GIFT – A Global Inventory of Floras and Traits for macroecology and biogeography

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Abstract

To understand how traits and evolutionary history shape the geographic distribution of plant life on Earth, we need to integrate high-quality and global-scale distribution data with functional and phylogenetic information. Large-scale distribution data for plants are, however, often restricted to either certain taxonomic groups or geographic regions. For example, range maps only exist for a small subset of all plant species and digitally available point-occurrence information is strongly biased both geographically and taxonomically. An alternative, currently rarely used resource for macroecological and botanical research are regional Floras and checklists, which contain highly curated information about the species composition of a clearly defined area, and which together virtually cover the entire global land surface. Here we report on our recent efforts to mobilize this information for macroecological and biogeographical analyses in the GIFT database, the Global Inventory of Floras and Traits. GIFT integrates plant distributions, functional traits, phylogenetic information, and region-level geographic, environmental and socio-economic data. GIFT currently holds species lists for 2,893 regions across the whole globe including ~315,000 taxonomically standardized species names (i.e. c. 80% of all known land plant species) and ~3 million species-by-region occurrences. In addition, GIFT contains information about the floristic status (native, endemic, alien and naturalized) and takes advantage of the wealth of trait information in the regional Floras, complemented by data from global trait databases. Based on a hierarchical and taxonomical derivation scheme, GIFT holds information for 83 functional traits and more than 2.3 million trait-by-species combinations and achieves unprecedented coverage in categorical traits such as woodiness (~233,000 spp.) or growth form (~213,000 spp.). Here we present the structure, content and automated workflows of GIFT and a corresponding web-interface (http://gift.uni-goettingen.de) as proof of concept for the feasibility and potential of mobilizing aggregated biodiversity data for global macroecological and biogeographical research.

Introduction

Worldwide, about 382,000 vascular plant species form the basis of our terrestrial biosphere and provide key ecosystem services to humanity (Willis, 2017). Despite the long history of botanical exploration of our planet, the global distribution is only known for a subset of all plant species at comparatively coarse spatial grains (e.g. WCSP, 2012). In contrast to smaller and better known taxa like birds and mammals (BirdLife International, 2018; IUCN, 2018), high-quality species-level range maps or atlas data of plants are only available for selected groups (e.g. conifers in Farjon & Filer, 2013; cacti in Barthlott *et al.*, 2015) or regions (e.g. Europe in Tutin *et al.*, 1964–1980; woody plants of China in Fang *et al.*, 2011). Many research questions at the forefront of biogeography and macroecology, however, require a detailed knowledge of global plant distributions and, additionally, of species-level functional traits and phylogenetic relationships (e.g. Morueta-Holme *et al.*, 2013; Weigelt *et al.*, 2015; König *et al.*, 2017).

Several national and international initiatives focus on mobilizing and aggregating plant distribution information. For instance, the Global Biodiversity Information Facility (GBIF, 2018), provides access to ~214 million point occurrences of vascular plant species. These records are invaluable for plant ecology and conservation-related research, as they provide information about key aspects of species identity, time and place (Powney & Isaac, 2015). However, taxonomic, geographical and temporal biases (Hortal *et al.*, 2015; Meyer *et al.*, 2016), as well as limited curation and standardization efforts and the lack of important meta-information, like, for example, the floristic status at a given location (native, non-native, naturalized, etc.), limit their usefulness for macroecological research. An alternative source of information are Floras and checklists which, in contrast, present highly curated accounts of the plant species known to occur in a certain region. Floras and checklists are often based on decades to centuries of exploration and regional botanical work, and have profited from the expertise of generations of botanists. They aim at providing (near-)complete floristic inventories for a given region and thus provide information on species presences and their floristic status, and additionally allow for the inference of local species absences (Lobo *et al.*, 2010; Jetz *et al.*, 2012). So far, extensive compilations of plant checklists exist only for certain geographic regions (e.g. Ulloa Ulloa *et al.*, 2017), taxonomic groups (e.g. Flann, 2009; WCSP, 2012), functional types (e.g. BGCI, 2017), or, for example, naturalized alien plants (van Kleunen *et al.*, 2015; Pyšek *et al.*, 2017).

In light of the increasing availability of biodiversity data, it is a major challenge to integrate various data types and to link data from different ecological domains representing species distributions, functional traits, phylogenetic relationships or environmental characteristics for analyses and cross-validation (König *et al.*, in prep.). Initiatives that integrate different types of distribution data with additional biotic or abiotic information are currently most comprehensive for particular geographic regions (e.g. BIEN for the Americas; Enquist *et al.*, 2016) or other taxa (e.g. Map of Life for vertebrates; Jetz *et al.*, 2012). However, the wealth of aggregated information in regional Floras and checklists (Frodin, 2001) allows for a near-global characterization of plant distributions. In combination with functional traits from the botanical literature or large trait databases (e.g. RBG Kew, 2008; Kattge *et al.*, 2011b) and ever-growing species-level phylogenies (e.g. Smith & Brown, 2018), this represents a promising basis for macroecological and biogeographic research.

Here, we present GIFT, the Global Inventory of Floras and Traits database, a new resource designed to integrate species distribution data and species-level functional traits of plants from regional Floras and checklists with phylogenetic information and geographic, environmental and socio-economic characteristics (**Fig. 1**). As such, the database architecture, workflows and data of GIFT facilitate a wide

array of macroecological and biogeographical analyses and may help to extent and validate other plant distribution and trait data resources. The general concepts outlined here may serve as a role model for aggregated species checklist and trait databases for other major taxonomic groups.

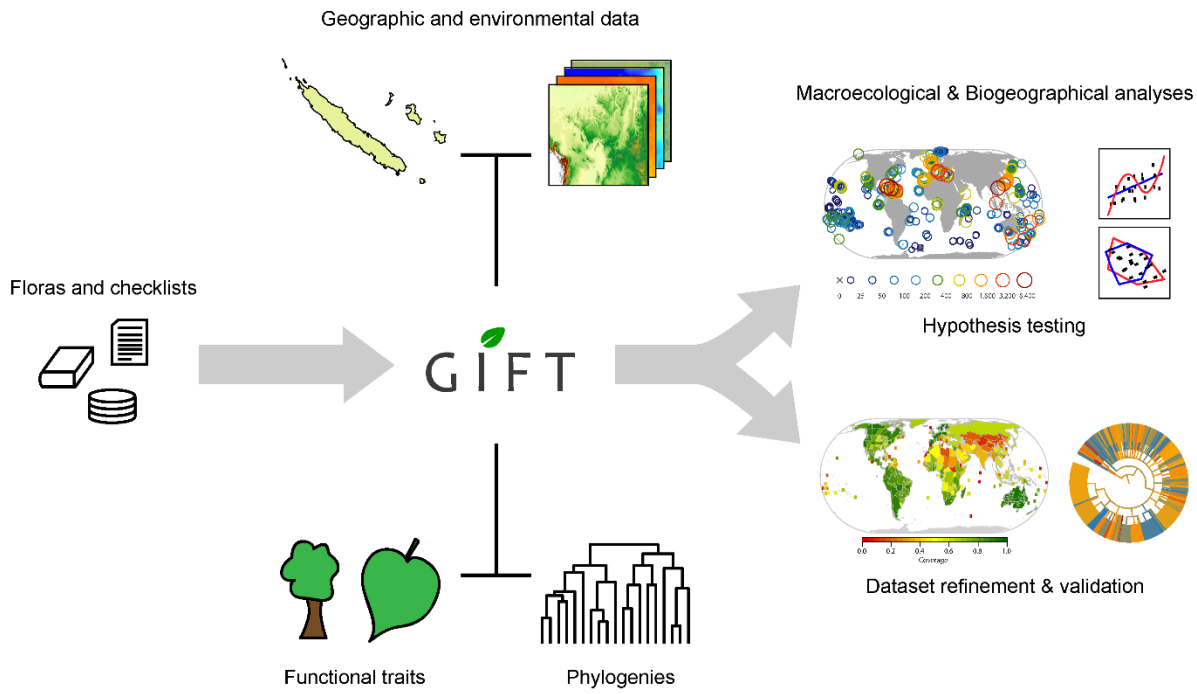

Fig. 1. Conceptual framework of the Global Inventory of Floras and Traits database (GIFT). The core information in GIFT are species occurrences in geographic regions (islands, political units, protected areas, biogeographical regions) based on Floras and checklist. At the level of the geographical regions, this information is linked to physical geographic, bioclimatic and socioeconomic properties. At the level of the species, functional traits, taxonomic placement and phylogenetic relationships are linked. This integration of species distribution data in the form of full regional inventories and regional and species characteristics allows for a wide variety of macroecological and biogeographical analyses of taxonomic, phylogenetic and functional diversity as well as for the refinement and validation of other plant distribution and trait datasets.

Content and structure of GIFT

Overview

Regional Floras and checklists are a rich source of information on species distributions that often also contain detailed descriptions of species traits and other information such as conservation status and human uses (Palmer & Richardson, 2012). In the past, botanical knowledge was recorded primarily in printed books (Frodin, 2001), which are labor-intensive to convert into structured data. These resources, however, are increasingly being made digitally available (e.g. Zuloaga *et al.*, 2004; Acevedo-Rodríguez & Strong, 2007) and modern regional inventory projects are set up as digital databases right from the start (e.g. Brach & Song, 2006; Jardim Botânico do Rio de Janeiro, 2016). In GIFT, we make use of this wealth of information, and collate and mobilize plant species lists and trait information from published and

unpublished Floras, catalogs, checklists and online databases into a single integrated and curated global database.

