

## APPLICATION

# GIFT—An R package to access the Global Inventory of Floras and Traits

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**Handling Editor:** Si-Chong Chen

## Abstract

1. Advancing knowledge of biodiversity requires global open-access databases. Having large-scale information on plant distributions, functional traits and evolutionary history will enable the scientific community to improve its understanding of the patterns and drivers of plant diversity on a global scale.
2. The Global Inventory of Floras and Traits (GIFT) is a global database of regional plant checklists that has proven successful in documenting biogeographical patterns of plants. Since the release of the first version of GIFT, the database kept on expanding. We introduce GIFT version 3.0, which contains 5169 plant checklists referring to 3400 regions worldwide. These checklists include a total of 371,148 land plant species, mostly vascular plants, of which 354,848 have accepted species names, and species-level data for 109 functional traits. This new version of GIFT relies on new resources for taxonomic name standardization, is matched to a new plant phylogeny, comes with a new trait aggregation workflow and includes additional environmental variables.
3. We also present the GIFT R-package, which contains all necessary functions to retrieve distributional, functional, phylogenetic, and environmental data from the GIFT database. The package comes with a dedicated website, <https://biogeomacro.github.io/GIFT/>, which includes three vignettes to guide users in retrieving data from GIFT.
4. The recent development of GIFT and its associated R-package provide ecologists with access to one of the largest plant databases. This will foster research into regional to global patterns of plant diversity and their underlying mechanisms. The ability to retrieve and cite data from any previous and current instance of the GIFT database will ensure the reproducibility of studies that utilise it.

## KEYWORDS

biodiversity, functional traits, global plant database, phylogeny, plant distributions, regional checklists, R-package, vascular plants

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## 1 | INTRODUCTION

Documenting and understanding species distributions and other dimensions of biodiversity requires global open-access data. While global databases with species ranges and trait information are available for some taxa, such as birds, mammals, amphibians and reptiles (BirdLife International, 2013; Myhrvold et al., 2015), equivalent data for plants still lag behind, although recent efforts have improved their spatial and taxonomic coverage. Together with the Botanical Information and Ecology Network (Enquist et al., 2016), the World Checklist of Vascular Plants (WCVP; Brown et al., 2023; Govaerts et al., 2021), the Global Naturalized Flora (van Kleunen et al., 2019) and the Global Biodiversity Information Facility (GBIF, [www.gbif.org](http://www.gbif.org)), the Global Inventory of Floras and Traits (GIFT; Weigelt et al., 2020) has contributed to improving our knowledge of plant distributions and multiple aspects of plant diversity. However, until now, the GIFT database of regional plant checklists and species-level traits has not been publicly available. Here, we present the latest update of the GIFT database, with the release of version 3.0, and the GIFT R-package, which grants open access for users to retrieve data.

### 1.1 | A short history of GIFT

GIFT is a global database of regional plant checklists, species-level functional traits and environmental region characteristics (Weigelt et al., 2020). Prior to GIFT and similar initiatives, plant diversity research using regional floras only considered the number of species per region and ignored species identities. However, a wide range of environmental predictors were already considered (e.g. in Kreft & Jetz, 2007). These earlier studies resulted in expert-drawn diversity maps (Barthlott et al., 1996; Mutke & Barthlott, 2005), estimated plant richness per ecoregion (Kier et al., 2005) and modelled global species richness patterns (Kreft & Jetz, 2007), the latter being recently updated (Cai, Kreft, Taylor, Denelle, et al., 2023). These efforts highlighted an under-representation of islands. To address this shortcoming, there has been a strong push for data collection for islands. With checklists now available for 1057 islands larger than 1 km<sup>2</sup>, representing 80.7% of the world's total island area (Weigelt et al., 2013), GIFT is the most comprehensive plant database for studying patterns of island biogeography. This high coverage has led to global assessments of vascular plants (Kreft et al., 2008; Weigelt & Kreft, 2013) and pteridophyte (Kreft et al., 2010) richness on islands, characterization of island environmental features (Weigelt et al., 2013; Weigelt & Kreft, 2013), and of the past and present drivers of plant diversity on islands (Cabral et al., 2014; Schrader et al., 2020; Weigelt et al., 2016).

