sPlotOpen – An environmentally-balanced, open-access, global dataset of vegetation plots

This manuscript is still work in progress

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Short Running Title

sPlotOpen: a global vegetation plot database

Abstract

Motivation: Assessing biodiversity status and trends in plant communities is critical for understanding, quantifying and predicting the effects of global change on ecosystems. Vegetation plots record the occurrence or abundance of all plant species co-occurring within delimited local areas. This allows inferring species absences, an information seldom provided by existing global plant datasets. Although many vegetation plots have been recorded, most are not available to the global research community. A recent initiative, called ‘sPlot’, compiled the first global vegetation plot database, and continues to grow and curate it. This large dataset, however, is challenging to work with because it is extremely unbalanced spatially, and because the data are not open-access. Here, we address both these issues by (a) resampling the vegetation plots using a novel algorithm and (b) securing permission from data holders to openly release data (from 105 local to regional datasets).

We thus present sPlotOpen, the largest open-access dataset of vegetation plots ever released. sPlotOpen can be used to explore global patterns of diversity at the plant community level, as ground truth data in remote sensing applications, or as a baseline for biodiversity monitoring.

Main types of variable contained: Vegetation plots (n = 95,104) recording cover or abundance of naturally occurring vascular plant species within delimited areas. sPlotOpen contains three partially overlapping, environmentally balanced datasets (~50,000 plots each), to be used as replicates in global analyses. Besides geographic location, date, plot size, biome, elevation, slope, aspect, vegetation type, naturalness, coverage of various vegetation layers and source dataset, plot-level data also include community-weighted means and variances of 18 plant functional traits from the 'TRY' database.

Spatial location and grain: Global, 0.01-40,000 m².

Time period and grain: 1888-2015, recording dates.

Major taxa and level of measurement: 42,677 vascular plant taxa, plot-level records.

Software format: Three main matrices (.csv), relationally linked.

Keywords

Biodiversity, Biogeography, Big-data, Database, Functional traits, Macroecology, Vascular plants, Vegetation plots

Background & Summary

Biodiversity is facing a global crisis. As many as 1 million species are currently threatened with extinction, the vast majority due to anthropogenic impacts such as land-use and climate change (1, 2). In addition, the rates of biodiversity homogenization and redistribution are accelerating (3, 4; 5). Biological assemblages are becoming progressively more similar to each other globally, as local and endemic species go extinct and are replaced by more widespread and competitive native or alien species (1; 5). Many terrestrial and marine species are also shifting their geographical distribution as a response to climate change (4), including animals hosting pathogens transmissible to humans (6; 7). This has profound potential impacts on ecosystems and human health (8; 9).

Plant communities are no exception to this biodiversity crisis (10; 11; 5). This is particularly worrying since terrestrial vegetation accounts for 80% (450 Gt C) of the living biomass on Earth (12). Given the central role of vegetation in ecosystem productivity, structure, stability and functioning (11), assessing biodiversity status and trends in plant communities is paramount for other kingdoms of life and human societies alike.

Monitoring trends in plant biodiversity requires adequate data across a range of spatiotemporal scales (13, 14). Large independent collections of plant occurrence data do exist at the global or continental extent via the Botanical Information and Ecology Network (BIEN) (15), the Global Inventory of Floras and Traits (GIFT) (16) or the Global Biodiversity Information Facility (GBIF) (https://www.gbif.org/). However, these databases suffer from one or several of the following limitations: (1) imbalance towards tree species only; (2) lack of data on how individual plant species co-occur and interact locally to form plant communities; or (3) coarse spatial resolutions (e.g., one-degree grid cells), which preclude intersection with high resolution remote sensing data and the assessment of biodiversity trends at the plant community level (17).

There is a long tradition among botanists and phytosociologists to record the cover or abundance of each plant species that occurs in a vegetation plot (here used as a synonym of 'relevé' or 'quadrat') of a given size (i.e. surface area) at a given time (e.g. 18). Compared to presence-only data, vegetation-plot data present many advantages. As all visible plant species are recorded, plots contain information on which plant species do, and do not, co-occur in the same locality at a given moment in time (19). This is important for testing hypotheses related to biotic interactions among plant species. Vegetation-plot data also provide crucial information on where and when a species was absent, therefore improving predictions from current species distribution models (20). Being spatially explicit, vegetation plots can be resurveyed through time to assess potential changes in plant species composition relative to a baseline (21; 22, 5). As they normally contain information on the relative cover or abundance of each species, vegetation plots are also more appropriate for detecting biodiversity changes than data representing only the occurrence of individual species (23, 24).

Globally, however, vegetation-plot data are very fragmented, as they typically stem from a myriad of local research and survey projects (25). These data often have fine grain (e.g., 1-10,000 m^2) but small spatial extents (e.g., 1-1,000 km^2)(26). With their disparate sampling protocols, standards and taxonomic resolutions, aggregating and harmonizing vegetation plot data proves extremely challenging (27). It is not surprising, therefore, that these data are rarely used in global-scale research on the biodiversity of plant communities (28; 29; 30).

The sPlot initiative tries to close this data gap. It consolidates numerous local to regional vegetation-plot datasets to create a harmonized and comprehensive global database of georeferenced terrestrial plant species assemblages (25). Established in 2013, sPlot (version 3) currently contains more than 1.9 million vegetation plots, and is fully integrated with the TRY database (31), from which it derives information on plant functional traits. The sPlot database is increasingly being used to study continental-to-global scale vegetation patterns, such as the relative contribution of regional vs. local factors on the global patterns of fern richness (32), the mechanisms underlying the spread and abundance of native vs. invasive tree species (33), and worldwide trait–environment relationships in plant communities (27).

Yet, most of these data are not open-access. Here, we secured permission from data holders in the sPlot database to openly release a dataset composed of 95,104 vegetation plots. We selected the plots to release using a replicated environmental stratification, in order to represent the entire environmental space covered by the sPlot database. This maximises the benefits of releasing these data for a wide range of potential uses. The selected vegetation plots stem from 105 databases and span 114 countries (Figure 1). This resampled dataset (sPlotOpen - hereafter) is composed of: (1) plot-level information, including metadata and basic vegetation structure descriptors; (2) the vascular plant species composition of each vegetation plot, including species cover or abundance information when available; and (3) community-level functional information obtained by intersection with the TRY database (31).