The original checklist data in GIFT consist of species names from the literature, their occurrences in the regional species lists and original trait information (yellow boxes in **Fig. 2**). All this information is linked to meta-data on the included literature references, species lists, traits and geographic entities (white boxes in **Fig. 2**). Semi-automated workflows allow a fast and reliable integration of new datasets and provide extensive curated and derived information (blue boxes in **Fig. 2**): (1) taxonomic match-up with taxonomic resources and name standardization (section 'Species names and taxonomic standardization'), (2) taxon placement according to a taxonomic backbone and phylogeny (section 'Taxonomic backbone and phylogeny'), (3) trait standardization and hierarchical and taxonomic trait derivation (section 'Functional traits'), (4) calculation of regional summary statistics like species richness or trait coverage (section 'Geographic regions') and (5) extraction and computation of geographic, environmental and socio-economic regional characteristics (section 'Geographic regions'). Based on this generic database framework, GIFT can be queried for complete species checklists of a certain taxonomic or functional group and floristic status (e.g. 'native angiosperms' or 'naturalized trees'). Alternatively, it is possible to extract distributional and functional information for a set of species, or to extract environmental information, species numbers and mean trait values for a set of regions. GIFT is currently stored on a MySQL 5.5.43 database server. Workflows for preparing, importing, processing, extracting and visualizing data are written in the R statistical programming language (R Core Team, 2018).

Checklists

GIFT currently contains 3,826 species lists referring to 2,893 different geographic regions which are based on 429 original checklist data sources (**Fig. 2**). Compared to other plant diversity databases which either focus on other types of distribution data (point occurrences, vegetation plots, range maps) or trait data (individual measurements), this represents a complementary resource of unprecedented extent. A full and up-to-date list of all data citations and their bibliographic references is available in **Appendix S 1** and at the GIFT website (http://gift.uni-goettingen.de), and publications based on GIFT are requested to cite the checklist resources the analyses are based upon (e.g in Weigelt *et al.*, 2016). Checklists and inventories stem from publically available sources as well as from unpublished sources with restricted access (4.2%). Meta-data on references and species lists further specify the type of the reference as provided (Flora, checklist, catalogue, identification key, survey, etc.), the taxonomic and floristic scope of the reference (e.g. all native and naturalized angiosperms), whether the species' floristic status is indicated and which functional traits are reported.

The actual distribution information is kept in a separate table that links the taxonomic names to the species lists they occur in and via those to geographic regions (**Fig. 2**, 'species occurrences'). For each species occurrence, we indicate, if known, whether this occurrence is native or not. For native species, we further indicate if species are endemic to the geographic entity of the species list or to the geographic entity of the entire reference, if indicated in the literature source. For non-native species, we additionally indicate whether they are naturalized or not (Richardson *et al.*, 2000). We also indicate whether the occurrence and the different kinds of floristic status information are questionable or doubtful according to the literature source as binary variables. Via the species names, occurrences are linked to species-level functional traits as well as to the taxonomic and phylogenetic backbone. Via the geographic regions, species and traits are linked to regional geographical characteristics (**Fig. 2**). Routines to export checklists

from GIFT and their meta-data as Darwin Core (Wieczorek *et al.*, 2012; Wieczorek *et al.*, 2014) and Humboldt Core (Guralnick *et al.*, 2018) archives, respectively, are currently being developed to allow easy integration with other kinds if distribution data (e.g. point occurrences from GBIF).

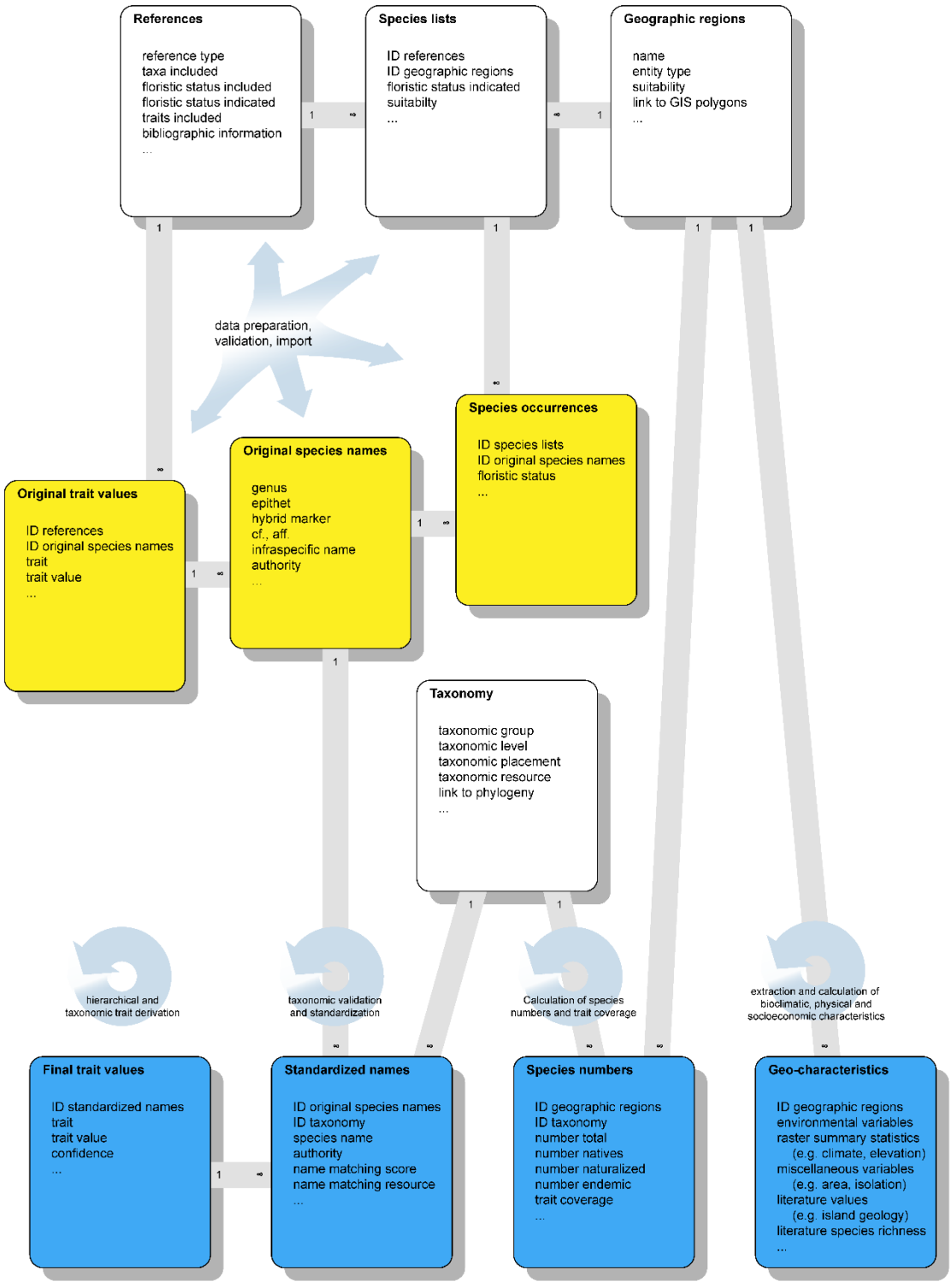

Fig. 2. Simplified structure of the Global Inventory of Floras and Traits database (GIFT). Meta-data on literature references, species lists and geographic regions builds the backbone of the database (top row). A reference can include several species lists (e.g. for different sub-regions) and a geographic region can be covered by several lists and references. Species lists vary in taxonomic and floristic scope (e.g. all native and naturalized angiosperms) and in the information content (floristic status, functional traits). Primary occurrence information, species names and functional trait data from the literature resources build the main block of original data (yellow). Automated workflows link those to taxonomically standardized working names, to a higher taxonomy and phylogeny of vascular plants and produce derived resources for analyses (blue). Grey bars indicate links among tables in a simplified way (most tables shown here represent several tables in the database).

Species names and taxonomic standardization

All species names enter the database in their original form including infraspecific information and author names where available. Species names derived from heterogeneous resources, referring to various geographic regions and published over a timespan of about one hundred years, inevitably vary in the taxonomic concepts applied (Jansen & Dengler, 2010). To compare species identities across different resources, we therefore submit all non-hybrid species names to a semi-automated taxonomic standardization and validation procedure based on taxonomic information provided by The Plant List 1.1 (TPL; The Plant List, 2013) and additional resources available via iPlant's Taxonomic Name Resolution Service (TNRS; Boyle *et al.*, 2013). Names of hybrid species are currently not standardized due to heterogeneous formats of their scientific names. The original names are nonetheless stored for further processing if needed. This procedure was exclusively developed to meet the needs of the GIFT database and has already been applied and described in Meyer et al. (2016).

First, all genus names not occurring in TPL are checked manually and spelling mistakes are corrected based on literature and online resources (e.g. Mabberley, 2008; IPNI, 2012). Entries that cannot be assigned to an established genus name at all (valid or not) are excluded from further steps. Second, all species names are compared automatically to all taxonomic names available for a particular genus in TPL based on pairwise orthographic distances (generalized Levenshtein distance; Levenshtein, 1966) between species epithets, infraspecific names, author names and the entire species names. We use both the absolute orthographic distance, which is the number of changes needed to transform one character string into the other (Levenshtein, 1966), and the relative orthographic distance, which relates the absolute orthographic distance to the length of the longer input string. Based on the orthographic distances of an original species name to all congeneric species listed in TPL, we determine the final working name hierarchically: First, we choose the best-matching species epithet. If multiple epithets match equally well, we choose those with best-matching infraspecific names (if infraspecific name available and if absolute orthographic distance < 4 and relative orthographic distance < 0.3), and then those with best-matching author names (if author names available and relative orthographic distance < 0.5). The specific matching thresholds at each step were derived seeking a balance between the number of names that cannot be matched and the number of names that are matched to the wrong species. Synonyms are linked to their accepted species names as suggested by TPL. If several names match equally well and lead to different accepted binomial species names, we first remove illegitimate and invalid names, then synonyms and then accepted names with poorer overall orthographic distance. In addition, all names are resolved using the TNRS application programming interface (API), which returns similar statistics on the name matching and the status of the matched names like the above-described approach using TPL. For choosing standardized binomial working names we give priority to TPL over TNRS, because of the possibility of adjusting our TPL name matching

approach. If a name does not match any name via TPL or TNRS with a relative orthographic distance < 0.25 for either the epithet or the full name, we keep the original name as working name. If not stated otherwise summary statistics below are based on these standardized binomial working names.