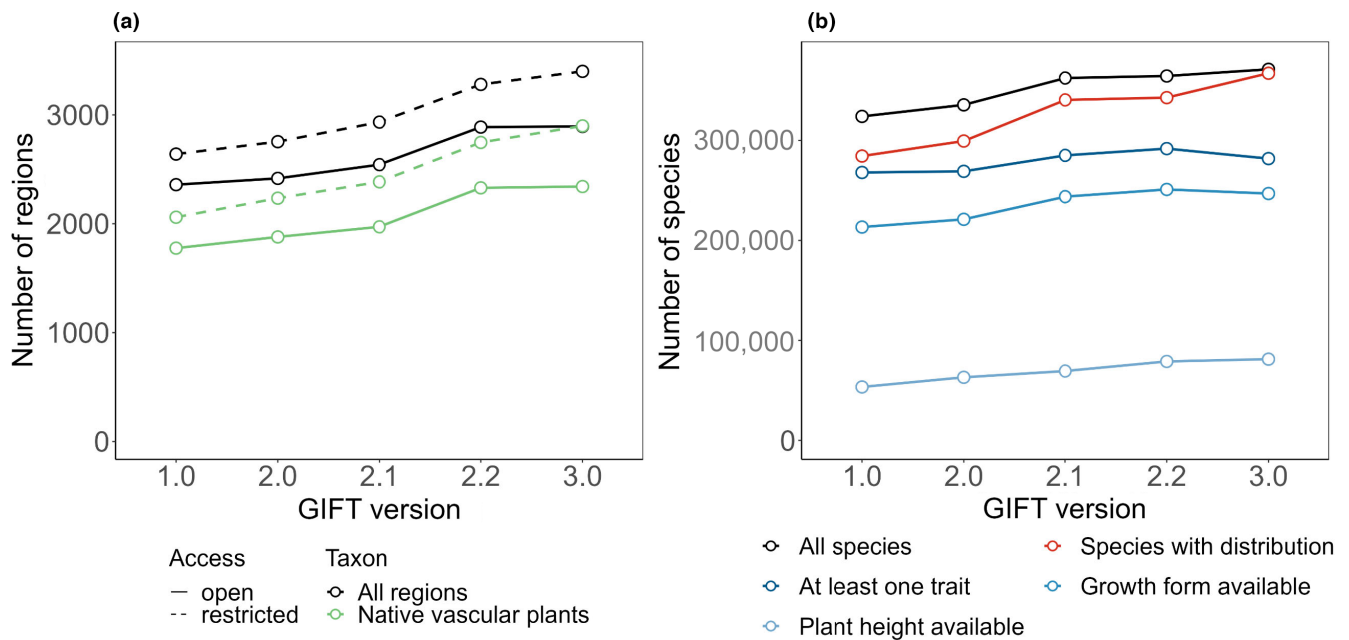
Making use of the species composition per region and the floristic status of occurrences, studies using the GIFT database provided global assessments for specific plant groups such as epiphytes (Taylor et al., 2022), phylogenetic diversity (Cai, Kreft, Taylor, Denelle, et al., 2023; Weigelt et al., 2015) and endemism (Cai, Kreft, Taylor, Schrader, et al., 2023), and  $\beta$ -diversity (König et al., 2017). Unlike

other databases where species composition is available at the plot level (e.g. sPlot; Bruehlheide et al., 2019) or comes from an aggregation of georeferenced occurrences (e.g. GBIF, [www.gbif.org](http://www.gbif.org)), regional-level species composition data in GIFT has high geographic coverage and is spatially less biased although being coarser in resolution/grain (König et al., 2019). There are also functional trait data in GIFT, which mainly come from species descriptions in floras, checklists and online databases, and are mainly available at the species level, whereas trait data in other databases like TRY (Kattge et al., 2011) are usually individual measurements making GIFT data a complementary addition. Functional traits in GIFT have been used to map the distribution of growth and life forms on a global scale (Taylor et al., 2023) and to address taxonomic and functional disharmonies between island and mainland floras (König et al., 2021; Razanajatovo et al., 2019; Taylor et al., 2019, 2021; Zizka et al., 2022). Finally, GIFT has also been used to advance our understanding of the distribution of alien plant species compared to native species (e.g. Bach et al., 2022; Omer et al., 2022; van Kleunen et al., 2015; Yang et al., 2021) as well as species interactions (Delavaux et al., 2019; Luo et al., 2023).

### 1.2 | From GIFT 1.0 to GIFT 3.0

Since the release of version 1.0 in 2018 (<https://gift.uni-goettingen.de/about>), the number of plant checklists and geographical regions in GIFT has steadily increased (Figure 1). GIFT 3.0 contains 5169 checklists, which is 50% more checklists than version 1.0. These checklists refer to 3400 georeferenced regions, of which 2899 regions have at least one checklist for all native vascular plants (Figure 1a). Different combinations of taxonomic group and floristic status can be queried, leading to different region numbers (Figure S1). Altogether, these regions cover the entire terrestrial surface of the Earth, as shown on the GIFT website: <https://gift.uni-goettingen.de/map> (Figure 2a). Unless otherwise noted, numbers in this manuscript refer to the data including restricted resources. Across all checklists, GIFT 3.0 includes a total of 1,161,174 original names (orig\_ID in the database, Figure S2) corresponding to a total of 371,148 standardized plant species (work\_ID in the database). GIFT 3.0 comes with more trait records than previous versions (Figure 1b, Figure S3), resulting in very high coverage of whole plant traits, such as growth form (246,901 species with growth form) and plant height (81,248 species) which are frequently mentioned in floras and checklists (Figure 1b). 281,836 species have at least one trait available.

