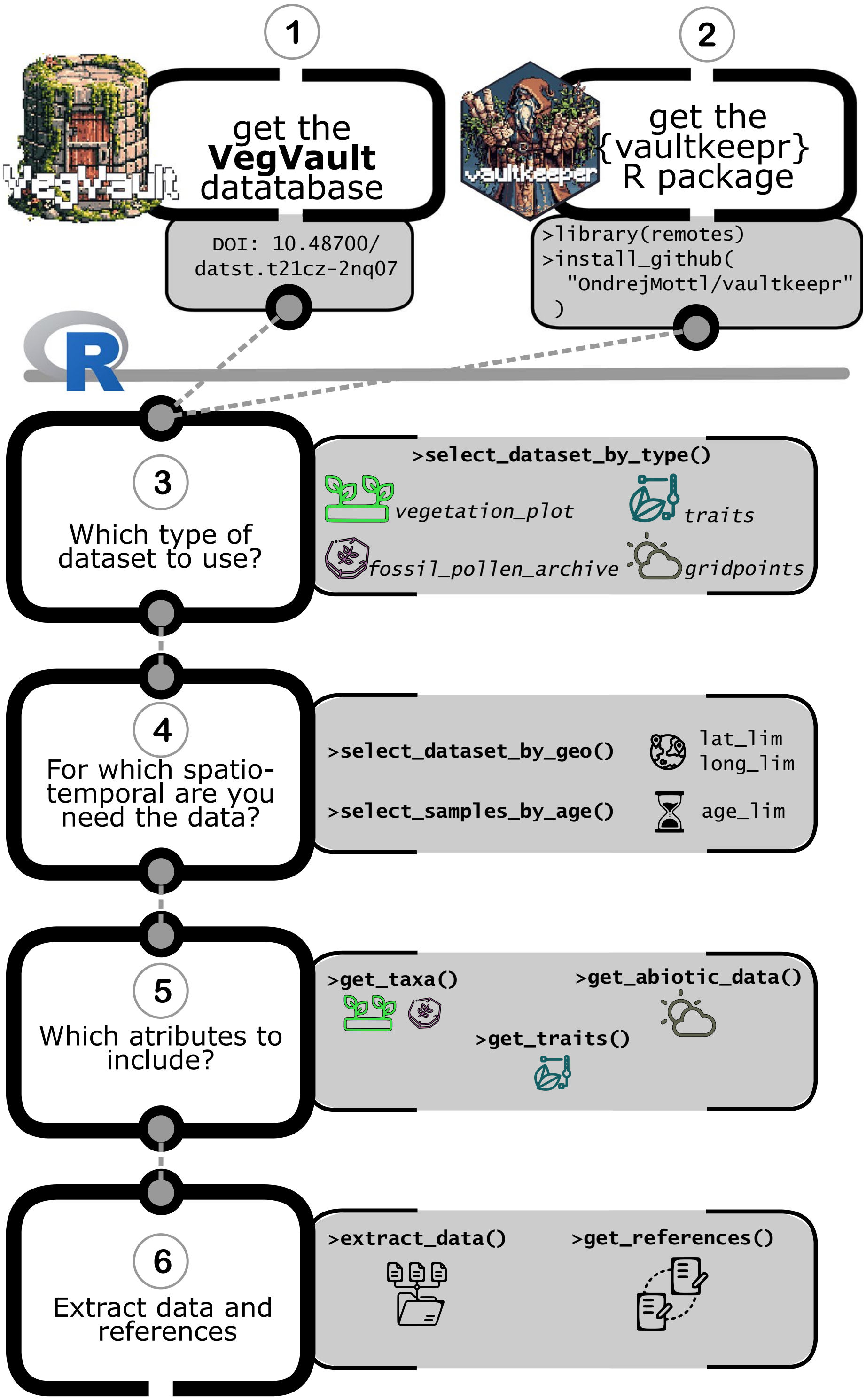
Table 34. Column names and types for table *AbioticDataReference*.

{vaultkeepr}: R-package for accessing the VegVault database. In order to make use of the VegVault as easily as possible and facilitate access to SQLite databases, we have developed an R-package called {*vaultkeepr*}, providing a suite of functions to effectively interact with the database directly from the R programming environment[50].