All original names, orthographic distances, matched names and meta-information about the matching are stored in the database (**Fig. 2**). Thus, the taxonomic standardization in GIFT is fully transparent and repeatable whenever taxonomic resources are updated or extended. Moreover, the stored information can be used to filter out names that did not match, matched only to a certain degree, or that do not lead to an accepted species name, allowing for rigorous sensitivity analyses of the effects of taxonomic uncertainties on the outcome of macroecological and biogeographical analyses.

Taxonomic backbone and phylogeny

All species working names are linked to a taxonomic backbone via their genus names. The taxonomy is based on the Angiosperm Phylogeny Group IV system for angiosperms (The Angiosperm Phylogeny Group, 2016), and on the Angiosperm Phylogeny Website version 13 (Stevens, 2013) and The Plant List 1.1 for gymnosperms, pteridophytes and bryophytes (The Plant List, 2013). Based on the taxonomic backbone, the database can be queried in two directions. First, species lists can be extracted including only species that belong to a certain taxon (e.g. only angiosperms). Second, geographic units can be chosen for which species lists cover a complete taxon of interest (e.g. all regions with Bixaceae checklists). In combination, species lists of a certain taxon can be produced for all regions where the required data is available. In addition, species-level functional traits can be aggregated at any desired taxonomic level and trait information for broad taxonomic groups can be used to derive species-level information for traits that are consistent across a larger taxonomic groups.

All seed plant species are linked to a global phylogeny with 353,185 terminal taxa (Smith & Brown, 2018) for phylogeographical analyses. Two versions of this phylogeny are included in the database in tabular form to extract checklist and trait information for particular clades and to visualize trait and taxonomic coverage across the phylogeny. In one version, species in GIFT not included in the phylogeny were added replacing all members of the genera they belong to with polytomies (Pearse *et al.*, 2015) and in the other version missing species were excluded to keep detailed phylogenetic relationships among the species covered by the phylogeny. In addition, all vascular plant species in GIFT are linked to a phylogeny with fewer terminal taxa but broader phylogenetic extent (i.e. including pteridophytes; Qian & Jin, 2016), which was used here to assess taxonomic coverage of distribution and trait data at the family level.

Functional traits

Species in GIFT are linked to functional trait information from currently 155 original resources. Most trait resources are Floras and checklists for which annotated information on traits have been extracted, but also large trait compilations with or without spatial context are incorporated (e.g. Zotz, 2013; BGCI, 2017). The range of functional traits currently covered by GIFT reflects different aspects of plant morphology, life history, reproduction, physiology, genetics, and ecology (**Table S 1**). The focus lies on aggregated trait information at the species level, making GIFT a valuable complementary resource to initiatives that collate large amounts of trait measurements at the individual level (e.g. Kattge *et al.*, 2011b; Enquist *et al.*, 2016).

Many trait resources provide equivalent information in various languages, using different terminologies or measurement units. The first step of trait processing in GIFT is therefore the standardization of primary trait data according to pertinent trait literature (Pérez-Harguindeguy *et al.*, 2013; Garnier *et al.*, 2017) (**Fig.**

3) using defined categorical levels (categorical traits) and units of measurement (numerical traits) (**Table S 1**). To retain the maximum information provided by the original resources, many categorical traits are defined at multiple levels of detail (e.g. life form 1 vs. life form 2). In the second trait processing step, the standardized trait values are therefore subjected to a hierarchical derivation procedure (**Fig. 3**). This procedure makes use of logical links and nestedness among many functional traits based on their definitions. For example, the value "tree" in the trait growth form implies the value "woody" in the trait woodiness. As such hierarchical trait derivation increases the amount of trait information in GIFT. In addition, hierarchical derivation ensures compatibility among different levels of detail of the same trait by automatically deriving values in coarser variations from available information in more detailed ones. We organize such hierarchical relationships between traits in a directed graph that can be easily traversed to fill data gaps (**Fig. S 1**). A tabular version of the graph is stored in the database for modifications (**Table S 2**). A similar derivation approach is implemented for taxonomic groups that are uniform with respect to a particular trait (taxonomic trait derivation). In this case, the basis of derivation is not the logical hierarchy of trait values, but that of taxonomic groups. For example, the genus *Abies* consists exclusively of monoecious trees (Farjon, 2010). Thus, all species of *Abies* can be characterized with respect to growth form "tree" and reproductive mode "monoecious" based only on their taxonomic position. Subsequently, the taxonomically derived species-level traits are subjected to the hierarchical derivation as outlined above.

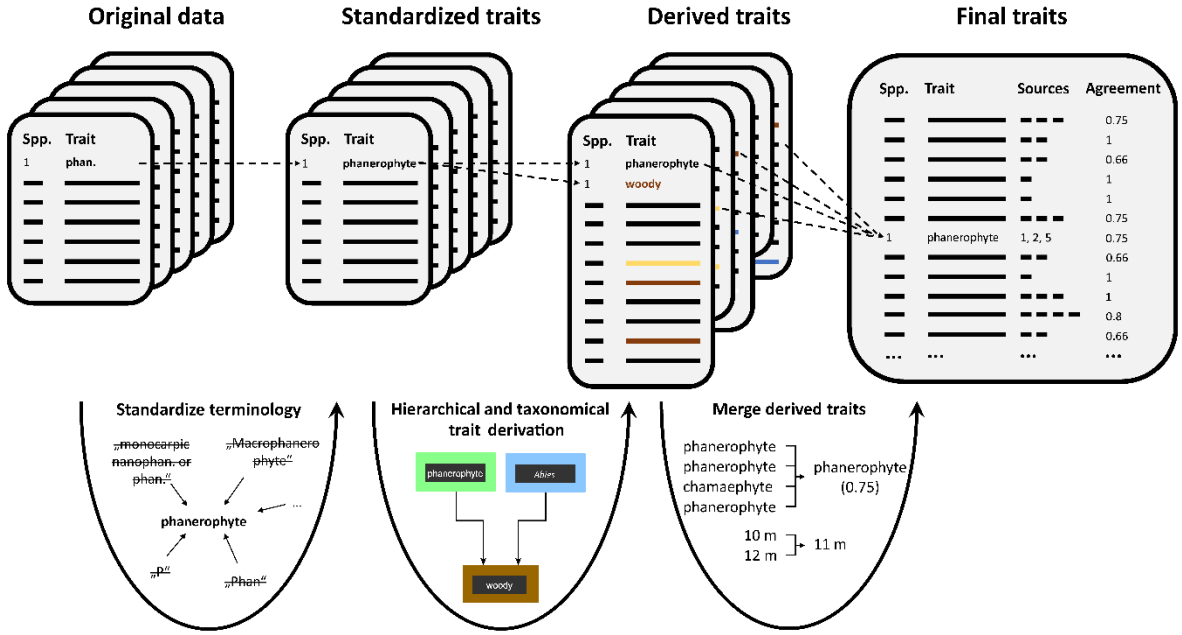

Fig. 3. Trait processing in GIFT. Original trait records entering GIFT are subjected to three processing steps: (1) Trait values are standardized with respect to language, terminology and measurement unit. (2) Additional trait values are derived hierarchically for traits that are logically nested (**Fig. S 1**), and taxonomically for species that belong to taxonomic groups that are uniform with respect to a particular trait. (3) Derived trait values are aggregated at the species level based on the consensus among resources (categorical traits) or summary statistics are computed based on the original values (numerical traits).

The original and derived trait data in GIFT may include several values per trait-species combination. To obtain a single, standardized value per trait and species, original and derived trait values are aggregated based on the consensus among resources (categorical variables, 66 % consensus threshold) or summary statistics are computed based on the original values (numerical variables, currently: mean, minimum and maximum) (**Fig. 3**). Trait derivation and aggregation for a given species are repeated each time a new trait record enters the database, such that the final values and consensus rates are continually re-evaluated in the light of new information. Throughout the entire procedure of trait processing, information can be traced back to their original reference and unstandardized value. This provides a basis for implementing advanced gap-filling (Schrodt *et al.*, 2015) and aggregation techniques (Kattge *et al.*, 2011a) in the future.

Geographic regions

As indicated in the original literature resources, each regional species checklist in GIFT unambiguously refers to a geographic region, e.g. an island, archipelago, a political or biogeographical unit, or a protected area. To make most out of the spatial delineation of the geographic regions, we assemble spatial polygons from the Biodiversity Information Standards Working Group (TDWG, 2007), the GADM database of Global Administrative Areas (Hijmans *et al.*, 2009), single island polygons extracted from GADM (see Weigelt *et al.*, 2013), the Global Island Database (UNEP-WCMC, 2013), the World Database on Protected Areas (UNEP-WCMC, 2014), or digitize regions manually according to the checklist literature resources. The regions vary in area by 13 orders of magnitude, ranging from small islands to large countries and botanical continents (**Fig. S 2**). Many regions may overlap with each other and small regions are frequently nested in larger ones (e.g. Yosemite National Park in California in the US). The degree of overlap is calculated automatically and recorded in the database to exclude overlapping entities or aggregate information for analyses.

For each original geographic region, a suite of 123 physical geographic, bioclimatic and socio-economic characteristics is computed for macroecological analyses based on the regions' spatial information and additional spatial datasets (**Fig. S 3**, **Table S 3**). Specifically, this includes (1) characteristics based on the spatial polygon itself like its area, centroid coordinates and geographic extent, (2) summary statistics (15 quantiles including minimum, median and maximum, mean, standard deviation, mode, number of unique values, Shannon diversity and number of cells) derived from raster layers like digital elevation models (Danielson & Gesch, 2011), global climatologies (e.g. CHELSA; Karger *et al.*, 2017) or human population density (Doxsey-Whitfield *et al.*, 2015), and (3) miscellaneous metrics calculated from additional spatial resources like biogeographic region affinity (Takhtajan, 1986) or island isolation (Weigelt & Kreft, 2013) (**Fig. S 3**c).