To facilitate studies of diversity-environment relationships, GIFT regions are linked to 213 environmental variables, including miscellaneous variables and variables derived from raster layers (Table S1). In GIFT 3.0, we added some recently published datasets including paleoclimatic variables (Brown et al., 2018; Karger et al., 2021), new bioclimatic variables (Brun et al., 2022), global soil temperature variables (Lembrechts et al., 2022), indices of climate stability (Owens & Guralnick, 2019) or aridity (Zomer et al., 2022) that were not available in previous versions. We also added the prediction of plant



**FIGURE 1** Amount of information in different versions of GIFT. (a) Number of regions available for different filters applied. Black lines represent the total number of regions per version, while green lines represent the number of regions with species lists of native vascular plants. Continuous lines represent the information directly available with the GIFT R-package and default Application Programming Interface settings, dashed lines represent numbers including restricted data which require contacting data owners before using them. (b) Number of species with certain trait or distribution information available in the different versions of GIFT. Black colour corresponds to the total number of species, red colour corresponds to species with distribution information, the three blue colours represent species with at least one available trait, growth form (e.g. tree, shrub, herb) or plant height values. The number of species with growth form available decreases slightly between version 2.2 and version 3.0 due to the change of the taxonomic backbone used to harmonize the species names.

richness per region extracted from the recent work of Cai, Kreft, Taylor, Denelle, et al. (2023). Extraction of raster values for GIFT regions now uses the exactextract R-package (Baston et al., 2022).

### 1.3 | Workflow updates

In addition to increasing the number of checklists, species, trait records and environmental variables, we have updated the taxonomic standardization of the original species names, since the superseded Plant List ([theplantlist.org/](http://theplantlist.org/)) was used in previous versions of GIFT. To standardize the original species names, GIFT now uses the World Checklist of Vascular Plants (Govaerts et al., 2021), the TNRS R-package (Maitner et al., 2023) and the additional resources used therein, namely The World Flora Online ([worldfloraonline.org/](http://worldfloraonline.org/)), Tropicos ([tropicos.org](http://tropicos.org)), and the USDA plant database ([plants.usda.gov](http://plants.usda.gov)). 99.1% of all original names could be matched and standardized to an existing species name using these resources. Of these standardized names, 95.6% are accepted species names in the above-mentioned resources (Figure S2). If a species name does not match, we keep the original species name. With this new taxonomic workflow, standardized species names also come with author names.

In GIFT 3.0, all standardized species names are linked to a phylogeny built using the U.PhyloMaker R-package (Jin & Qian, 2022) which is stored in the database and accessible via the GIFT R-package. For seed plants, it is based on the GBOTB megatree from Smith and

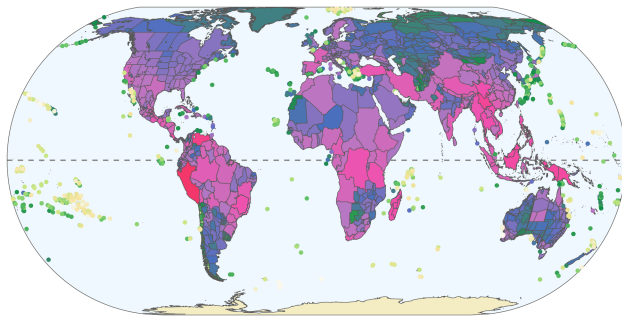
Brown (2018) and for pteridophytes, on Zanne et al. (2014), both standardized according to WCVP. Missing species and genera were bound to their respective genera and families using 'Scenario 3' from the U.PhyloMaker R-package.

The aggregation of a trait value at the species level is different depending on whether a trait is categorical or continuous. When querying a categorical trait for a given species, the most frequent category is returned as the trait value, alternative trait values are indicated and the proportion of references that agree on a given trait value is given. For continuous traits, the aggregated trait value can be the minimum, mean (e.g. for average plant height) or maximum (e.g. for maximum plant height) of all trait values from the different references included in GIFT. To acknowledge the variation across references, the coefficient of variation is returned.

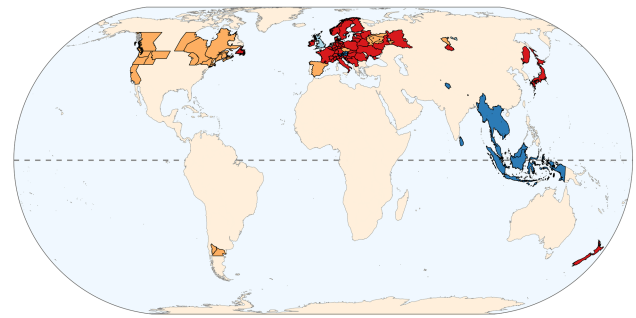
### 1.4 | Package functionality

The GIFT R-package contains 27 functions (Table 1) that allow users to retrieve plant checklists matching specific criteria, species distribution information, functional traits, environmental variables, spatial information and a phylogeny. Most of these functions allow retrieving tables at the global scale or only for a subset of regions or plant species. The GIFT R-package comes with a website (<https://biogeomacro.github.io/GIFT/>), with vignettes, tutorials and detailed documentation for each function. The R-package calls an