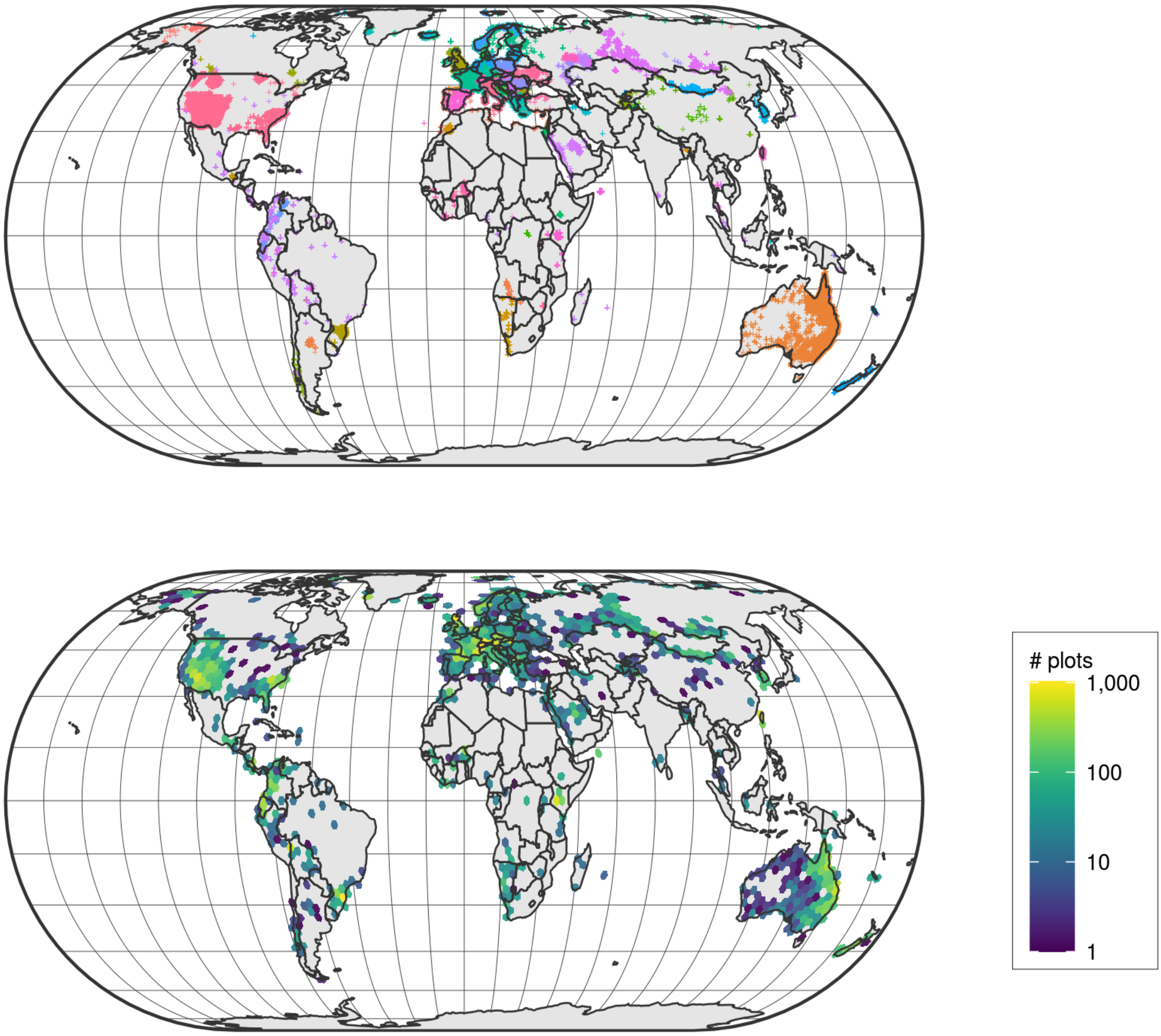

Figure 1: Top: Global distribution of all vegetation plots contained in sPlotOpen (n = 95,104). Each color represents a different source dataset (n = 105 - different datasets might have the same color). Bottom: Spatial distribution of vegetation plot density for the environmentally-balanced dataset selected by the first resampling iteration (n = 49,787).

Densities are calculated in hexagonal cells with a spatial resolution of approximately 70,000 km². Map projection is Eckert IV.

Methods

Vegetation plot data sources

We started from the sPlot database v2.1 (created in October 2016), which contains 1,121,244 unique vegetation plots and 23,586,216 species records. sPlot mostly focuses on natural and semi-natural vegetation, and hardly contains data on vegetation shaped by intensive and repeated human interference, such as cropland or ruderal communities. Data originate from 110 different vegetation-plot datasets of regional, national or continental extent, some of which stemming from regional or continental initiatives (see 25 for more information). For instance: 48 vegetation-plot datasets derive from the European Vegetation Archive (EVA) (19); three major African datasets derive from the Tropical African Vegetation Archive (TAVA); and multiple vegetation datasets in the USA and Australia derive from the VegBank (34; 35) and TERN's AEKOS (36) archives, respectively. Data from other continents (South America, Asia) or countries were contributed as separate standalone datasets. The metadata of each individual vegetation-plot dataset stored in sPlot are managed through the Global Index of Vegetation-Plot Databases GIVD (37), using the GIVD code as the unique dataset identifier.

Resampling method

Data in the sPlot database are unevenly distributed across vegetation types and geographic regions (see 27). Mid-latitude regions in developed countries (mostly Europe, the USA and Australia) are overrepresented in sPlot, while regions in the tropics and subtropics are underrepresented, which is a typical geographical bias in biodiversity data (e.g., 38; 4). To reduce this imbalance as much as possible, we performed a stratified resampling approach, using several environmental variables available at global extent as sampling strata.

First, we removed vegetation plots without geographical coordinates or with a location uncertainty higher than 3 km. We also removed vegetation plots identified by the respective data contributors as being from wetlands and from anthropogenic vegetation types, since these data were available only for few geographic regions, mostly in Europe. This resulted in a total of 799,400 out of the initial set of 1,121,244 vegetation plots.

We then ran a global principal component analysis (PCA) on a matrix of terrestrial grid cells based on 30 climatic and soil variables. For climate, we used the 19 bioclimatic variables from CHELSA v1.2 (39), as well as two other bioclimatic variables reflecting the growing-season length (growing degree days above 1 °C - GDD1 - and 5 °C - GDD5), which were derived from CHELSA's monthly average temperatures. Specifically, we summed the number of days of those months with average temperature greater than 1 °C or 5 °C, respectively. In addition, we considered an index of aridity and a layer for potential evapotranspiration from the Consortium of Spatial Information (CGIAR-CSI 40). For soil, we extracted seven variables from the SoilGrids database (41), namely: (1) soil organic carbon content in the fine earth fraction; (2) cation exchange capacity; (3) pH; as well as the fractions of (4) coarse fragments; (5) sand; (6) silt; and (7) clay.
The results of this PCA represents the full environmental space of all terrestrial habitats on Earth at a spatial resolution of 2.5 arcmin, totaling 8,384,404 terrestrial grid cells, irrespective of whether a grid cell hosted vegetation plots or not (Figure S1). We then subdivided the PCA ordination space, represented by the first two principal components (PC1–PC2), which accounted for 47% and 23% of the total environmental variation in terrestrial grid cells, into a regular 100 × 100 grid. This PC1-PC2 two-dimensional space was subsequently used to balance our sampling effort across all PC1-PC2 grid cells for which vegetation plots were available. After excluding 42,878 vegetation plots for which no PC1 or PC2 values were available, due to missing data in the bioclimatic or soil variables, we projected

the remaining 756,522 vegetation plots onto this PC1-PC2 grid. We finally calculated how many vegetation plots occurred in each PC1-PC2 grid cell (Figure 2).

In total, vegetation plots were available for 1,720 PC1-PC2 grid cells out of the 4,125 PC1-PC2 grid cells covered by the 8,384,404 terrestrial grid cells of the geographical space. We then resampled those PC1-PC2 grid cells (n = 858) with more than 50 vegetation plots, which is the median number of plots occurring across occupied grid cells in sPlot. This threshold of 50 vegetation plots represents a compromise between selecting a high number of plots, and keeping the resampled dataset as much balanced as possible across the PC1-PC2 environmental space. To select these 50 vegetation plots we used the heterogeneity-constrained random resampling algorithm from Lengyel et al. (2011) [42]. This approach optimizes the selection of a subset of vegetation plots that encompasses the highest variability in species composition while avoiding peculiar and rare communities, which may represent outliers. As such, our approach maximizes variability over representativeness when resampling vegetation plots. We quantified the variability in plant species composition among the 50 randomly selected vegetation plots by computing the mean and the variance of the Jaccard's dissimilarity index (43) between all possible pairs of these 50 vegetation plots (n = 1,225). More precisely, for a given PC1-PC2 grid cell containing more than 50 vegetation plots, we generated 1,000 random selections of 50 vegetation plots and ranked each selection according to the mean (ascending order) and variance (descending order) value of the Jaccard's dissimilarity index. Ranks from both sortings were summed for each random selection, and the selection with the lowest summed rank was considered to provide the most balanced/even representation of vegetation types within the focal grid cell. Where a grid cell contained less than 50 plots, we retained all of them. In this way, we reduced the imbalance towards over-sampled climate types while ensuring that the resampled dataset represents the entire environmental gradient covered by the original sPlot database. We repeated the whole resampling procedure three times to get three different environmentally-balanced, resampled subsets of our vegetation plots. These three resampling iterations can therefore be used as separate replicates, albeit these are not completely independent, as the same plots might have been drawn in different iterations. In addition, those plots located in PC1-PC2 grid cells with less than 50 vegetation plots are completely shared by all three iterations.