For families and higher taxonomic groups, we automatically calculate the number of all species, native species, naturalized species and endemic species for all regions that are covered by checklists for the given combination of taxonomic group and floristics status. Additionally, we calculate for the same taxonomic groups and floristic subsets the percent trait coverage for all functional traits covered by the database. It is hence possible to extract and visualize for which regions and taxa what information in terms of species checklists and functional traits is available. Based on the various checklist resources available for each geographic region, we decide whether the checklist information should theoretically completely cover the whole native vascular or angiosperm flora. This, however, is only a rough and subjective estimate and given the huge amount of unexplored plant diversity especially in the tropics and only partial completeness of the according Floras, it needs further evaluation. To this end, we are currently

incorporating species numbers and richness estimates from the literature (Frodin, 2001; Kreft & Jetz, 2007) into the database and develop workflows to compare them to the species numbers derived from the checklists. Regions deviating considerably from these literature values can be excluded from analyses if needed. The same way regional trait coverage can be used to exclude regions with little trait information from analyses on trait patterns.

Versioning

This paper describes GIFT version 1.0. New data are incorporated into GIFT in chunks and each time new data are added or workflows are modified, a new version is released. Changes will be documented at http://gift.uni-goettingen.de/about. Old versions are backed up and can be restored to reproduce analyses carried out on older versions of the database.

Current state

Geographic coverage

Initially, GIFT started with the collection of Floras and checklists for oceanic islands and the basic workflows have been developed for various projects focusing on island plant diversity (Weigelt, 2015; Weigelt *et al.*, 2016). Island floras usually host a comparatively limited set of species and have clearly defined geographic boundaries. As such, they have attracted a lot of scientific interest in the past, leading to a high availability of island Floras and checklists. GIFT therefore offers a very comprehensive overview over the floristic composition of 1,845 of the world's islands, which has already led to a variety of studies on island biodiversity patterns and their determinants (Weigelt *et al.*, 2013; Cabral *et al.*, 2014; e.g. Weigelt *et al.*, 2015; Weigelt *et al.*, 2016; Lenzner *et al.*, 2017). More recently, GIFT has been expanded to mainland floras, currently covering 1,048 distinct regions, to support comparative analyses of continental and insular floras (e.g. König *et al.*, 2017) and extensive studies of global plant diversity.

In total, GIFT currently includes 2,963,438 species-by-region occurrences for 315,164 standardized species names across 2,893 geographic regions covering the whole globe. For 92.7 % of the occurrences the native status and for 47.5 % endemism is reported. 2,062 have at least one checklist for all native vascular plants, together covering all floristic kingdoms and biomes and 79.1 % of the earth's land surface excluding Antarctica (**Fig. 4**a). After removing overlapping entities to avoid pseudo-replication, up to 1,841 regions and 58.2 % land surface coverage remain when prioritizing small entities (> 100 km²) over large entities, and 1,555 regions and 73.1 % land surface coverage remain when prioritizing large entities over small entities (single islands always prioritized over island groups). Geographic coverage varies with focal taxonomic group (**Fig. 4**, **Table 1**) and floristic status (**Fig. S 4**), and is highest for native species. The largest gaps for native vascular plant floras are currently located in Tropical Africa, the Middle East, Central Eurasia, and South East Asia (**Fig. 4**). Data gaps in GIFT do not necessarily represent true knowledge gaps. Floras of the countries of the former USSR, West Africa, Madagascar, Java and India, for example, are available and are currently in the process of being incorporated.

Since many Floras refer to entire countries of various sizes, and some of the resources in GIFT use broad distributional classifications (e.g. WCSP, 2012; BGCI, 2017), many mainland regions in GIFT are relatively large (mean area = 170,287 km², median = 30,454 km²), especially in comparison to an average island (3,265 km²; **Fig. S 2**). However, GIFT also includes mainland regions of small sizes like protected areas and small political units, since smaller units span smaller environmental gradients, and thus provide a tighter

link between taxonomic, functional and phylogenetic species composition and aggregated abiotic conditions (Pearson & Dawson, 2003).

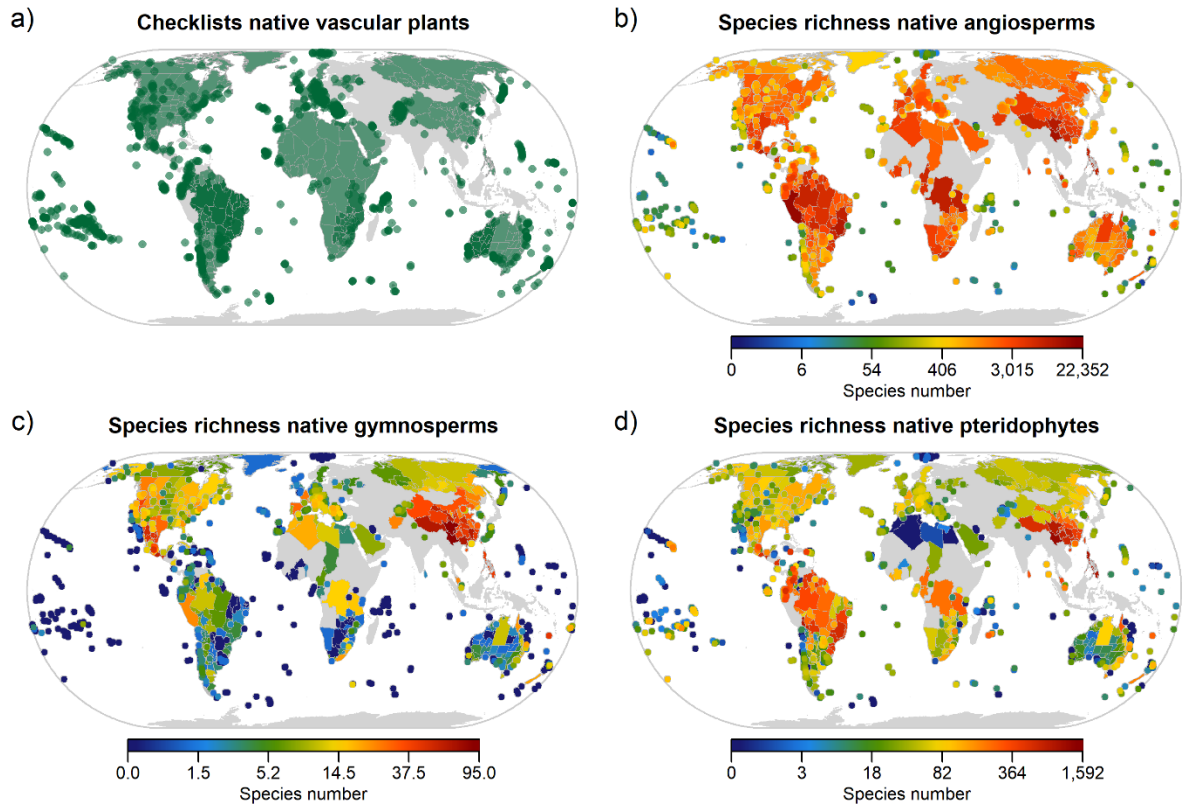

Fig. 4. Spatial coverage of checklist data currently stored in GIFT. a) Regions with checklist data for native vascular plants. Darker green shade indicates overlapping regions. b-d) Checklist coverage and species richness of major taxonomic groups for regions with theoretically complete inventories. Polygons are plotted sequentially in order of decreasing area to show smaller regions on top of larger regions, in the case where they overlap. Regions <25,000 km² are plotted as points.

Taxonomic coverage

GIFT currently includes 324,136 taxonomically standardized species from all major groups of land plants (Embryophyta). 277,580 of which are resolved to accepted species names. The focus for the collection of species lists and traits lies on vascular plants (Tracheophyta, 322,002 species) and in particular on angiosperms (Angiospermae; 308,963 species; **Table 1**). On average, 79.3% of all accepted species per plant family according to TPL are covered by distribution data. Taxonomic coverage of distribution data does not show a significant phylogenetic signal (Abouheif's Cmean = 0.03, p = 0.142; Abouheif, 1999), i.e. it exhibits no detectable bias towards certain clades (**Fig. 5**). The 324,136 species names in total derive from 717,117 unstandardized original names (after genus name correction and exclusion of hybrid names) that differ in spelling or in the availability of author names or infraspecific information. 98.2 % of all original names could be matched and standardized to an existing species name using our approach to match TPL or using the TNRS API. For 90.5 % of all names, the synonymy could be resolved. Only 3.6 % of

all working names are names that were adopted unchanged from the original names because they could not be adequately matched to taxonomic resources.

Table 1. Current content of GIFT for selected major plant groups in terms of number of regions with supposedly full inventories for native species, unstandardized taxonomic names, standardized species names, species with resolved taxonomy, and trait records.

Taxonomic group	Regions	Names	Species	Species resolved	Trait records
Embryophyta	53	717117	324136	277580	2307100
Tracheophyta	2062	714781	322002	275610	2306973
Pteridophyta	2079	24241	11888	8408	54772
Gymnospermae	2211	4031	1151	1051	12352
Angiospermae	2218	686509	308963	266151	2239849
Orchidaceae	2478	64508	28155	27029	192332
Asteraceae	2218	58492	27755	24450	167300
Fabaceae	2218	46999	21000	18416	145895
Poaceae	2431	38464	12368	11215	130492
Rubiaceae	2431	29485	14260	13545	96684
Lamiaceae	2431	18120	7882	7560	61708

Trait coverage

In total, there are 3,475,337 original trait records referring to 550,892 original taxon names. Hierarchical trait derivation yields an additional 1,261,718 trait records. After aggregating original and derived trait records, i.e. resolving species names and combining trait records for identical species, 2,307,100 species-trait combinations for 267,978 standardized species remain for ecological analyses (**Table 1**).

The majority of trait information in GIFT refers to morphological characteristics (**Table S 1**) such as woodiness (234,214 species) climbing habit (223,280 species), or growth form (213,372 species). Life history traits such as life form (100,607 species) or life cycle (84,206 species) are the second most common trait category. Other categorical traits are considerably rarer, e.g. photosynthetic pathway (31,534 species), dispersal syndrome (8,204 species), or pollination syndrome (4,511 species). Also quantitative traits such as maximum plant height (53,449 species), mean seed mass (23,874 species) or mean specific leaf area (2,304 species) are comparatively poorly covered. As such, GIFT represents a complimentary resource to existing trait databases which provide more records for numerical traits frequently measured in the field at the individual level (Pérez-Harguindeguy *et al.*, 2013), but have considerable lower coverage in terms of whole plant traits like, for example, growth form (84,459 species in BIEN 4.1 (Enquist *et al.*, 2016) and 99,217 species in TRY 4.1 (Kattge *et al.*, 2011b)) or life form (12,708 species in TRY 4.1).