## (a) Native vascular plants

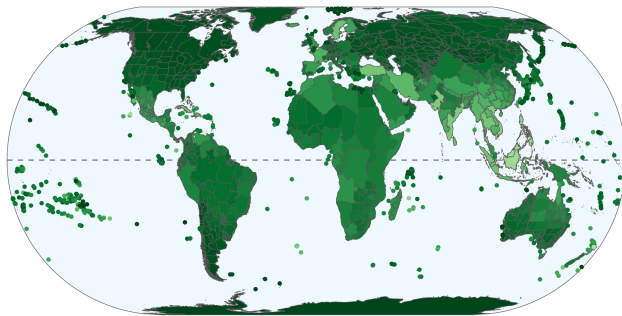


Species number 1 10 100 1000 10 000 40 000

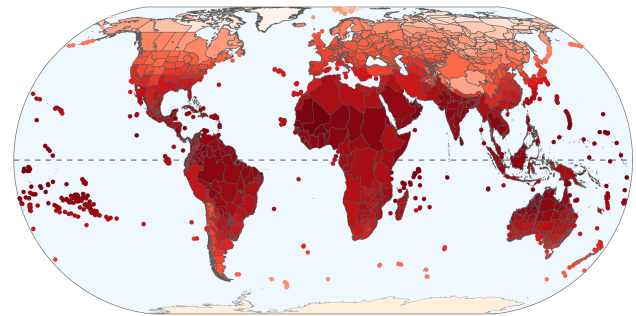
(b) Distribution map of *Impatiens glandulifera*

Status ■ native ■ naturalized ■ non-native ■ unknown

## (c) Growth form coverage of native vascular plants (d) Mean annual temperature



Coverage (%) 0 25 50 75 100



°C -20 -10 0 10 20 30

**FIGURE 2** Different facets of GIFT by geographic region. (a) Richness of native vascular plants, with a log-transformed colour scale, based on `GIFT_richness()`. (b) Distribution of *Impatiens glandulifera* with its floristic status in each region as indicated in the primary references used in GIFT, based on `GIFT_species_distribution()`. (c) Coverage for the growth form of vascular plants based on `GIFT_coverage()`. (d) Mean annual temperature (°C) per region based on `GIFT_env()`. The projection used for all panels is Eckert IV (EPSG: 54012). R-code to generate such figures based on functions from the GIFT R-package is accessible in the main vignette of the R-package <https://biogeomacro.github.io/GIFT/articles/GIFT.html>. The `GIFT_shapes()` function was used to retrieve the spatial polygons associated with each region.

Application Programming Interface (API), and the API then accesses the database to retrieve the desired data. If necessary, the API can also be called programmatically or through the browser independently of the R-package ([https://biogeomacro.github.io/GIFT/articles/GIFT\\_API.html](https://biogeomacro.github.io/GIFT/articles/GIFT_API.html)).

Most of the functions are interconnected and interdependent (Figure S4). Some arguments are shared with other functions, such as the identification numbers for references (`ref_ID`), checklists (`list_ID`), unstandardized species names (`name_ID`), standardized species names (`work_ID`), traits (`trait_ID`) and regions (`entity_ID`). We provide the possibility to extract and work with any existing version of the database. Each of the functions presented below has an argument called `GIFT_version` that allows retrieving data from a specific instance of the database (Table 1). Because all versions are available through the R-package, analyses can be reproduced even after the database has been updated.

A small number of data providers have asked to restrict access to their data at this time. This implies that among all the data that can be retrieved with the R-package, a small proportion of references (6.7%, Figure 1a) are restricted. These data have mostly been contributed by data owners who plan to publish their data independently before

making them publicly available via GIFT or come from large online databases that are better accessed directly (e.g. WCVP; Govaerts et al., 2021). A password-protected API, that can be made available upon request, is needed to retrieve these restricted data. On top of the password-restricted API, approval from the data providers is needed. The `GIFT_coverage()` function gives an overview of the potential information available in the restricted references and can be run before considering its use. Regardless, all data sources, open access and restricted, used in studies using GIFT data should be cited.

## 2 | REGIONAL PLANT CHECKLISTS

The main function of the package, `GIFT_checklists()`, allows one to retrieve plant checklists for regions that meet certain criteria. A complete tutorial on how to use this function is available in the main vignette of the package, <https://biogeomacro.github.io/GIFT/articles/GIFT.html>, and, in the following, the main options are presented. `GIFT_checklists()` returns a list with two objects: the metadata of the regions matching the input criteria, together with the identification numbers of the corresponding references and checklists, and a table

TABLE 1 Overview of the 27 functions available in the GIFT R-package.