Functions include accessing the database, extracting datasets, filtering samples, and accessing specific taxa and traits. Therefore, we suggest all users to use the SQLite database accompanied by {*vaultkeepr*} R package to retrieve only project-specific data without the need to load data into memory.

This package is a well-tested interface (>95% code coverage). See Fig. 9 for details about individual steps to retrieve the data from VegVault. For more about the package, the function documentation and examples of code usage, please see {*vaultkeepr*} website (https://bit.ly/vaultkeepr). Here we present 3 examples of potential projects and how to obtain data for such projects from VegVault using {*vaultkeepr*} R-package. Note that we are specifically not trying to do any analysis, only presenting a way to obtain data, which can be used for such follow-up projects:

- Figure 10A: The first example demonstrates how to retrieve data for the genus *Picea* across North America by selecting both contemporary and fossil pollen plot datasets, filtering samples by geographic boundaries and temporal range (0 to 15,000 cal yr BP), and harmonizing taxa to the genus level. The resulting dataset allows users to study spatiotemporal patterns of *Picea* distribution over millennia.
- Figure 10B: In the second example, the project aims to do species distribution modelling for plant taxa in the Czech Republic based on contemporary vegetation plot data and mean annual temperature. The project includes selecting datasets and extracting relevant abiotic data.
- Figure 10C: The third example focuses on obtaining data to be able to reconstruct plant height for South and Central America between 6–12 cal kyr BP (thousand calibrated years before present). This example project showcases the integration of trait data with paleo-vegetation records to subsequently study historical vegetation dynamics and functional composition of plant communities.



```
>library(remotes)
>install_github(
  "OndrejMottl/vaultkeepr"
 )
```

Fig. 9 Schematic workflow of accessing and extracting data from VegVault database using {*vaultkeepr*} R package. (**1**) Download VegVault database (v1.0.0; https://doi.org/10.48700/datst.t21cz-2nq07); (**2**) Download {*vaultkeepr*} R package from GitHub (current version 0.0.6; https://doi.org/10.5281/zenodo.14964737); (**3**) In the R programming environment[50], the user has to select which type(s) of datasets they would like to extracted. A minimum of one *Dataset Type (see* **Data Records** section for more details*)* must be specified when using the '*vaultkeepr::select_dataset_by_type()*' function; (**4**) When the user is interested in data from a specific region, they can specific the geographical coordinates of a rectangular extent using the '*vaultkeepr::select_dataset_by_geo()*' function to only get *Samples* from the individual *Datasets* that were recorded within the region of interest. Additionally, the user can specify the temporal focus by filtering data within a specific period using the '*vaultkeepr::select_samples_by_age()*'; (**5**) The user may also specify any further attributes to be added to the data compilation. Specifically: '*get_taxa()*'—When extracting contemporary or past vegetation (fossil pollen) records, the user most likely wishes to add information about the abundance of individual *Taxa* in each

Sample. To do so, the user can use the ‘*vaultkeepr::get_taxa()*’ function. In addition, the user can standardise the taxonomy, so that the extracted *Taxa* can be compared. The parameter ‘*classify_to*’ within the ‘*vaultkeepr::get_taxa()*’ function allows the user to specify a taxonomic level (species, genus or family) on which the data should be comparable (see **Methods** about *Taxa* classification). Furthermore, the user can select specific *Taxa* based on taxonomy by using the ‘*vaultkeepr::select_taxa_by_name()*’ function. ‘*get_traits()*’—When wishing to link the *Trait* data with the vegetation records, the user can use ‘*vaultkeepr::get_traits()* function to extract all *Trait Samples* of the earlier specified spatio-temporal extent. Moreover, similarly to the ‘*vaultkeepr::get_taxa()*’ function, the user can specify the taxonomic level to which the data should be standardised by using the ‘*classify_to*’ parameter. Please note that the user has to decide in their further analysis how they want to aggregate the measured traits per taxonomic group, e.g. by taking the mean. Further, the user can select a specific *Trait Domain* (of the six available; see **Methods** about details) by using the ‘*vaultkeepr::select_traits_by_domain_name()*‘ function. ‘*get_abiotic_data()*‘—When wishing to link vegetation or trait records with abiotic data, the abiotic data can be obtained by the ‘*vaultkeepr::get_abiotic_data()*‘ function. The user can specify in which mode the abiotic data should be linked, which can be either “*nearest*” (i.e., geographically closest records), “*mean*” or “*median*” (summarising all abiotic records within a set geographical and/or temporal distance). This can be further tweaked by its parameters ‘*limit_by_distance_km*‘ and ‘*limit_by_age_years*‘. Furthermore, specific abiotic variables can be chosen by the ‘*vaultkeepr::select_abiotic_var_by_name()*‘ function; **6)** When defined all specifications for data extraction, the user can execute the extraction using ‘*vaultkeepr::extract_data()*‘. This will result in a “ready-for-analyses” data compilation. Moreover, the user can use the ‘*vaultkeepr::get_references()*‘ function to obtain all references required (and/or suggested) for such compilation (see **Internal Dataset Structure** section for more details about the hierarchical structure of references). Finally, see the **Usage Notes** section for examples of data processing and extracting using {vaultkeepr} R package.