To illustrate patterns in the geographic and taxonomic trait coverage of GIFT, we use the overall coverage across all traits as well as four exemplary traits (growth form, plant height, life form and seed mass). Geographically, most trait information per species is available in Europe and some comparatively species-poor temperate islands (**Fig. 6**a). Also, non-tropical parts of the Americas, Africa and Australia are well

covered, whereas tropical regions in Africa and South-East Asia are least well covered with respect to their plant functional characteristics. However, geographic coverage varies strongly among individual functional traits. Frequent traits such as growth form are available for most species in almost every floristic region, whereas the coverage of less well-covered traits is strongly dependent on the geographic scope of the main contributing resources (**Fig. 6**). Life form *sensu* Raunkiær (1907), for example, is widely available throughout Europe, but rarely reported for species in other regions of the world (**Fig. 6**d). Likewise, plant height and seed mass exhibit uneven geographical coverage distributions, with highest coverage in Australia, South Africa and Europe (**Fig. 6**c&e).

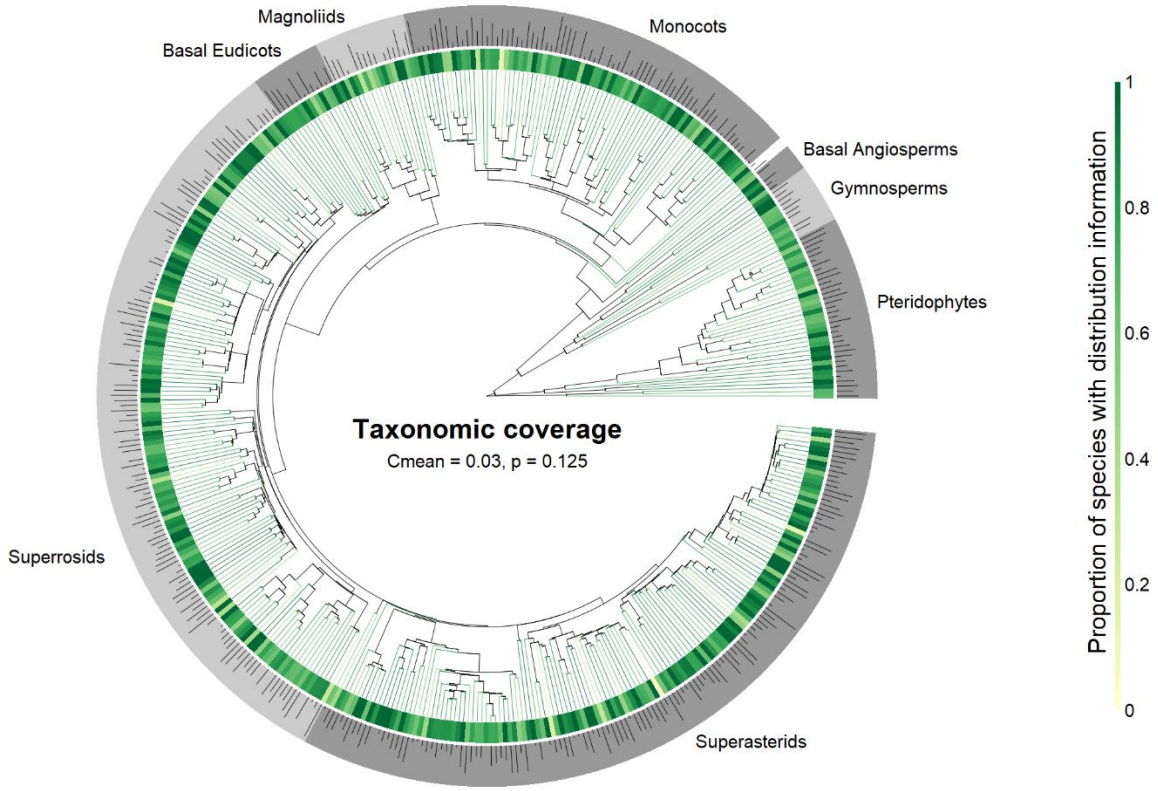

Fig. 5. Taxonomic coverage of distribution data in GIFT at the family level. Tip color and inner ring color indicate the proportion of species with distribution information relative to all species of a given family, the grey outer ring delimits major clades of vascular plants. The height of bars in the outer ring is proportional to $\log_{10}$ total family species richness. Phylogenetic signal in taxonomic coverage was assessed as Abouheif's Cmean, a measure of phylogenetic autocorrelation based on the sum of the successive squared differences between values of neighbouring tips in the phylogeny (Abouheif, 1999).

The taxonomic coverage of trait information in GIFT has small, yet significant phylogenetic signal (Cmean = 0.21, $p < 0.001$, **Fig. S 5**a). That is there is a mild bias towards certain taxonomic groups, e.g. monocots, in overall coverage of trait data. Examining phylogenetic signal at the level of individual traits reveals interesting patterns (**Fig. S 5**b-e). For example, plant height is very well covered for the graminid clade (leftmost group within the monocots, **Fig. S 5**c), and Raunkiær life form is particularly well covered in gymnosperms and monocots (**Fig. S 5**d).

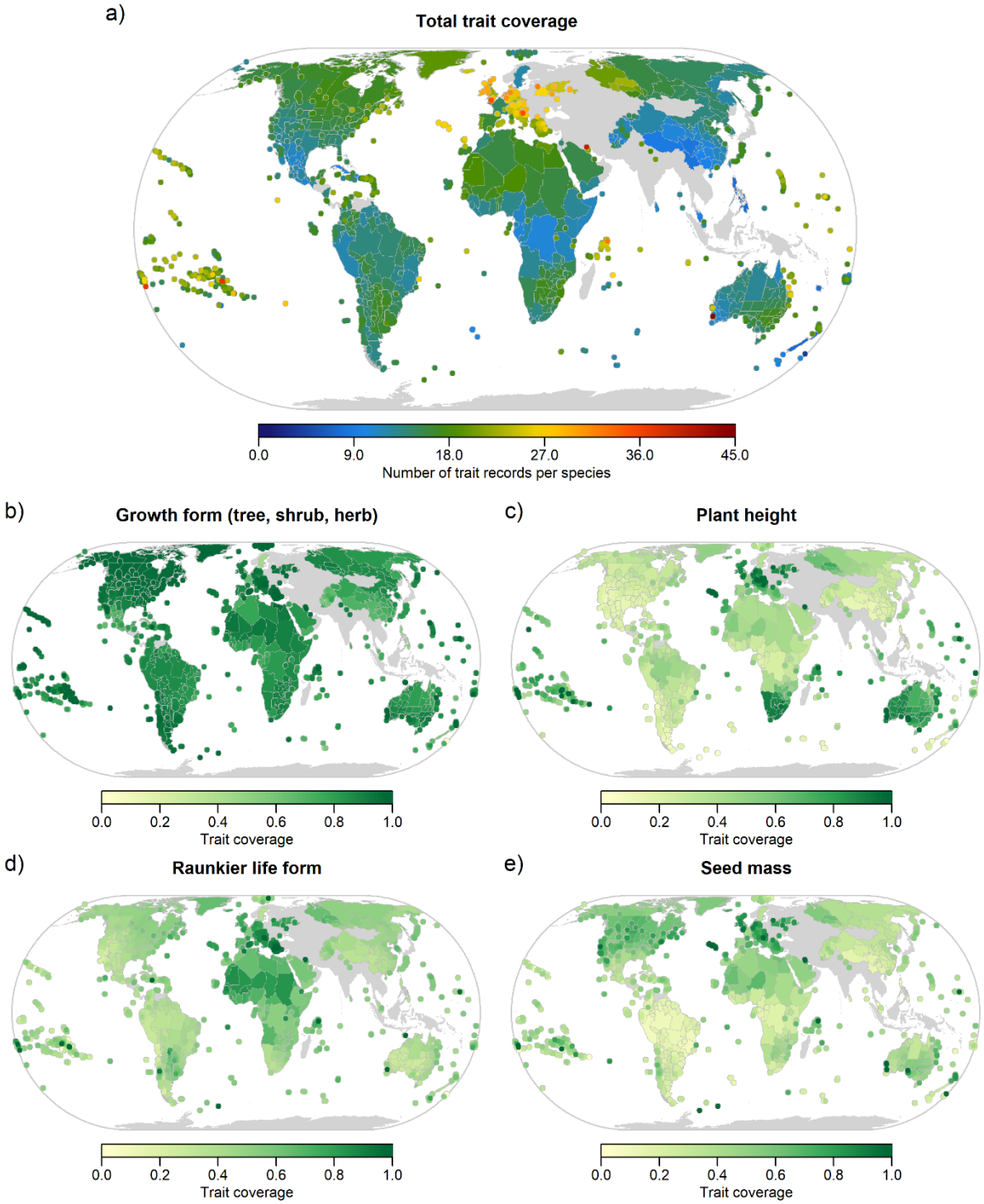

Fig. 6. (a) Total number of trait records per native angiosperm species per region and (b-e) trait coverage per region (number of native angiosperm species with trait information/number of all native angiosperm species) for exemplary traits with characteristic geographic patterns in coverage. Polygons are plotted sequentially in order of decreasing area to show smaller regions on top of larger regions, in the case where they overlap. Regions <25,000 km² are plotted as points.

Web interface

A live overview over the current content of GIFT is available through a web interface at http://gift.uni-goettingen.de. It provides summary statistics and allows producing customized richness and trait coverage maps for every combination of taxonomic group and floristic subset based on the species numbers and trait coverage values in the database. It is possible to see for which regions and taxa what information in terms of species checklists and functional traits is available and to browse the bibliographic references.