Category	Functions	Description
Regional checklists and species distributions	GIFT_checklists()	Checklists for regions matching certain criteria
	GIFT_checklists_conditional()	Metadata of checklists for regions matching certain criteria
	GIFT_checklists_raw()	Checklists by reference (ref_ID)
	GIFT_lists()	Metadata of checklists and regions per reference
	GIFT_species_distribution()	Distributions of individual plant species
Species names, taxonomy and phylogeny	GIFT_phylogeny()	Phylogeny linked to standardized species names
	GIFT_species_lookup()	Taxonomic information per species name
	GIFT_species()	All standardized species available
	GIFT_taxonomy()	Taxonomy lookup
	GIFT_taxgroup()	Assigns taxonomic groups to species
Traits	GIFT_traits()	Aggregated trait values per species
	GIFT_traits_meta()	Metadata for traits
	GIFT_traits_raw()	Non-aggregated reference-level trait values
	GIFT_traits_tax()	Trait values at taxonomic group level
Spatial and environmental data	GIFT_env()	Environmental data per region
	GIFT_env_meta_misc()	Metadata for miscellaneous environmental variables
	GIFT_env_meta_raster()	Metadata for environmental raster layers
	GIFT_spatial()	Regions matching spatial input
	GIFT_regions()	Miscellaneous information per region
	GIFT_shapes()	Spatial polygons of selected or all regions
	GIFT_overlap()	Spatial overlap between GIFT regions and external polygon resources
	GIFT_no_overlap()	Pairwise overlap between GIFT regions
Utils	GIFT_coverage()	Taxonomic and trait coverage per region
	GIFT_references()	Metadata per reference
	GIFT_richness()	Species richness per region and taxonomic group
	GIFT_versions()	Versions of GIFT available
	western_mediterranean	Spatial polygon of the western Mediterranean basin (example data)

with the species composition per checklist and region. By default, the standardized species names and their floristic status are returned in this table but the original non-standardized species names can also be returned on request.

GIFT\_checklists() allows one to define a taxonomic and a floristic group of interest. The taxonomic group can take several values, for example all vascular plants (taxon\_name="Tracheophyta") or other taxonomic groups within land plants (e.g. a plant family, taxon\_name="Orchidaceae"). All available options can be viewed by running the GIFT\_taxonomy() function. The floristic\_group indicates whether the species retrieved should be native, naturalized, endemic or if all species should be retrieved. Both arguments have a companion argument, complete\_taxon and complete\_floristic respectively, which can be set to TRUE or FALSE. These arguments define whether only regions that are covered by checklists of the entire taxonomic group or floristic status should be retrieved or if regions covered for only a subset can be returned. For example, with taxon\_name="Tracheophyta", a region covered only by an orchid checklist will only be retrieved if complete\_taxon=FALSE. Equivalently, with floristic\_group="native", a region covered only by lists of

endemic species or only trees will only be retrieved if complete\_floristic=FALSE. More detailed explanations can be found in the main vignette of the package.

Second, GIFT\_checklists() works with or without spatial restriction. By default, there is no restriction, meaning that regions covered by checklists meeting the other criteria will be retrieved all over the world. It is also possible to provide a shapefile or a set of coordinates to spatially constrain the query. As an example, we provide a shape of the western Mediterranean basin, which can be retrieved using the western\_mediterranean data function. Regions that correspond to, fall inside or intersect the spatial input can then be retrieved. Another important consideration is whether users want to retrieve several checklists for nested and overlapping regions or if only non-overlapping regions should be considered. This can be easily set with the remove\_overlap argument. Overlapping regions can be removed in favour of smaller or larger regions (above or below a user-defined area threshold) in case of overlap (see Figures S5 and S6 and the main tutorial on the website <https://biogeomacro.github.io/GIFT/articles/GIFT.html>). We also provide the option to remove overlapping regions only if they belong to the same reference (see

the advanced vignette for more details [https://biogeomacro.github.io/GIFT/articles/GIFT\\_advanced\\_users.html#by-ref\\_id](https://biogeomacro.github.io/GIFT/articles/GIFT_advanced_users.html#by-ref_id)). If one is interested in retrieving the species richness of a particular taxonomic and floristic group per region, one can use the alternative function `GIFT_richness()`.

### 3 | DISTRIBUTION OF INDIVIDUAL PLANT SPECIES

To look up if a plant species is included in GIFT, users can call the `GIFT_species_lookup()` function. This function can search for both original or standardized species names and returns all references in which the focal species name occurs as well as the original species name as found in these references. The complete list of standardized plant species names available in the GIFT database can be retrieved with the function `GIFT_species()`. Second, the function `GIFT_species_distribution()` returns a list of regions where the focal plant species occurs. The floristic status of the species is provided, allowing for quick identification of regions where the focal plant is native, naturalised or endemic. The argument `aggregation` allows to aggregate this information at the region level, with a note indicating whether the original references disagree on the status. An example using *Impatiens glandulifera*, an annual plant native to the Himalayas that is now considered naturalized in many areas, is shown in [Figure 2b](#). This example illustrates that the floristic status must be treated with caution. While *Impatiens glandulifera* is considered native to the Himalayas, some references also classify it as native to Southeast Asia. This type of conflict, which occurs for many species, may be due to conflicting references, the fact that the floristic status refers to the original species names before taxonomic standardization, or errors in the references. Alternatively, GIFT data can be used via the `bRacatus` R package to estimate a georeferenced occurrence record's probability of being true or false and its biogeographic status based on a probabilistic framework (Arle et al., 2021).