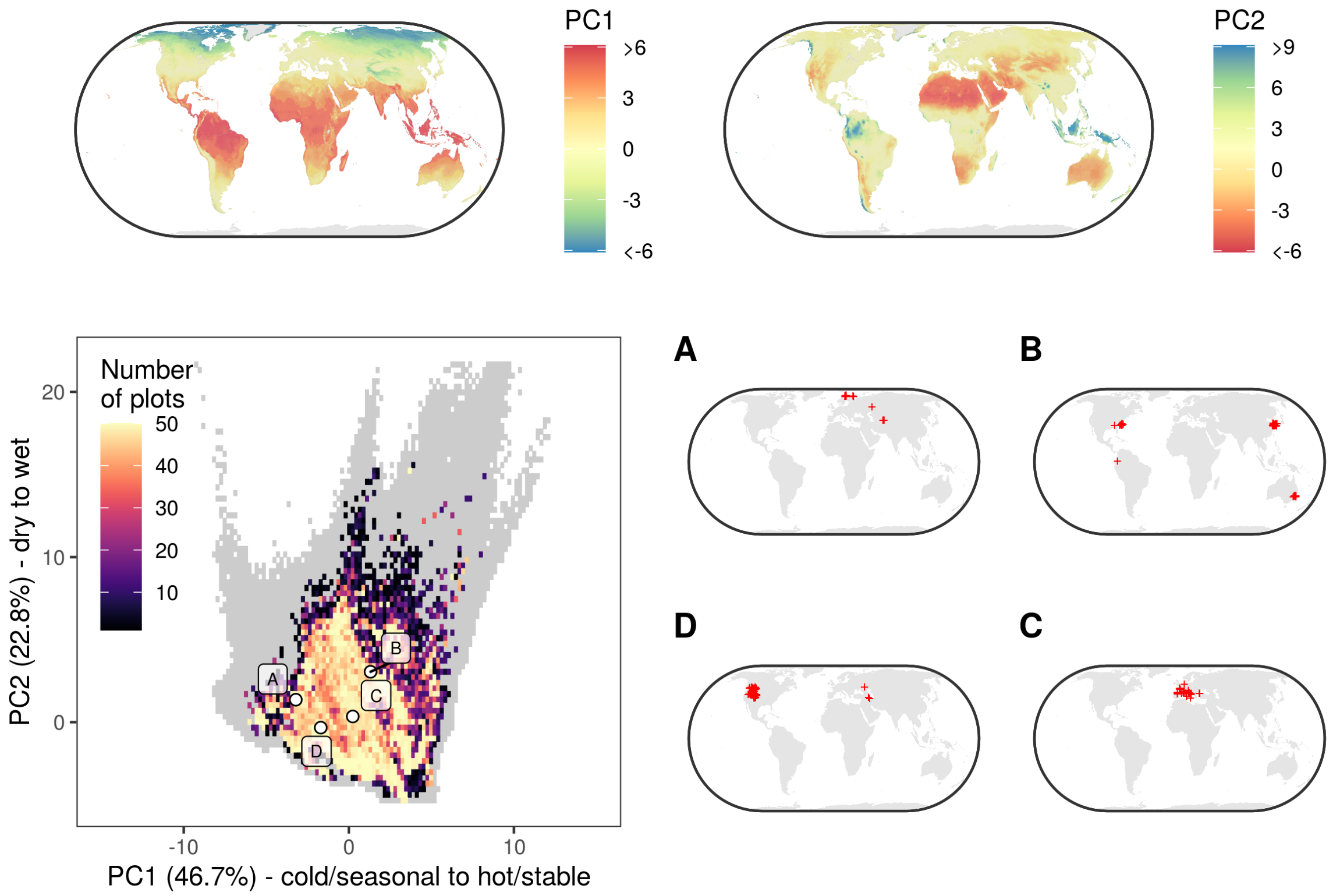

Figure 2: Distribution of vegetation plots from sPlotOpen in the global environmental space based on a principal component analysis (PCA) using 30 climate and soil variables. Top: Spatial distribution of PCA values across all terrestrial grid cells (n = 8,384,404, spatial grain = 2.5 arcmin). Bottom Left: Distribution of plots compared to the distribution of all terrestrial 2.5 arc-minute cells (gray background) in the PCA space. Only the plots in the environmentally-balanced dataset selected by the first resampling iteration are shown (n = 49,787). The PCA space was divided into a 100 × 100 regular grid. The first and second PCA axis explained 47% and 23% of the total variance. Bottom right: Geographic distribution of the vegetation plots contained in four randomly selected grid cells.

Permission to release the data as open access

The resampling procedure resulted in 56,486, 56,501 and 56,494 vegetation plots selected during resampling iteration #1, #2 and #3, respectively, for a total 107,238 unique vegetation plots. Since the sPlot database is a consortium of independent datasets whose copyright belongs to the data contributor, we used this preliminary potential selection to ask each dataset's custodian (i.e., either the owner of a dataset or its authorized representative in case of a collective dataset) for permission to release the data of selected vegetation plots as open access. For 12,134 unique vegetation plots, permission could not be granted because, for instance, the data are unpublished, confidential or sensitive. The number of vegetation plots for which the open-access permission was not granted in resampling iteration #1, #2 and #3 were 6,699, 6,690 and 6,705, respectively.

To mitigate the imbalance due to the exclusion of these confidential plots, we created a 'consensus' dataset. We started from resampling iteration #1, and replaced the 6,699 plots not granted as open access, with plots selected in the second and third iteration, for which such permission could be granted ('reserve' plots, hereafter). We imposed the constraint that each candidate vegetation plot in the reserve pool should belong to the same environmental stratum, i.e., the same PC1-PC2 grid cell, of the confidential vegetation plot, even if we acknowledge that this procedure does not maximize the variability in plant species composition of the replacement plots. Even after drawing from reserves, there were 3,150 plots that could not be replaced. These were distributed across 279 PC1-PC2 grid cells (16.2% of occupied cells), each cell having on average 11 irreplaceable plots (min = 1, median = 5, max = 50).

Trait information

For each vegetation plot for which open access could be granted, we computed the community-weighted mean and variance for eighteen plant functional traits derived from the TRY database v3.0 (31). These traits were selected among those that describe the leaf, wood and seed economics spectra (44; 45), and are known to either affect different key ecosystem processes or respond to macroclimatic drivers, or both (25). The eighteen plant functional traits (all concentrations based on dry weight) were: (1) leaf area [mm^2]; (2) stem specific density [g cm^{-3}]; (3) specific leaf area [$m^2 kg^{-1}$]; (4) leaf carbon concentration [mg g^{-1}]; (5) leaf nitrogen concentration [mg g^{-1}]; (6) leaf phosphorus concentration [mg g^{-1}]; (7) plant height [m]; (8) seed mass [mg]; (9) seed length [mm]; (10) leaf dry matter content [g g^{-1}]; (11) leaf nitrogen per area [g m^{-2}]; (12) leaf N:P ratio [g g^{-1}]; (13) leaf $\delta^{15}N$ [per million]; (14) seed number per reproductive unit; (15) leaf fresh mass [g]; (16) stem conduit density [mm^{-2}]; (17) dispersal unit length [mm]; and (18) conduit element length [μm].

Because missing values were particularly widespread in the species-trait matrix, we calculated community-weighted means using the gap-filled version of these traits we received from TRY (31). Gap-filling was performed at the level of individual observations and relies on a hierarchical Bayesian modeling (R package 'BHPMF', 46; 47). This is a Bayesian machine learning approach, with no a priori assumptions, except for the data being missing completely at random. The algorithm "learns" from the data, i.e. if there was a phylogenetic signal in the data, this was used to fill the gaps but where no such signal was apparent, none was introduced. After gap-filling, we transformed to the natural logarithm all gap-filled trait values and averaged each trait by taxon (i.e., at species, or genus level). The gap-filling approach was run only for species having at least one trait observation (n = 21,854). Additional information on the gap-filling procedure is available in [25].