Applications and outlook

Curated regional plant species composition data from Floras and plant checklists, and diverse information on species characteristics and their environment as integrated in GIFT (**Fig. 1**) allows to move global plant diversity research beyond using species richness as a proxy for biodiversity (Barthlott *et al.*, 2005; Kreft & Jetz, 2007; Kreft *et al.*, 2008). Examining the drivers of taxonomic, functional and phylogenetic diversity and turnover (Tuomisto, 2010; Qian *et al.*, 2013; Lamanna *et al.*, 2014; Weigelt *et al.*, 2015; König *et al.*, 2017) may help to disentangle the mechanisms underlying global plant diversity more directly (Graham *et al.*, 2014). Functional biogeography, for example, combines the mechanistic focus of functional ecology with the large eco-evolutionary scales of biogeography (Violle *et al.*, 2014) and thus provides a direct link between measures of organismal performance and a wide range of abiotic and biotic conditions. Although functional biogeographical approaches already provided significant insights into patterns and drivers of functional diversity (Moles *et al.*, 2014; Reichstein *et al.*, 2014; Engemann *et al.*, 2016; Butler *et al.*, 2017), the availability and representativeness of data on plant traits and distributions remains a limiting factor. Together with distribution and floristic status information available in GIFT (e.g. native, naturalized, endemic), functional traits may help to better understand the biogeographic history of plant life on Earth and its anthropogenic stressors. Analyses of endemic species and their traits, for example, can shed light on the evolution of new species and their contribution to current biogeographic patterns (Weigelt *et al.*, 2016). Naturalized alien species and their traits help to understand the role of humans in changing plant assemblages and may teach us how new habitats and regions are colonized. Knowledge on the composition of native vs. alien floras (see www.glonaf.org; van Kleunen *et al.*, 2015; Pyšek *et al.*, 2017) allows to tackle pressing questions in invasion ecology, for example what native floras are susceptible to plant invasions and how regional plant composition changes due to the naturalization of alien species (Winter *et al.*, 2009).

Apart from direct use as data source for macroecological or biogeographical research, GIFT is also a valuable resource to validate or expand other distribution or trait datasets (**Fig. 1**). Having near-global and full taxonomic coverage of distribution data (**Fig. 4**) and several functional traits (**Table S 1**), GIFT can help to assess the representativeness of macroecological datasets and to overcome data limitations to find answers to fundamental questions in functional biogeography and macroecology (FitzJohn *et al.*, 2014; e.g. Scheffer *et al.*; König *et al.*, in prep.). It may for example help to estimate whether data from resources like GBIF or TRY are sufficiently complete or representative for analyses of a given taxon, region or functional group (Meyer *et al.*, 2016; König *et al.*, in prep.). Alternatively, GIFT can also be used to infer the floristic status of plant point occurrences (e.g. to tell apart native and non-native species), to identify unlikely or dubious occurrences or to infer local species absences. The latter may be particularly useful for species distribution modelling where random pseudo-absences are commonly used when true absences are not known (Lobo *et al.*, 2010; Barbet-Massin *et al.*, 2012). Furthermore, GIFT can be used to define regional species pools of local plant communities (Karger *et al.*, 2016), for example, for identifying

likely source regions of species that colonize oceanic islands (König *et al.*, 2019). Defining the regional species pool or inferring the floristic status may not only be important for macroecological studies but also for field projects at the local to regional scale.

The aggregated nature of data in GIFT, i.e. distribution data at the level of geographic regions and functional traits at the species level allow to achieve taxonomic and geographic coverage which currently is not available in databases of more highly resolved distribution and trait data (e.g. point occurrences and individual level trait measurements) (König *et al.*, in prep.). It is a mid-term goal of GIFT to reach full global coverage of vascular plant checklists. Already now, 79.1 % of the global land surface is covered and further Floras and checklists covering missing parts are currently processed. Realistically, GIFT will reach about 90% spatial coverage in 2019 and will serve as a representative resource for analyses of global plant diversity. In the meantime, regions already covered by coarse geographical units will be complemented by finer-scale data, and new literature resources will be included to update outdated checklists. Once the availability of checklists per region has further increased, workflows to spatially aggregate them will be developed. This will include the identification of conflicting information and choice of the best and most up-to-date information as well as derivation of the floristic status from small to large regions and vice-versa.

A major challenge regards the evaluation of checklist quality and completeness in GIFT (Hortal *et al.*, 2015). The species richness data sets currently being included allow for a comparison of expected and actual species numbers, but also the integration of other data like, for example, point occurrence information as provided by GBIF or vegetation plot data (Bruelheide *et al.*, 2018) may help to estimate completeness of the regional checklists in GIFT and eventually to update them. Furthermore, the lack of cosmopolitan or regionally common species in checklists, an uneven representation of expected higher taxa, or deviances from expected ecological relationships like, for example, the species area relationship or the latitudinal diversity gradient may be used to flag potentially incomplete checklists (Santos *et al.*, 2010). Also conflicting information, like species endemic in one region and native in another (currently 0.39 % of 246,583 species across 2,258 non-overlapping regions) or species not occurring in a region but present in a nested region (currently 5.73 % of 504,389 native species occurrences across 614 regions that are nested in 114 larger regions), can be used to flag potentially incomplete regions. Regions with incomplete checklists can then be excluded from analyses or survey effort can be included in statistical models and data acquisition can be prioritized for those regions (Meyer *et al.*, 2016).

In conclusion, GIFT offers a novel integrated database framework to study the geographic distribution of plant life across the globe. The integration of regional plant checklists with functional traits, phylogenetic relationships and regional environmental characteristics allows for the extraction of well-curated, high quality macroecological datasets for hypothesis testing and the validation and extension (Maitner, 2018)of alternative resources. In addition, the outlined database framework can serve as an example for other taxa with insufficiently complete information at the level of individual species and for an integration of comparable data types such as vegetation plots or surveys. The spatially nested structure of regions in GIFT allows for an ongoing inclusion of resources to improve inventory quality and spatial resolution in future database releases.

Data accessibility

GIFT integrates various data types from different data domains such as species names, distributions, traits, taxonomy, phylogenies and environmental data. The database structure is relational and highly complex, and data in GIFT may exhibit systematic gaps, biases and uncertainties that users need to account for. Additionally, the data stem from resources with various terms of use. Data from GIFT is therefore currently available upon request. Derived diversity metrics and individual regional checklists without sharing restrictions by the data providers will be be shared without conditions. More complex and larger scale data are available within scientific collaborations. However, we are currently developing data extraction tools (comparable to those in the BIEN R package; Maitner, 2018) that enable users to retrieve data from GIFT and prepare them for macrocological and biogeographical analyses (https://github.com/BioGeoMacro/GIFT-export). Once these tools have reached a status that allows easy handling of the complex content of the database, consideration of data restrictions of the original data sources and evaluation of potential biases, GIFT will become publicly available. Already now, naturalized alien species occurrences from GIFT are included in and accessible via the global naturalized alien flora (GloNAF) database (van Kleunen *et al.*, 2019) and first trait data (e.g. plant growth form) will be published and made publicly available via the online portals of TRY (https://www.try-db.org) and GIFT (http://gift.uni-goettingen.de). The GIFT website also provides an interactive visualization of the geographic coverage of checklist and trait information in GIFT and allows the user to discover data. Here, users can select taxonomic groups and floristic subsets to map aggregated patterns of species richness or percent trait coverage for a given trait across the covered geographic regions. Furthermore, unrestricted species distributions from GIFT will be implemented in the near future for visualization on the Map of Life website (https://mol.org/).

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Author Contributions

PW and HK conceived the GIFT database. All authors led the collection of checklist and trait data. PW and CK developed the workflows for importing and processing data in GIFT and for calculating derived variables. PW and CK performed the analyses presented here and all authors contributed to writing the manuscript.

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Supplementary Material

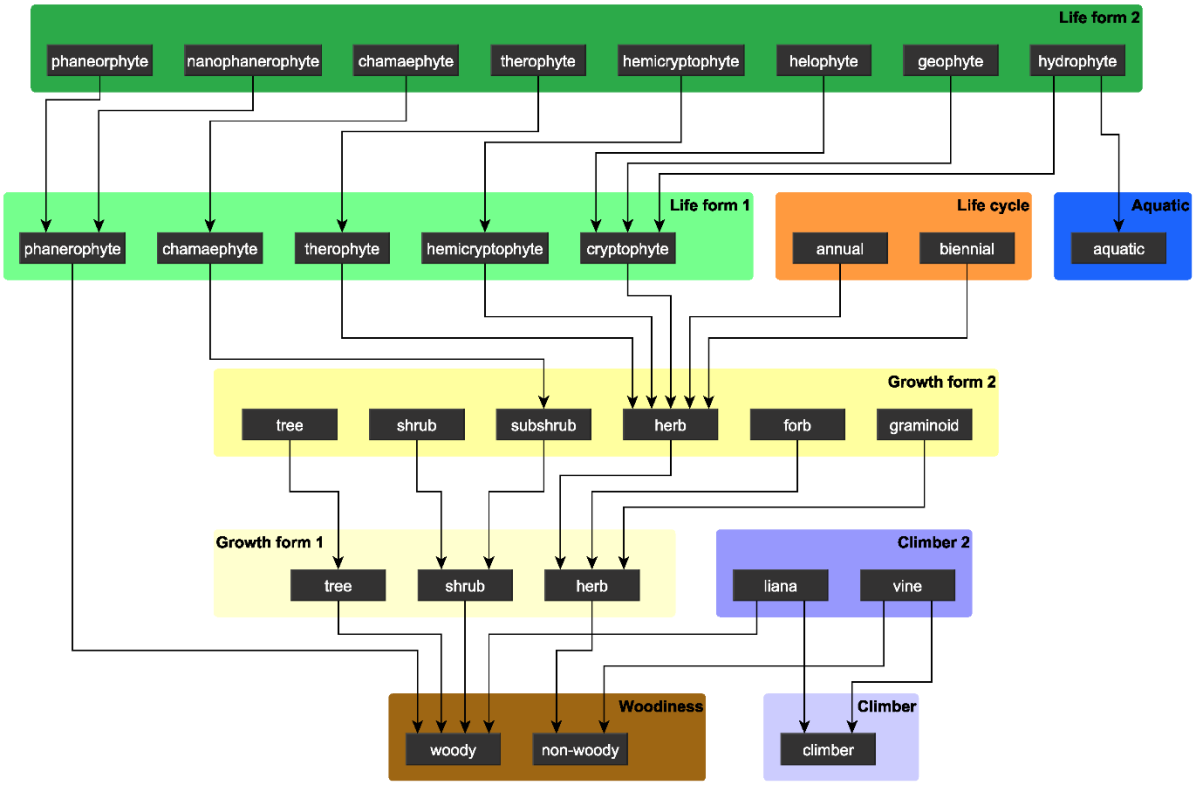

Fig. S 1. Main module of the directed graph used for hierarchical trait derivation in GIFT, defining unambiguous relationships among 30 categorical levels from five functional traits (life form, life cycle, aquatic, growth form, climber and woodiness). Some traits are represented in multiple versions (e.g. growth form) to account for varying levels of detail of original information. The full list of parent-child relationships used for trait derivation in GIFT (71 connections among 89 categorical levels) is given in **Table S 2**.