### 4 | TAXONOMY

The GIFT database includes original species names as taken from the original references as well as standardized species names and statistics about the standardization process. Several functions in the package, such as `GIFT_checklists()` or `GIFT_species_lookup()`, can return the original species names before standardization and information about the standardization process. It is important to provide this information because the floristic status of species refers to the original species names, not the standardized names. For example, a subspecies may be described as endemic in a reference and standardized to its parent species which is actually considered non-endemic native, resulting in a misleading floristic status for that standardized species. Species names derived from infraspecific taxa or synonyms are therefore highlighted. We also provide matching scores in percentage for genera, epithets and overall species

names between the original species name and the accepted species names. These harmonization statistics can hence be used to filter for only accepted species ([Figure S2](#)), or species that were not subspecies before standardization, and so forth. Therefore, functions that allow to retrieve plant checklists, species distributions or raw functional traits, namely `GIFT_checklists()`, `GIFT_species_distribution()` and `GIFT_traits_raw()`, allow the inclusion in their output of both the original and harmonized species names, as well as details about the standardization and the service used. The original and taxonomically harmonized names come with an identification number (`name_ID` and `work_ID`, respectively) and allow tracing back the taxonomic standardization or to run a preferred alternative taxonomic standardization (Grenié et al., 2023). There are 1,161,174 original species names for 371,148 standardized species names in GIFT 3.0 ([Figure S2](#)).

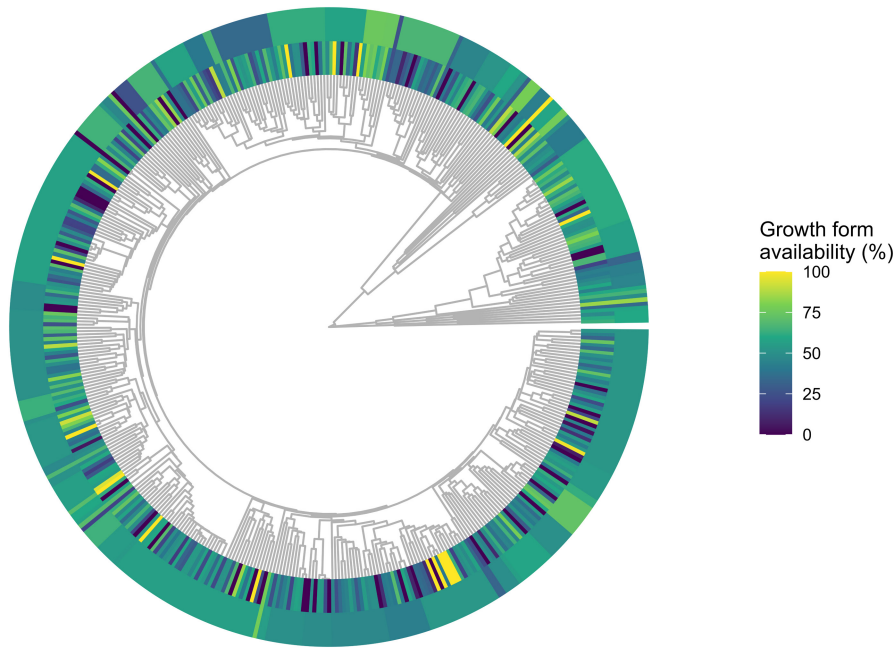
The taxonomy of GIFT assigns species to their respective genera, families and orders up to higher group levels such as Angiosperms, Spermatophytes and so forth. It is stored in a table that can be accessed with `GIFT_taxonomy()`. This function returns a table which can be translated into the Newick tree format (Archie et al., 1986) in which each taxon, down to the genus level, is placed between a left and right border. The `GIFT_taxgroup()` function can be used to place any of the accepted plant species names within this taxonomy and to retrieve their higher taxonomic groups (e.g. family, order or higher group).

### 5 | PHYLOGENY

The phylogeny in GIFT is based on existing megatrees (Jin & Qian, 2022; Smith & Brown, 2018; Zanne et al., 2014), includes all vascular plants from the GIFT database and can be accessed with the function `GIFT_phylogeny()` from version 3.0 onward. Higher taxonomic groups from the taxonomy of GIFT that form monophyletic groups in the phylogeny can be used to retrieve a phylogeny for a taxonomic subset of the entire phylogeny. The phylogeny can be retrieved as a tree object, which can then be used directly with other R-packages such as `phytools` (Revell, 2023) or `ape` (Paradis et al., 2023), or as a table mimicking the Newick format (Archie et al., 1986). The phylogeny, in combination with data from the previously described functions, allows the calculation of phylogenetic diversity metrics at the checklist or region level or the estimation of trait coverage along the phylogeny of vascular plants ([Figure 3](#)).