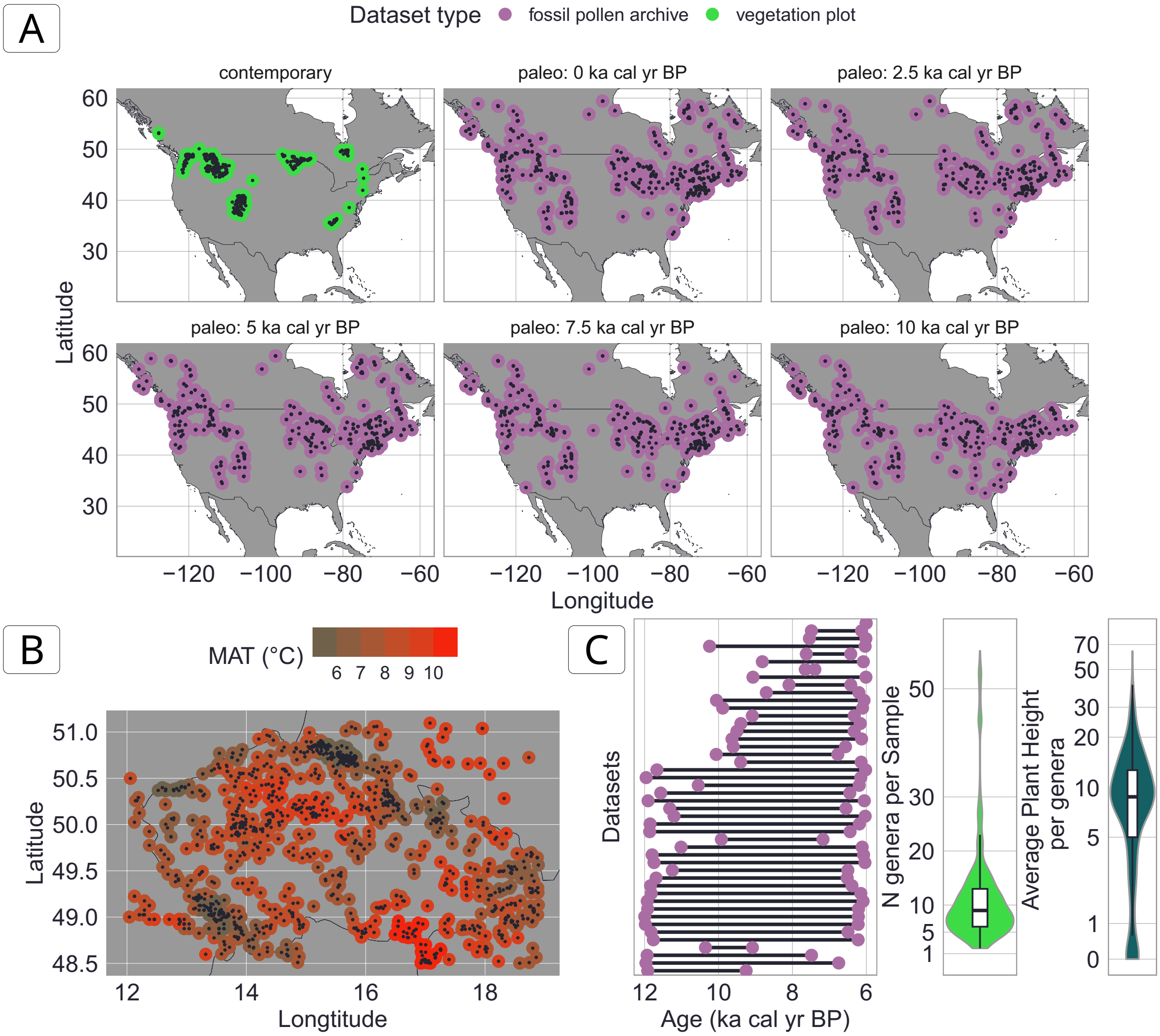


Fig. 10 Visualisation of example data usage of VegVault using {*vaultkeepr*} package. See **Usage Notes** section for details about the aim of each data compilation. (**A**) The individual points represent vegetation data (*Samples*

for fossil pollen or contemporary vegetation plots) within each age time slice. (**B**) Each point represents one contemporary vegetation plot. The colour represents the Mean Annual Temperature (MAT) associated with that plot. Note that several vegetation plots can have the same value due to sharing the same closest *gridpoint* (see Fig. 2). (**C**) The left figure represents the temporal length of fossil pollen *Datasets*, which are available for Central and South America between 6 and 12 ka BP (thousand years before present). The middle figure represents the distribution of various genera present in this data assembly. The right figure represents the distribution of average *Plant height Trait* per each genus present in the data assembly. The code to reproduce these figures can be accessed from the GitHub repository titled *VegVault* (https://github.com/OndrejMottl/VegVault/tree/v1.0.0-website_rewiev), which can be accessed as https://doi.org/10.5281/zenodo.16987345.

Column name	Data type	Description
reference_id	integer	ID of a *Reference* (unique)
reference_detail	character	Text of a *Reference* (i.e., citation)
mandatory	Integer (Boolean)	Is the *Reference* mandatory to report while using the data? Most primary sources of the data have a license, which requires correct attribution.

Table 35. Column names and types for table *References*.

Data availability

The VegVault v1.0.0 relational database (SQLite; ~110 GB) is publicly archived in the National Repository ('REPO') and available at https://doi.org/10.48700/datst.t21cz-2nq07. The deposit consists of a single SQLite file comprising 31 linked tables with 87 fields, containing >480,000 datasets, >13,000,000 samples, >100,000 taxa, six vegetation trait domains, >11,000,000 trait values, and eight abiotic variables. The database schema and field definitions are detailed in the