Community-weighted means (CWM) and variances (CWV) were calculated for every plant functional trait *j* and every vegetation plot *k* as follows (48):

$$CWM_{j,k} = \sum_{i}^{n_k} p_{i,k} t_{i,j} \tag{1}$$

$$CWV_{j,k} = \sum_{i}^{n_k} p_{i,k} (t_{i,j} - CWM_{j,k})^2 \tag{2}$$

where n_k is the number of species with trait information in vegetation plot *k*, $p_{i,k}$ is the relative abundance of species *i* in vegetation plot *k* calculated as the species' fraction in cover or abundance of total cover or abundance, and $t_{i,j}$ is the mean value of species *i* for trait *j*.

Data Records

sPlotOpen contains 95,104 unique vegetation plots from 105 constitutive datasets (Table 1) and from 114 countries covering all continents except Antarctica (Figure 1). This is the result of pooling together the three environmentally-balanced datasets from resampling iterations #1, #2 and #3 containing 49,787, 49,811 and 49,789 plots, respectively, after excluding the set of plots not granted as open access by data contributors. The number of plots shared across all three resampling iterations is 19,672, while 14,939 plots are shared between two iterations. Replacing confidential plots in resampling iteration #1 with reserves from the other two iterations in the same PC1-PC2 grid cell, resulted in a consensus version containing 53,262 plots. sPlotOpen only contains the species composition of vascular plants; information on the composition of bryophytes and lichens was discarded since it was only available for a minority of plots (n = 11,001 and n = 6,801, respectively). Information on the size (surface area) of the vegetation survey is available for 67,022 plots, and ranges between 0.03 and 40,000 m^2 (mean = 377 m^2; median = 100 m^2). Specifically, sPlotOpen contains 12,894 plots with size smaller than 10 m^2, 25,742 with size 10-100 m^2, 24,750 plots with size 100-1,000 m^2 and 3,075 plots with size greater or equal to 1,000 m^2. Similarly, only for a minority of plots (n = 24,167) information on the exact group of plants sampled in the field is available (e.g., complete vegetation, only trees, only trees > 1 m height, and so on). However, as most data were collected using the phytosociological method, we deem safe to assume that, unless otherwise specified, plots contain information on all vascular plants. We retained plots with incomplete vegetation, because they were mostly located in the tropics, i.e., in areas where vegetation plots are particularly scarce otherwise. The average number of vascular plant species per vegetation plot ranges between 1 (i.e. monospecific stands) and 271 species (mean = 20; median = 16).

By capping the number of vegetation plots in overrepresented environmental conditions, the resampling procedure described above strongly reduced the bias in the distribution of vegetation plots within the PC1-PC2 environmental space. Yet, due to the lack or scarcity of data from some geographical regions, like the tropics, there is some remaining imbalance in the spatial distribution of vegetation plots across geographical regions (Figure 1). This is evident when comparing the number of plots across continents or biomes. When considering the first resampling iteration only (n = 49,787), Europe is by far the best represented continent, with 15,920 vegetation plots. The least represented continents are Africa and South America, with 3,709 and 5,498 vegetation plots, respectively. Some residual imbalance remains also when considering biomes. With the exception of the 'Temperate mid-latitudes' biome, which includes 14,100 vegetation plots, all other biomes have a number of plots comprised between 1,558 ('Polar and subpolar zone') and 6,245 ('Subtropics with year-round rain') vegetation plots (Figure 3, left). Despite this residual imbalance, all the Whittaker biomes are covered by sPlotOpen (Figure 3, right), and our resampling algorithm has resulted in a much more balanced dataset than many other global datasets that are available, such as GBIF.

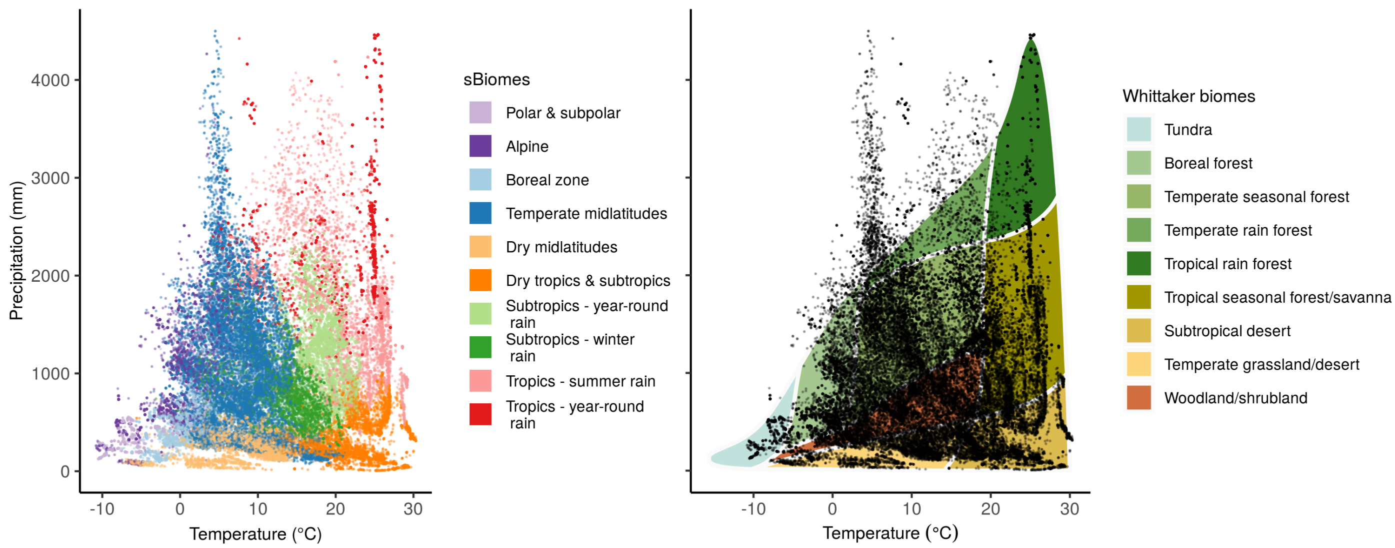

Figure 3: Distribution of vegetation plots in the first resampling iteration of sPlotOpen (n = 49,787) in the two-dimensional climatic space represented by mean annual temperature and mean annual precipitation. Left: plots are color coded based on sBiomes, i.e., sPlot's definition of biomes (25), which derives from Schultz (2005)(49) ecozones, modified to include also the alpine biome from Körner et al. (2017)(50). Right: the same plots superimposed onto Whittaker (1975) biomes (51), as adapted by Rickleff (2008)(52) and plotted using the *R* package *plotbiomes*.

Almost one third of the 95,104 vegetation plots in sPlotOpen belong to forests (n = 38,282), one half to non-forest vegetation (n = 45,735), with 11.6 % of plots remaining unassigned (n = 11,087). When not directly done by data providers, the assignment of plots to forests and non-forests was based on multiple lines of evidence, including the plot-level information on the cover of the tree layer, as well as traits of species composing a plot, such as growth form and height. In short, a plot record was considered as forest if the cover of the tree layer, or alternatively, the sum of the (relative) cover of all tree taxa (scaled by the sum of all cover values, in percentage), was greater than 25%. It was considered a non-forest record if the sum of relative cover of low-stature, non-tree and non-shrub taxa was greater than 90%. For an extensive explanation of this classification scheme, we refer the reader to Bruelheide et al. (2019) [25]. Even if the proportion of forest vs. non-forest vegetation plots is relatively well-balanced, the geographical distribution of vegetation plots belonging to different vegetation types is likely not balanced in the geographical space, as it depends on the idiosyncrasies of the constitutive datasets composing the sPlot database. For instance, the data from New Zealand only include plots collected in non-forest ecosystems, while data from Chile only refer to forests. We urge potential users to carefully read the description of each individual dataset in GIVD and to contact the custodians of each dataset for further information.