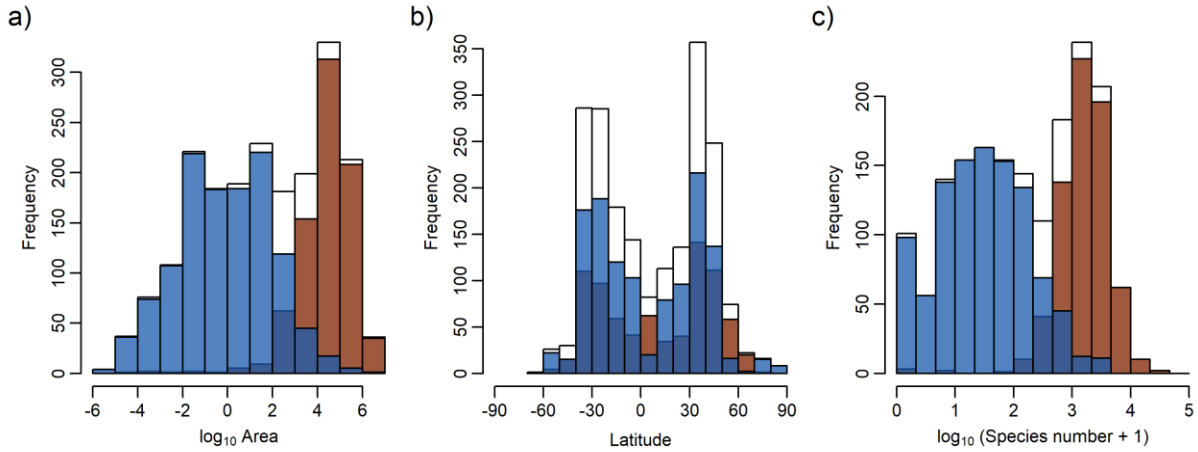

Fig. S 2. Frequency distributions of 2007 geographic regions in GIFT with information on native vascular plant species composition and spatial properties for a) region area (km²), b) latitude and c) species richness of native vascular plants. Blue bars = islands, brown = mainland regions, white = total, dark blue = overlap of mainland and island bars.

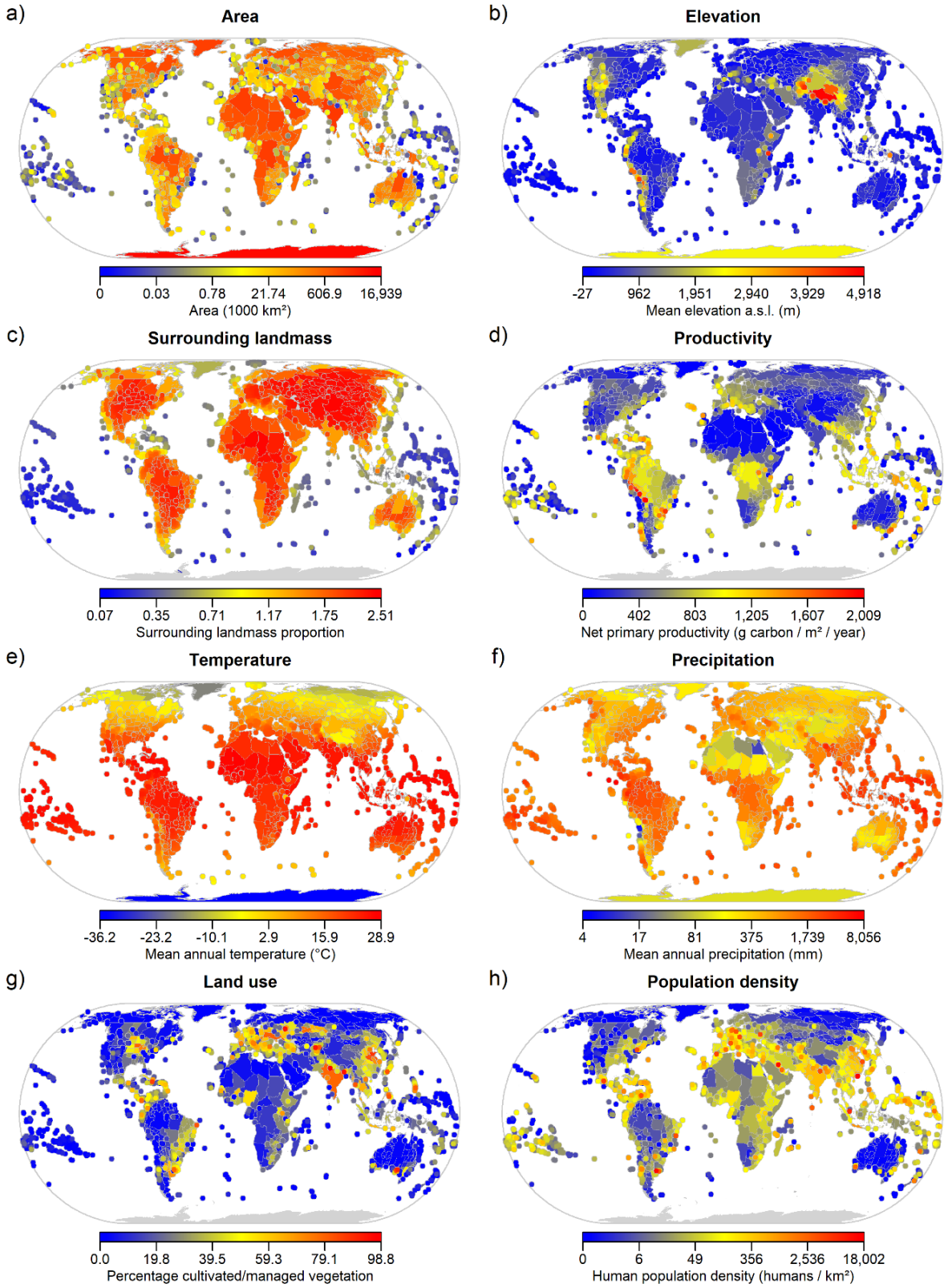

Fig. S 3. Selected environmental variables in GIFT. For a full list of geographic, environmental and socio-economic variables and source references see **Table S 3**. Polygons are plotted sequentially in order of decreasing area to show smaller regions on top of larger regions, in the case where they overlap. Regions <25,000 km² are plotted as points.

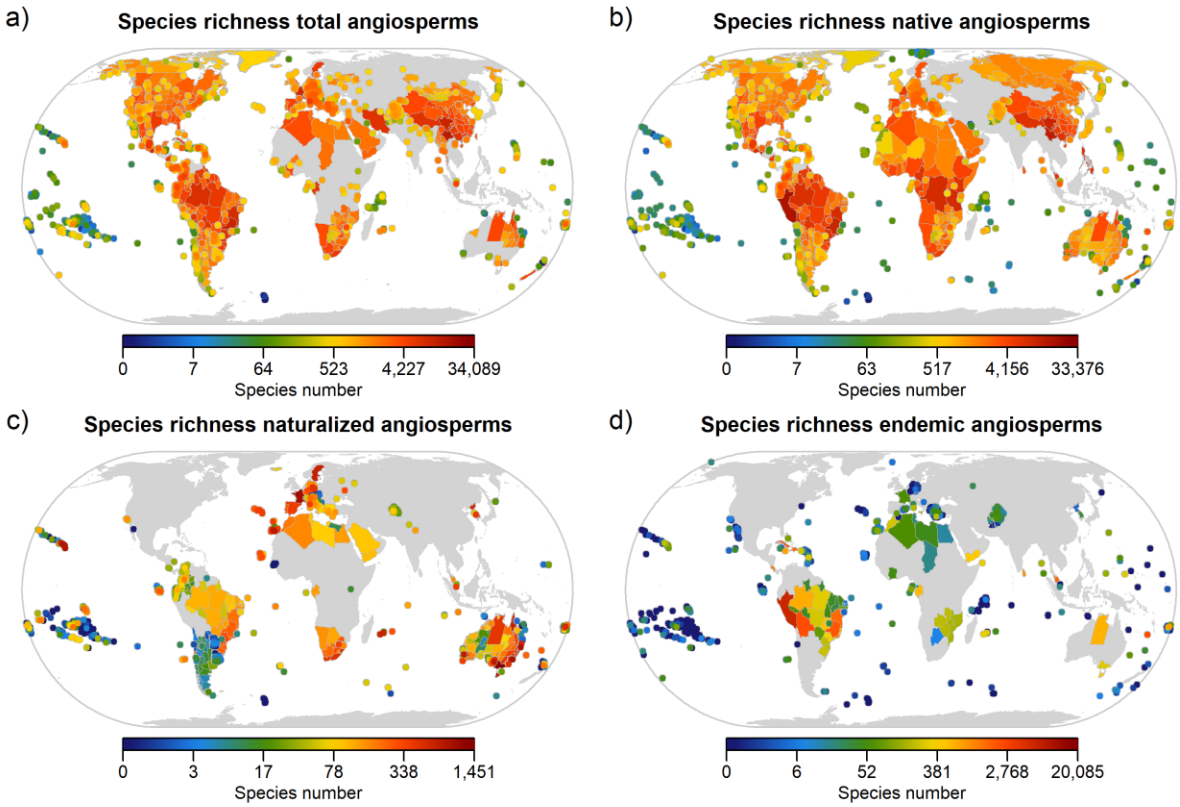

Fig. S 4. Spatial coverage of floristic subsets in GIFT. Species richness of total angiosperms (a) refers to regions with information on both native and introduced angiosperm species or species with unresolved floristic status. Most commonly resources in GIFT include information on native species (b), while information on introduced naturalized (c) and endemic species (d) is considerably rarer. Endemism information is most common for island regions. Polygons are plotted sequentially in order of decreasing area to show smaller regions on top of larger regions, in the case where they overlap. Regions <25,000 km² are plotted as points.