manuscript (**Data Records**, Fig. 4; Tables 5–35**)**. The database can be queried with any SQLite-compatible client or accessed programmatically via the companion R package {*vaultkeepr*} (see **Usage Notes**). Version history and change logs are stored in the internal *version_control* table, and subsequent releases will be issued as versioned updates in the same repository.

Code availability

The VegVault database is built on SQLite, chosen for its robustness and compatibility with various data types. The VegVault v1.0.0 is available at the *National Repository*[44] ('*REPO*') under https://doi.org/10.48700/datst.t21cz-2nq07. The database itself is under *CC B 4.0* licence, see **Usage Notes** section. VegVault utilizes several tools and software to facilitate data management and access. All code used to generate the VegVault dataset is publicly available under the MIT licence. The GitHub repository *VegVault* used to integrate all data together and migrate them into SQLite database (can be accessed as https://doi.org/10.5281/zenodo.16987345). See **Methods** section and Fig. 1 for details about individual GitHub repositories. To enable easy access and manipulation of data, {*vaultkeepr*} R package has been developed as an open access software under MIT licence (https://bit.ly/vaultkeepr). The code to create the figures in this manuscript is available under https://doi.org/10.5281/zenodo.16987345.

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Author contributions

O.M. conceived the study and programmed all related code. S.G.A.F. provided strategic guidance during the development of the project and manuscript, including decisions on data presentation and structure. F.G., I.S. and S.G.A.F. provided critical feedback on the technical infrastructure and database design. O.M. and S.G.A.F. wrote the first draft of the manuscript. S.G.A.F., F.G. and I.S. contributed to multiple rounds of revision. All authors approved the final version of the manuscript.

Competing interests

The authors declare no competing interests.

Additional information

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