Database Organization

sPlotOpen is organized into three main matrices, relationally linked through the key column *'PlotObservationID'*.

The **'header'** matrix contains plot-level information for the 95,104 vegetation plots, including: metadata (e.g., plot ID, ownership, sampling date, geographical location, positional accuracy); sampling design information (e.g., the total surface area used during the vegetation survey); and a plot-level description of vegetation structure (e.g., vegetation type, percentage cover of each vegetation layer), vegetation type, and naturalness level (i.e., whether a plot belongs to the same formation that would occupy the site without human interference). Plots in Europe are also classified according to the EUNIS habitat classification (column *'ESY'*), based on the habitat classification expert system described in Chytrý et al. (2020) [53]. For each vegetation plot, we further provide information on the dataset it originates from, based on the IDs used in GIVD. We also report four binary fields describing whether a plot belongs to the three resampling iterations (columns *'Resample_1'*, *'Resample_2'*, *'Resample_3'*), or to the first resampling iteration after the inclusion of replacement plots (column *'Resample_1_consensus'*). A brief summary of all the 47 variables in the header matrix is provided in Table 2.

The **'DT'** matrix contains data on the species composition of each plot. It is structured in a long format and contains 1,945,384 records from 42,680 vascular plant taxa, mostly resolved at the species level. For each record, we report both the taxon name as originally contributed by the data custodian (column *'Original_species'*), and the taxon name after taxonomic standardization (column *'Species'*). For details on the taxonomic standardization, please see 'Technical Validation' below. For each species we also provided cover/abundance values. These follow different standards across the datasets constituting the sPlot database. We, therefore, provide both the cover/abundance value as reported in the original data (column *'Original_abundance'*), together with the abundance scale that was originally used (column *'Abundance_scale'*). This can take seven values: 'CoverPerc' = percentage cover; 'pa' = presence-absence; 'x_BA' = basal area (m^2/ha, only for woody species); 'x_IC' = individual count, i.e., number of individuals in plot; 'x_SC' = stem count, i.e., number of stems in plot; 'x_IV' = importance value index; 'x_PF' = presence frequency. The great majority of entries, however, use the percentage cover scale (n= 1,709,000). Finally, for each entry, we calculated a *'Relative_cover'*, i.e., the cover/abundance of a given taxon divided by the total cover/abundance of all taxa in that vegetation plot.

The **'CWM_CWV'** matrix contains the community-weighted means and variances calculated for each of the 18 functional traits mentioned above. It also contains three additional columns. The column *'Species_richness'* returns the number of species recorded in each plot. The columns *'Trait_coverage_cover'* and *'Trait_coverage_pa'* return, respectively, the proportion of total cover and species in a plot for which functional trait information was available. Functional trait information was available for 21,854 species. The average proportion of species in each plot for which we have functional trait information is 0.85 (median = 0.95). For 42,012 plots, the coverage is complete, while we do not have functional trait information for any of the species occurring in 482 plots. When considering relative cover, the average trait coverage is 0.87. As many as 68,041 and 74,151 plots have functional trait information for 80% or more of the species or relative cover, respectively.

sPlotOpen contains two additional objects. The **'metadata'** matrix contains plot-level metadata, which provide information on the origin of each individual vegetation plot. This object contains 15 columns, with information on the dataset of origin (column *'GIVD_ID'* - 37), author or surveyor names (columns *'Releve_author'* and *'Releve_coauthor'*), bibliographic references both at the dataset (column *'DB_BIBTEXKEY'*) and plot level (*'Plot_Biblioreference'* and *'BIBTEXKEY'*), when available. Similarly, the column *'Project_name'* provides information on the project in which a vegetation plot was collected.

When available, we also provide information on the numbering of the plots in the publication where they originally appeared (columns *'Nr_table_in_publ'*, *'Nr_releve_in_table'*), or in the dataset where they were initially stored (*'Original_nr_in_database'*). In the case of nested plots (n = 1,851), we also provide the original plot and subplot IDs (columns: *'Original_plotID'*, *'Original_subplotID'*). The last two columns report plot-level *'Remarks'*, and the unique identifier produced by Turboveg when the vegetation plot was first stored (*'GUID'*).

Finally, the object **'references'**, contains all the bibliographic references formatted according to a BibTex standard. Each reference is tagged with a key corresponding to the fields *'DB_BIBTEXKEY'* and *'BIBTEXKEY'* in the metadata. We further provide an R function (*'sPlotOpen_citation'*) to create reference lists, based on a selection of plots and/or datasets.

Except for the 'reference' file (format .bib), all objects/matrices are provided in tab-delimited .txt files. All objects, including the *'sPlotOpen_citation'* function, are also compiled inside an .RData object.

Technical Validation

The original sPlot database has a nested structure and consists of several individual datasets, each validated and maintained by its respective dataset custodian. In many cases, individual datasets are also collections whose vegetation plots were provided by their respective owners (the person who performed the actual vegetation survey) or by someone who digitized the original data from the scientific published or grey literature. We obviously have no direct control over the individual vegetation plots that we provide here in sPlotOpen. Yet, all these vegetation plots stem from trained professional botanists, or published scientific work, and are accompanied by detailed information on the sampling protocols used, thus ensuring data quality and reliability.

Before integration into the sPlot database, each dataset was further checked for consistency and, if it was in a different format, we converted it to a Turboveg 2 dataset (54). During this conversion, we checked that all datasets contained the required metadata information, and cross-checked that each plot was located within the geographic scopes of its respective dataset. All individual Turboveg 2 datasets were then integrated into a Turboveg 3 database, and exported to comma-separated files. Finally, we harmonized all the taxonomic names from all datasets, based on the sPlot's taxonomic backbone (55). This backbone matched all the taxonomic names (without nomenclatural authors) from all datasets in sPlot 2.1 and TRY v3.0 (31) to their resolved version based on the Taxonomic Name Resolution Service web application (TNRS version 4.0; 56). This allowed us to (1) harmonize all datasets to a common nomenclature, and (2) link the sPlot database to the TRY database (31). The final backbone only retained matched taxonomic names at the rank of species or higher. Additional detail on the taxonomic resolution is reported in [25], while a description of the workflow, including R-code, is available in [55].

Usage Notes

The sPlotOpen database can be downloaded from https://www.idiv.de (link to PlantHub). Users are urged to cite the original sources when using sPlotOpen in addition to the present paper, particularly when using data contained in BioTIME (57). For two datasets (AF-00-009, AF-CD-001), the identification of taxa at species level is still in progress. Data on lichens and mosses, where available (e.g., dataset NA-GL-001), can be obtained on request from the respective dataset custodian or sPlot coordinator. As most of the constitutive datasets remain under continuous development, sPlotOpen users are encouraged to get in touch with the custodian(s) of the data they are planning to use (custodian names are reported in https://www.idiv.de/en/splot).

The data included in the present paper represent the subset of sPlot for which we were able to secure permission for making these data open. The additional data in sPlot are available under sPlot's Governance and Data Property Rules (https://www.idiv.de/en/splot). Using the full sPlot dataset is also recommended if a stratification is desired that is different from the environmental factors used here, for example by geographical region or plot size.

Code Availability

The R code used to produce sPlotOpen from the sPlot 2.1 database is contained in the *sPlotOpen_code* GitHub repository: (https://github.com/fmsabatini/sPlotOpen_Code/). This manuscript was produced using the Manubot workflow (58). The code for reproducing this manuscript is stored in the *sPlotOpen_manuscript* GitHub repository: (https://github.com/fmsabatini/sPlotOpen_Manuscript).