### 6 | FUNCTIONAL TRAITS

GIFT 3.0 includes data for 109 different functional traits and a total of 5,679,014 trait records aggregated at the species level ([Figure S3](#)). The different traits are distributed across six categories: morphological, ecological, physiological, reproductive, genetic or life history (Weigelt et al., 2020). Coverage varies considerably among traits with, for example, the growth form being available



**FIGURE 3** Phylogenetic coverage of the plant trait 'growth form'. The phylogeny is based on Jin and Qian (2022) and was extracted from Global Inventory of Floras and Traits using the GIFT\_ phylogeny() function and pruned to genus level (one tip per genus). The two outer rings illustrate the growth form coverage either at the genus level (inner ring) or at the family level (outer ring). Growth form coverage was calculated as the proportion of species covered per genus and family respectively. The R-code to generate this figure is accessible in the main vignette of the R-package <https://biogeomacro.github.io/GIFT/articles/GIFT.html>.

for 246,901 plant species while dispersal syndrome is available for only about 9600 species. Metadata for each of these traits can be viewed by calling the `GIFT_traits_meta()` function. When having a list of traits of interest, users may start by calling this metadata function to retrieve their identification number (`trait_ID`). Once this number is known, users can call the functions `GIFT_traits_raw()` or `GIFT_traits()` to receive one or several traits at a time. The functions return the raw traits or the aggregated trait data at the species level, respectively. In GIFT, there is also trait information collected at the higher taxonomic level. For example, all species belonging to the genus *Abies* are woody. This data can be retrieved using `GIFT_traits_tax()`. Querying the raw traits acknowledges the variation of trait values across references and is therefore of interest to ecologists working at the species level. The primary references for these trait values are also returned. `GIFT_traits()` returns trait values aggregated at the species level. For categorical traits (such as e.g. growth form), the function returns the most frequent trait value, along with an agreement score. This score indicates the percentage of references that leads to this most frequent value out of all references that provide information about this trait. For example, if a plant is described as *tree* in two sources and as *shrub* in a third one, then the value *tree* is returned with an agreement score of 66%. Users can decide on a threshold at which they trust the trait values, or they can include the agreement score and the associated uncertainty in their statistical analysis. For continuous traits, the number of references used to aggregate the trait value is given, together with the coefficient of variation of the continuous value listed in the different references.

Trait records in GIFT can be actual values taken from the references but they can also be logically derived from available information (König et al., 2017). For example, a species can have its growth form described as *tree*, and since all trees are phanerophytes, the life form value of this plant species is set to

*phanerophyte*. Whether a trait is derived or not is indicated in the raw trait table returned by `GIFT_traits_raw()`. Trait derivation can introduce biases in the proportional representation of trait categories in assemblages. For example, since all trees are phanerophytes, but not all herbs are therophytes, this derivation leads to an overrepresentation of phanerophytes. Similarly, references of only trees (Beech et al., 2017) or only epiphytes (Zotz et al., 2021) introduce biases at the assemblage level. Trait values only based on a reference or a derivation that introduces a bias can be filtered out by setting the `bias_deriv` or `bias_ref` arguments to `FALSE`. More details about the arguments of these two functions can be found in the main vignette of the package (<https://biogeomacro.github.io/GIFT/articles/GIFT.html>).

Finally, the `GIFT_coverage()` function can be used to map the coverage of a particular trait for a given taxonomic and floristic group. In this case, the argument `what` of the function has to be set to "trait\_coverage". Figure 2c maps the coverage of the maximal vegetative height per plant using this function. This function is complementary to the GIFT website <https://gift.uni-goettingen.de/map>, where trait coverage can be mapped, and can be used to compare data including or excluding restricted references. In addition, this function can be used to indicate whether a combination of region, taxonomic group and floristic status is covered by at least one checklist for public and restricted data in comparison.

## 7 | ENVIRONMENTAL VARIABLES PER REGION

A major line of research in macroecology and biogeography is to identify the environmental drivers underpinning species distributions and diversity gradients (McGill, 2019). To facilitate such research, GIFT 3.0. contains 213 variables, distributed across 34

miscellaneous variables and 179 raster layers (Table S1). Raster layers mostly contain continuous metrics that provide insights into macroclimatic, topographic, edaphic or paleoclimatic variables or sometimes categorical information like the distribution of soil classes (Hengl et al., 2017). Miscellaneous variables provide information on the geography, geometry, floristic regions, isolation and other characteristics of the GIFT regions based on the region's spatial shapes and additional feature layers. The two metadata functions `GIFT_env_meta_misc()` and `GIFT_env_meta_raster()` provide an overview of all environmental variables and the underlying data layers. Each of these functions returns the list of available raster layers or miscellaneous variables along with their names and references. Once the names of the variables of interest have been identified, users can call the `GIFT_env()` function for a list of GIFT regions, using their identification number (`entity_ID`).

When calling a miscellaneous variable, such as the area or the biome that encapsulates the region of interest, a single value is returned. For raster layers, however, users need to provide a set of summary statistics. Indeed, as the raster layers have a finer resolution than most of the GIFT regions, the environmental information needs to be aggregated. For example, one can ask for the average temperature of the raster cells falling into a GIFT region (`GIFT_env(rasterlayer = "wc2.0_bio_30s_01", sumstat = "mean")`, Figure 2d) or for the standard deviation of the precipitation values (`GIFT_env(rasterlayer = "wc2.0_bio_30s_12", sumstat = "sd")`). The desired summary statistics must be passed to the `GIFT_env()` function using the `sumstat` argument.