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Author contributions

FMS wrote the first draft of the manuscript, with considerable input from JL and HB. JL and TH wrote the resampling algorithm. FMS set up the GitHub projects, curated the database, and produced the graphs. He also coordinated the sPlot consortium. SMH wrote the Turboveg software, which holds the sPlot database. JK provided the trait data from TRY and FS performed the trait data gap filling. HB secured the funding for sPlot as a strategic project of iDiv. All other authors contributed data and/or helped set up the database and/or helped develop the resampling algorithm. All authors contributed to revising and approved the manuscript.

Competing interests

The authors declare no competing interests.

Biosketch

sPlot is a collaborative initiative to integrate existing local and national vegetation-plot datasets into a global harmonized database. It was initiated in 2013, within the sDiv working group “Plant trait-environment relationships across the world’s biomes”. Since then, it became established as the largest vegetation-plot databases worldwide and coordinates a consortium of 251 individual active members, representing 167 local and national datasets. sPlot’s overarching scientific goal is the exploration of all aspects of global plant community diversity, including taxonomic, functional and phylogenetic diversity, across biomes, vegetation types, taxonomic or functional guilds and scales. Central to sPlot’s mission are the exploration of the relationships between environmental drivers, trait variation, and assembly processes in local plant communities worldwide.

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Luis Cayuela, Lucía Gálvez-Bravo, Ramón Pérez Pérez, Fábio de Albuquerque, Duncan Golicher, Rakan Zahawi, Neptalí Ramírez-Marcial, Cristina Garibaldi, Richard Field, José Rey Benayas, … Regino Zamora
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Supplementary Material

Table 1: List of databases contributing to sPlotOpen, the environmentally-balanced, open-access, global dataset of vegetation plots. Databases are ordered based on their ID in the Global Index of Vegetation Databases (GVID ID).

GIVD ID	Dataset name	Custodian	Deputy custodian	Nr. open-access plots	Ref
00-00-001	ForestPlots.net	Oliver L. Phillips	Aurora Levesley	169	59
00-00-003	SALVIAS	Brian Enquist	Brad Boyle	3403	
00-00-004	Vegetation Database of Eurasian Tundra	Risto Virtanen		519	
00-00-005	Tundra Vegetation Plots (TundraPlot)	Anne D. Bjorkman	Sarah Elmendorf	309	60
00-RU-001	Vegetation Database Forest of Southern Ural	Vasiliy Martynenko	Pavel Shirokikh	68	
00-RU-002	Database of Masaryk University`s Vegetation Research in Siberia	Milan Chytrý		158	61
00-RU-003	Database Meadows and Steppes of Southern Ural	Sergey Yamalov	Mariya Lebedeva	238	
00-TR-001	Forest Vegetation Database of Turkey - FVDT	Ali Kavgacı		45	
AF-00-001	West African Vegetation Database	Marco Schmidt	Georg Zizka	258	62
AF-00-003	BIOTA Southern Africa Biodiversity Observatories Vegetation Database	Norbert Jürgens	Ute Schmiedel	1015	63
AF-00-006	SWEA-Dataveg	Miguel Alvarez	Michael Curran	1675	
AF-00-008	PANAF Vegetation Database	Hjalmar S. Kühl	TeneKwetche Sop	884	
AF-00-009	Vegetation Database of the Okavango Basin	Rasmus Revermann	Manfred Finckh	378	64
AF-BF-001	Sahel Vegetation Database	Jonas V. Müller	Marco Schmidt	556	65
AF-CD-001	Forest Database of Central Congo Basin	Kim Sarah Jacobsen	Hans Verbeeck	140	66
AF-ET-001	Vegetation Database of Ethiopia	Desalegn Wana	Anke Jentsch	67	67
AF-MA-001	Vegetation Database of Southern Morocco	Manfred Finckh		621	68
AF-ZW-001	Vegetation Database of Zimbabwe	Cyrus Samimi		31	69
AS-00-001	Korean Forest Database	Tomáš Černý	Jiri Dolezal	1039	70
AS-00-003	Vegetation of Middle Asia	Arkadiusz Nowak	Marcin Nobis	314	71
AS-00-004	Rice Field Vegetation Database	Arkadiusz Nowak		32	
AS-BD-001	Tropical Forest Dataset of Bangladesh	Mohammed A.S. Arfin Khan	Fahmida Sultana	87	
AS-CN-001	China Forest-Steppe Ecotone Database	Hongyan Liu	Fengjun Zhao	117	72
AS-CN-002	Tibet-PaDeMoS Grazing Transect	Karsten Wesche		58	73
AS-CN-003	Vegetation Database of the BEF China Project	Helge Bruelheide		24	74

GIVD ID	Dataset name	Custodian	Deputy custodian	Nr. open-access plots	Ref
AS-CN-004	Vegetation Database of the Northern Mountains in China	Zhiyao Tang		124	
AS-EG-001	Vegetation Database of Sinai in Egypt	Mohamed Z. Hatim		143	75
AS-ID-001	Sulawesi Vegetation Database	Michael Kessler		24	
AS-IR-001	Vegetation Database of Iran	Jalil Noroozi	Parastoo Mahdavi	277	
AS-KZ-001	Database of Meadow Vegetation in the NW Tien Shan Mountains	Viktoria Wagner		13	76
AS-MN-001	Southern Gobi Protected Areas Database	Henrik von Wehrden	Karsten Wesche	1032	77
AS-RU-001	Wetland Vegetation Database of Baikal Siberia (WETBS)	Victor Chepinoga		9	78
AS-RU-002	Database of Siberian Vegetation (DSV)	Andrey Korolyuk	Andrei Zverev	3634	79
AS-RU-004	Database of the University of Münster - Biodiversity and Ecosystem Research Group's Vegetation Research in Western Siberia and Kazakhstan	Norbert Hölzel	Wanja Mathar	207	
AS-SA-001	Vegetation Database of Saudi Arabia	Mohamed Abd El-Rouf Mousa El-Sheikh		711	80
AS-TJ-001	Eastern Pamirs	Kim André Vanselow		221	81
AS-TW-001	National Vegetation Database of Taiwan	Ching-Feng Li	Chang-Fu Hsieh	912	
AS-YE-001	Socotra Vegetation Database	Michele De Sanctis	Fabio Attorre	236	82
AU-AU-002	AEKOS	Ben Sparrow		10976	36
AU-NC-001	New Caledonian Plant Inventory and Permanent Plot Network (NC-PIPPN)	Jérôme Munzinger	Philippe Birnbaum	98	83
AU-NZ-001	New Zealand National Vegetation Databank	Susan K. Wiser		1127	84
AU-PG-001	Forest Plots from Papua New Guinea	Timothy J.S. Whitfeld	George D. Weiblen	60	85
EU-00-002	Nordic-Baltic Grassland Vegetation Database (NBGVD)	Jürgen Dengler	Łukasz Kozub	54	86
EU-00-011	Vegetation-Plot Database of the University of the Basque Country (BIOVEG)	Idoia Biurrun	Itziar García-Mijangos	2142	87
EU-00-013	Balkan Dry Grasslands Database	Kiril Vassilev	Armin Macanović	269	88
EU-00-016	Mediterranean Ammophiletea Database	Corrado Marcenò	Borja Jiménez-Alfaro	783	89
EU-00-017	European Coastal Vegetation Database	John A.M. Janssen		356	
EU-00-018	The Nordic Vegetation Database	Jonathan Lenoir	Jens-Christian Svenning	1735	90

GIVD ID	Dataset name	Custodian	Deputy custodian	Nr. open-access plots	Ref
EU-00-019	Balkan Vegetation Database	Kiril Vassilev	Hristo Pedashenko	484	91
EU-00-020	WetVegEurope	Flavia Landucci		127	92
EU-00-022	European Mire Vegetation Database	Tomáš Peterka	Martin Jiroušek	2560	93
EU-AL-001	Vegetation Database of Albania	Michele De Sanctis	Giuliano Fanelli	31	94
EU-AT-001	Austrian Vegetation Database	Wolfgang Willner	Christian Berg	2310	95
EU-BE-002	INBOVEG	Els De Bie		119	
EU-BG-001	Bulgarian Vegetation Database	Iva Apostolova	Desislava Sopotlieva	160	96
EU-CH-005	Swiss Forest Vegetation Database	Thomas Wohlgemuth		2134	97
EU-CZ-001	Czech National Phytosociological Database	Milan Chytrý	Ilona Knollová	1287	98
EU-DE-001	VegMV	Florian Jansen	Christian Berg	15	99
EU-DE-013	VegetWeb Germany	Florian Jansen	Jörg Ewald	587	100
EU-DE-014	German Vegetation Reference Database (GVRD)	Ute Jandt	Helge Bruelheide	762	101
EU-DK-002	National Vegetation Database of Denmark	Jesper Erenskjold Moeslund	Rasmus Ejrnæs	332	
EU-ES-001	Iberian and Macaronesian Vegetation Information System (SIVIM) - Wetlands	Aaron Pérez-Haase	Xavier Font	580	
EU-FR-003	SOPHY	Emmanuel Garbolino	Patrice De Ruffray	7986	102
EU-GB-001	UK National Vegetation Classification Database	John S. Rodwell		3182	
EU-GR-001	KRITI	Erwin Bergmeier		22	
EU-GR-005	Hellenic Natura 2000 Vegetation Database (HelNatVeg)	Panayotis Dimopoulos	Ioannis Tsiripidis	620	103
EU-GR-006	Hellenic Woodland Database	Ioannis Tsiripidis	Georgios Fotiadis	17	104
EU-HR-001	Phytosociological Database of Non-Forest Vegetation in Croatia	Zvjezdana Stančić		193	105
EU-HR-002	Croatian Vegetation Database	Željko Škvorc	Daniel Krstonošić	585	
EU-HU-003	CoenoDat Hungarian Phytosociological Database	János Csiky	Zoltán Botta-Dukát	46	106
EU-IT-001	VegItaly	Roberto Venanzoni	Flavia Landucci	754	107
EU-IT-010	Vegetation database of Habitats in the Italian Alps – HabItAlp	Laura Casella	Pierangela Angelini	247	108
EU-IT-011	Vegetation-Plot Database Sapienza University of Rome (VPD-Sapienza)	Emiliano Agrillo	Fabio Attorre	967	109
EU-LT-001	Lithuanian Vegetation Database	Valerijus Rašomavičius	Domas Uogintas	81	

GIVD ID	Dataset name	Custodian	Deputy custodian	Nr. open-access plots	Ref
EU-LV-001	Semi-natural Grassland Vegetation Database of Latvia	Solvita Rūsiņa		369	110
EU-MK-001	Vegetation Database of the Republic of Macedonia	Renata Ćušterevska		28	
EU-NL-001	Dutch National Vegetation Database	Stephan M. Hennekens	Joop H.J. Schaminée	1098	111
EU-PL-001	Polish Vegetation Database	Zygmunt Kącki	Grzegorz Swacha	692	112
EU-RO-007	Romanian Forest Database	Adrian Indreica	Pavel Dan Turtureanu	166	113
EU-RO-008	Romanian Grassland Database	Eszter Ruprecht	Kiril Vassilev	82	114
EU-RS-002	Vegetation Database Grassland Vegetation of Serbia	Svetlana Aćić	Zora Dajić Stevanović	217	115
EU-RU-002	Lower Volga Valley Phytosociological Database	Valentin Golub	Andrey Chuvashov	383	116
EU-RU-003	Vegetation Database of the Volga and the Ural Rivers Basins	Tatiana Lysenko		174	117
EU-RU-011	Vegetation Database of Tatarstan	Vadim Prokhorov	Maria Kozhevnikova	206	118
EU-SI-001	Vegetation Database of Slovenia	Urban Šilc	Filip Küzmič	1029	119
EU-SK-001	Slovak Vegetation Database	Milan Valachovič	Jozef Šibík	2394	120
EU-UA-001	Ukrainian Grasslands Database	Anna Kuzemko	Yulia Vashenyak	301	121
EU-UA-006	Vegetation Database of Ukraine and Adjacent Parts of Russia	Viktor Onyshchenko	Vitaliy Kolomiychuk	96	
NA-00-002	Tree Biodiversity Network (BIOTREE-NET)	Luis Cayuela		241	122
NA-CA-003	Database of Timberline Vegetation in NW North America	Viktoria Wagner	Toby Spribille	63	123
NA-CA-004	Understory of Sugar Maple Dominated Stands in Quebec and Ontario (Canada)	Isabelle Aubin		13	124
NA-CA-005	Boreal Forest of Canada	Philippe Marchand	Yves Bergeron	57	
NA-GL-001	Vegetation Database of Greenland	Birgit Jedrzejek	Fred J.A. Daniëls	441	125
NA-US-002	VegBank	Robert K. Peet	Michael T. Lee	14965	126
NA-US-006	Carolina Vegetation Survey Database	Robert K. Peet	Michael T. Lee	3263	127
NA-US-014	Alaska-Arctic Vegetation Archive	Donald A. Walker	Amy Breen	771	128
SA-00-002	VegPáramo	Gwendolyn Peyre	Xavier Font	2010	129
SA-AR-002	Vegetation Database of Central Argentina	Melisa Giorgis	Alicia T.R. Acosta	86	
SA-BO-003	Bolivia Forest Plots	Michael Kessler	Sebastian Herzog	44	
SA-BR-002	Forest Inventory, State of Santa Catarina, Brazil (IFFSC Project)	Alexander Christian Vibrans	André Luís de Gasper	1561	130

GIVD ID	Dataset name	Custodian	Deputy custodian	Nr. open-access plots	Ref
SA-BR-003	Grasslands of Rio Grande do Sul, Brazil	Eduardo Vélez-Martin	Valério D. Pillar	306	
SA-BR-004	Grassland Database of Campos Sulinos	Gerhard E. Overbeck	Valério D. Pillar	147	
SA-CL-002	SSAForests_Plots_db	Alvaro G. Gutiérrez		155	
SA-CL-003	Chilean Park Transects - Fondecyt 1040528	Aníbal Pauchard	Alicia Marticorena	44	131
SA-EC-001	Ecuador Forest Plot Database	Jürgen Homeier		166	

Table 2: Description of the variables contained in the 'header' matrix, together with their range (if numeric) or possible levels (if nominal or binary) and the number of non-empty (i.e., non NA) records. Variable types can be n - nominal (i.e., qualitative variable), o - ordinal, q - quantitative, or b - binary (i.e., boolean), or d - date . Additional details on the variables are in Bruelheide et al. (2019) [25]. GIVD codes derive from Dengler et al. (2011) [37]. Biomes refer to Schultz 2005 [49], modified to include also the world mountain regions by Körner et al. (2017)[50]. The column ESY refers to the EUNIS Habitat Classification Expert system described in Chytrý et al. (2020) [53].

Variable	Range/Levels	Unit of Measurement	Nr. of plots with information	Type
GIVD_ID			95104	n
Dataset			95104	n
Continent	Africa, Asia, Europe, North America, Oceania, South America		95104	n
Country			95104	n
Biome	Alpine, Boreal zone, Dry midlatitudes, Dry tropics and subtropics, Polar and subpolar zone, Subtropics with year-round rain, Subtropics with winter rain, Temperate midlatitudes, Tropics with summer rain, Tropics with year-round rain		95104	n
Date_of_recording	1888-07-05 - 2015-02-03	dd-mm-yyyy	80085	d
Latitude	-54.82303 - 80.149116	° (WGS84)	95104	q
Longitude	-162.741433 - 176.4221	° (WGS84)	95104	q
Location_uncertainty	1 - 2750	m	95075	q
Releve_area	0.03 - 40000	m^2	67022	q
Plant_recorded	All vascular plants, All trees & dominant understory, Dominant trees, Only dominant species, Dominant woody plants >= 2.5 cm dbh, All woody plants, Woody plants >= 1 cm dbh, Woody plants >= 2.5 cm dbh, Woody plants >= 5 cm dbh, Woody plants >= 10 cm dbh, Woody plants >= 20 cm dbh, Woody plants >= 1 m height, Not specified		95104	n
Elevation	-30 - 5960	m a.s.l.	62968	q
Aspect	1 - 360	°	42178	q