## 8 | OUTLOOK

The GIFT R-package provides easy-to-use functions for accessing the GIFT database. This tool will support a range of new studies on plant biogeography while allowing for their reproducibility. In parallel, we continue integrating new plant checklists into the GIFT database to increase the coverage of underrepresented regions or environments of the world, to bridge the gap between local and regional studies of plant diversity (Puglielli & Pärtel, 2023) and to increase the coverage of functional traits. Additions will be made to the beta version of GIFT, which will be turned into a new stable version once enough additions have been made and checked for consistency. Updates to the package are submitted to the CRAN repository and archived on the Zenodo repository, with each new release having its own DOI (version 1.2.0 of the package is archived at <https://zenodo.org/record/8256512>).

### AUTHOR CONTRIBUTIONS

Pierre Denelle and Patrick Weigelt developed the GIFT R-package and the associated GitHub website. Patrick Weigelt led the development of the database infrastructure and API. All authors worked on the advancement of the GIFT database. Pierre Denelle led the writing of the manuscript to which all authors contributed critically.

### ACKNOWLEDGEMENTS

We thank Martin Turjak, Matthias Grenié and other beta-testers of the R-package for providing useful insights. HK acknowledges funding from the DFG as part of the research unit FOR 2716 DynaCom and research training group RTG 1644 Scaling Problems in Statistics.

### CONFLICT OF INTEREST STATEMENT

All authors have no conflict of interest to declare.

### PEER REVIEW

The peer review history for this article is available at <https://www.webofscience.com/api/gateway/wos/peer-review/10.1111/2041-210X.14213>.

### DATA AVAILABILITY STATEMENT

The GIFT R-package is available for download from CRAN at <https://CRAN.R-project.org/package=GIFT>. The development version of the package is available at <https://github.com/BioGeoMacro/GIFT>. An associated website with tutorials is available at <https://biogeomacro.github.io/GIFT/> and an interactive overview of the data available can be found at <https://gift.uni-goettingen.de>. A permanent archive of the version 1.2.0 of the package is available on Zenodo at <https://zenodo.org/record/8256512> (Denelle et al., 2023).

### AUTHORSHIP GUIDELINES

Publications using the GIFT database should cite all primary sources (Table S2) that were used as well as the version of GIFT and the original publication of the GIFT database (Weigelt et al., 2020). All primary references in GIFT are available with the `GIFT_references()` function. If GIFT data are retrieved through the R-package, this paper should also be cited. We also encourage authors to provide the R-scripts used to retrieve the data as supplementary files to their study to promote traceability and reproducibility. A few data contributors of GIFT asked to restrict access to their data for now. These data can be accessed through the R-package specifying a password-protected API (provided by the authors of this article upon request) and their use requires contacting the authors of the primary restricted data and asking for permission to use them. We encourage researchers using GIFT to contact us if any help is needed regarding the use of GIFT data.

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## SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

**Figure S1:** Number of regions retrieved with GIFT\_checklists() using different criteria for GIFT 3.0. The first red lollipop corresponds to the black dashed line in Figure 1a. For the yellow and green lollipops, the taxonomic group is set to Tracheophyta, i.e. vascular plants and complete\_taxon is set to TRUE. With complete\_floristic = TRUE, the number of regions with the floristic status set to native is higher than with the floristic status set to all because it is easier to get a complete knowledge of only native species in a region than for all species. For the blue and purple lollipops, the floristic status is set to native and complete\_floristic is set to TRUE. With complete\_taxon = TRUE, the number of regions with angiosperms is higher than with vascular plants because it is easier to get a complete knowledge of only angiosperms in a region than for all vascular plants.

**Figure S2:** Number of original unstandardized (green) and standardized (purple) species names compared across versions of

GIFT. In GIFT 3.0, the new taxonomic workflow using the World Checklist of Vascular Plants (Govaerts et al., 2021) allows to classify species as accepted or not. The majority (95.6%) of standardized names are considered as accepted.

**Figure S3:** Number of trait records, and number of traits available in the different versions of GIFT. Panel (a) indicates how many trait values are available (a record is a value of a particular trait at the species level) and panel (b) shows the total number of traits.

**Figure S4:** Dependency graph of the 27 functions in the GIFT R package. Each circle represents one function. If one function uses another one, then it is connected to it with a grey arrow. Functions are colored according to their category (Table 1). The metadata function `GIFT_versions()` is removed from this graph because it is a metadata function that connected to all other functions.

**Figure S5:** Principle of the argument `remove_overlap` and `area_th_mainland` in `GIFT_spatial()`. If `remove_overlap` is set to `TRUE`, overlapping regions are removed. Depending on the value of

`area_th_mainland` in  $\text{km}^2$ , the smaller or larger regions are kept.

**Figure S6:** Principle of the argument `overlap_th` in `GIFT_spatial()`. `overlap_th` expresses in percentage and defines above which threshold regions are considered as overlapping.

**Table S1:** Number of miscellaneous variables and raster layers available in all versions of the GIFT database. Numbers in italics indicate variables that are only accessible through the password-protected restricted API.

**Table S2:** List of references used to produce the figures of this article.

**How to cite this article:** Denelle, P., Weigelt, P., & Kreft, H. (2023). GIFT—An R package to access the Global Inventory of Floras and Traits. *Methods in Ecology and Evolution*, 14, 2738–2748. <https://doi.org/10.1111/2041-210X.14213>