Variable	Range/Levels	Unit of Measurement	Nr. of plots with information	Type
Slope	0 - 90	°	51246	q
is_forest	FALSE = 45735; TRUE = 38282		84017	b
ESY			39632	n
Naturalness	1 = Natural, 2 = Semi-natural		60192	o
Forest	FALSE = 36282; TRUE = 33170		69452	b
Shrubland	FALSE = 58245; TRUE = 11207		69452	b
Grassland	FALSE = 33800; TRUE = 35652		69452	b
Wetland	FALSE = 59196; TRUE = 10256		69452	b
Sparse_vegetation	FALSE = 66177; TRUE = 3275		69452	b
Cover_total	1 - 990	%	19407	q
Cover_tree_layer	0.5 - 150	%	12094	q
Cover_shrub_layer	0.5 - 170	%	16804	q
Cover_herb_layer	0.2 - 199	%	29668	q
Cover_moss_layer	1 - 100	%	9681	q
Cover_lichen_layer	1 - 90	%	708	q
Cover_algae_layer	1 - 100	%	41	q
Cover_litter_layer	1 - 107	%	3161	q
Cover_bare_rocks	1 - 100	%	2747	q
Cover_cryptogams	1 - 90	%	772	q
Cover_bare_soil	-1 - 99	%	2746	q
Height_trees_highest	1 - 99	m	8220	q
Height_trees_lowest	1 - 90	m	447	q
Height_shrubs_highest	0.1 - 9.9	m	3389	q
Height_shrubs_lowest	0.1 - 9	m	263	q
Height_herbs_average	0.1 - 600	cm	5901	q
Height_herbs_lowest	1 - 150	cm	490	q
Height_herbs_highest	1 - 600	cm	1083	q
SoilClim_PC1	-6.233 - 8.172		95104	q
SoilClim_PC2	-4.824 - 15.466		95104	q
Resample_1	FALSE = 45317; TRUE = 49787		95104	b
Resample_2	FALSE = 45293; TRUE = 49811		95104	b
Resample_3	FALSE = 45315; TRUE = 49789		95104	b
Resample_1_consensus	FALSE = 41842; TRUE = 53262		95104	b

Supplementary Material

Figure S1

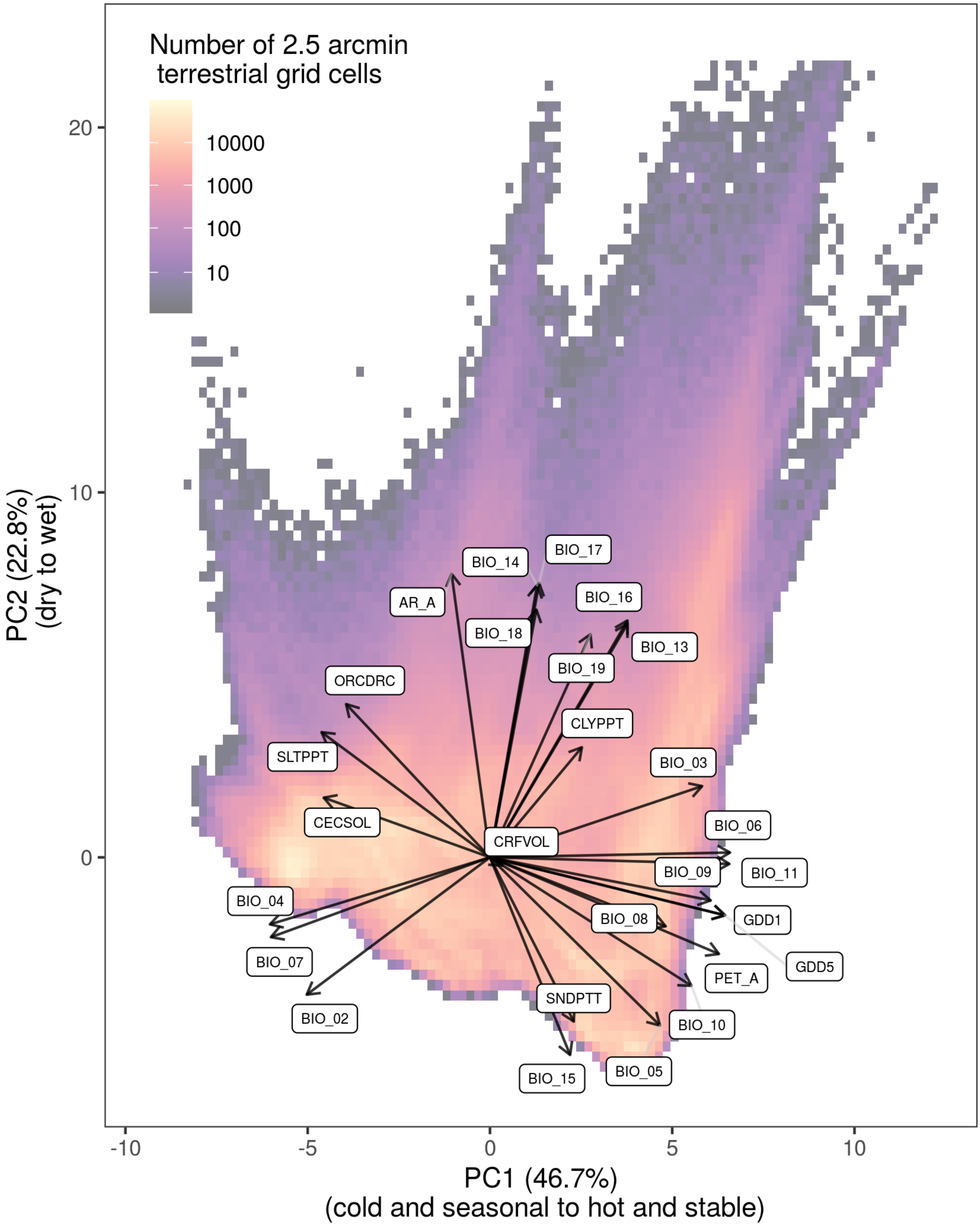

Figure S1: Global principal component analysis (PCA) of the world environmental conditions. The PCA is based on the matrix of all terrestrial grid cells (n = 8,384,404, spatial grain = 2.5 arcmin) by 30 environmental variables. The PCA space represents the full environmental space of all terrestrial habitats on Earth, irrespective of whether a grid cell hosted vegetation plots from the sPlotOpen or not. The PCA space is divided into a 10,000 regular tiles (100 x 100), and the number of 2.5 arcmin terrestrial grid cells counted for each tile. Abbreviations - Climate - Bio1 = Annual Mean Temperature, Bio2 = Mean Diurnal Range, Bio3 = Isothermality, Bio4 = Temperature Seasonality, Bio5 = Max Temperature of Warmest Month, Bio6 = Min Temperature of Coldest Month, Bio7 = Temperature Annual Range, Bio8 = Mean Temperature of Wettest Quarter, Bio9 = Mean Temperature of Driest Quarter, Bio10 = Mean Temperature of Warmest Quarter, Bio11 = Mean Temperature of Coldest Quarter, Bio12 = Annual Precipitation, Bio13 = Precipitation of Wettest Month, Bio14 = Precipitation of Driest Month, Bio15 = Precipitation Seasonality, Bio16 = Precipitation of Wettest Quarter, Bio17 = Precipitation of Driest Quarter, Bio18 = Precipitation of Warmest Quarter, Bio19 = Precipitation of Coldest Quarter. Soil - CECSOL = Cation Exchange capacity of soil, ORCDRC = Soil Organic Carbon Content, PHIHOX = Soil pH, BLDFIE = Bulk Density, CLYPPT = Clay mass fraction, SLTPPT = Silt mass fraction, SNDPPT = Sand mass fraction, CRFVOL = Coarse fragments.