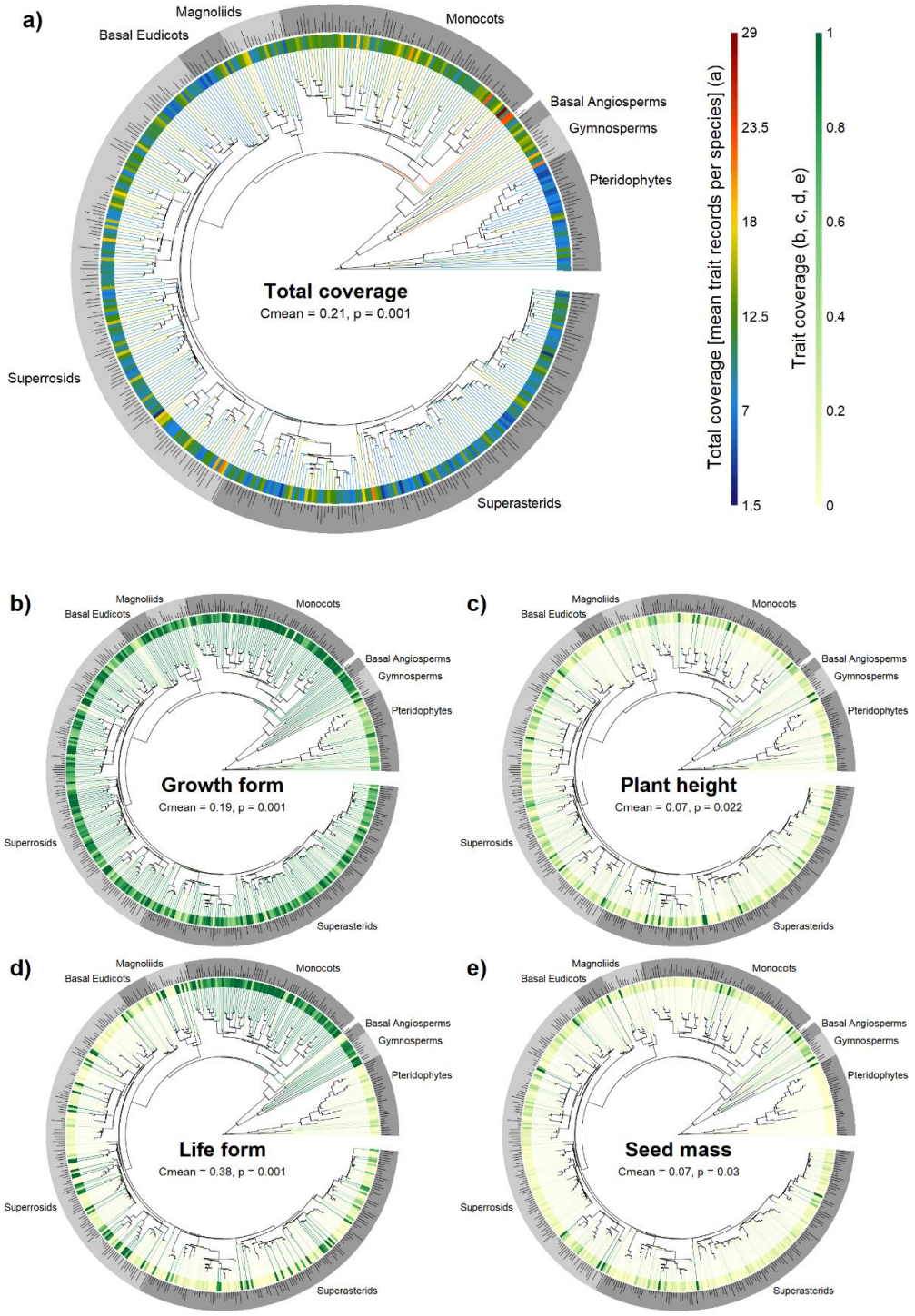

Fig. S 5. Taxonomic trait coverage of GIFT across all functional traits at the family level (a; mean trait records per species) and for four selected functional traits individually (b-e; number of species with trait information/total number of species). Tip color and inner ring color denote trait coverage per family, outer ring delimits major clades of vascular plants. The height of bars in the outer ring is proportional to $\log_{10}$ family size. Phylogenetic signal in taxonomic coverage was assessed as Abouheif's Cmean, a measure of phylogenetic autocorrelation based on the sum of the successive squared differences between values of neighbouring tips in the phylogeny (Abouheif, 1999).

Table S 1. Functional traits in GIFT, their broader trait categories, type, units and factor levels respectively and the number of species covered in GIFT.

ID	Category	Trait	Trait variant	Type	Unit/Level	Species number
1.1.1	Morphology	Woodiness	Woodiness 1	categorial	woody, non-woody, variable	234214
1.2.1	Morphology	Growth form	Growth form 1	categorial	herb, shrub, tree, other	213372
1.2.2	Morphology	Growth form	Growth form 2	categorial	herb, graminoid, forb, subshrub, shrub, tree, palm, other	165540
1.3.1	Morphology	Epiphyte	Epiphyte 1	categorial	obligatory, facultative, terrestrial	206699
1.3.2	Morphology	Epiphyte	Epiphyte 2	categorial	holoepiphyte, hemiepiphyte, prim_hemiepiphyte, sec_hemiepiphyte, facultative, terrestrial	70816
1.4.1	Morphology	Climber	Climber 1	categorial	obligatory, facultative, self-supporting	223280
1.4.2	Morphology	Climber	Climber 2	categorial	liana, vine, self-supporting	93098
1.5.1	Morphology	Parasite	Parasite 1	categorial	obligatory, facultative, independent	209609
1.6.1	Morphology	Plant height	Plant height min	numeric	m	28859
1.6.2	Morphology	Plant height	Plant height max	numeric	m	53449
1.6.3	Morphology	Plant height	Plant height mean	numeric	m	16127
1.7.1	Morphology	Aquatic	Aquatic 1	categorial	aquatic, semiaquatic, terrestrial	148432
1.8.2	Morphology	DBH	DBH max	numeric	cm	25
1.8.3	Morphology	DBH	DBH mean	numeric	cm	25
2.1.1	Life history	Lifecycle	Lifecycle 1	categorial	annual, biennial, perennial, variable	84206
2.3.1	Life history	Life form	Life form 1	categorial	phanerophyte, chamaephyte, hemicryptophyte, cryptophyte, therophyte	81198
2.3.2	Life history	Life form	Life form 2	categorial	nanophanerophyte, phanerophyte, chamaephyte, hemicryptophyte, geophyte, hydrophyte, helophyte, therophyte, lithophyte	100607
2.4.1	Life history	Deciduousness	Deciduousness 1	categorial	deciduous, evergreen, variable	8069
3.1.1	Reproduction	Self fertilization	Self fertilization 1	categorial	present, absent	3538
3.10.1	Reproduction	Seed length	Seed length min	numeric	mm	1196
3.10.2	Reproduction	Seed length	Seed length max	numeric	mm	1344
3.10.3	Reproduction	Seed length	Seed length mean	numeric	mm	535
3.11.1	Reproduction	Seed width	Seed width min	numeric	mm	100
3.11.2	Reproduction	Seed width	Seed width max	numeric	mm	277
3.12.1	Reproduction	Seed height	Seed height min	numeric	mm	7
3.12.2	Reproduction	Seed height	Seed height max	numeric	mm	148
3.13.1	Reproduction	Fruit length	Fruit length min	numeric	cm	962
3.13.2	Reproduction	Fruit length	Fruit length max	numeric	cm	1096
3.13.3	Reproduction	Fruit length	Fruit length mean	numeric	cm	520
3.14.1	Reproduction	Fruit width	Fruit width min	numeric	cm	380
3.14.2	Reproduction	Fruit width	Fruit width max	numeric	cm	432
3.14.3	Reproduction	Fruit width	Fruit width mean	numeric	cm	561
3.15.1	Reproduction	Fruit height	Fruit height min	numeric	cm	54
3.15.2	Reproduction	Fruit height	Fruit height max	numeric	cm	54
3.15.3	Reproduction	Fruit height	Fruit height mean	numeric	cm	54
3.16.1	Reproduction	Fruit type	Fruit type 1	categorial	achene, baccate, berry, capsule, drupe, follicle, lomentum, nut, pod, pome, schizocarp, siliqua, utricle, other	5883
3.17.1	Reproduction	Dehiscence	Dehiscence 1	categorial	dehiscent, indehiscent	5513
3.18.1	Reproduction	Fruit dryness	Fruit dryness 1	categorial	dry, fleshy	2559
3.19.1	Reproduction	Seed volume	Seed volume min	numeric	mm^3	2805
3.19.2	Reproduction	Seed volume	Seed volume max	numeric	mm^3	2805
3.19.3	Reproduction	Seed volume	Seed volume mean	numeric	mm^3	2805
3.2.1	Reproduction	Seed mass	Seed mass min	numeric	g	22655
3.2.2	Reproduction	Seed mass	Seed mass max	numeric	g	22655
3.2.3	Reproduction	Seed mass	Seed mass mean	numeric	g	23874
3.20.1	Reproduction	Monocarpy	Monocarpy	categorial	monocarp, polycarp	88
3.3.1	Reproduction	Dispersal syndrome	Dispersal syndrome 1	categorial	anemochorous, zoochorous, autochorous, hydrochorous, unspecialized	8204
3.3.2	Reproduction	Dispersal syndrome	Dispersal syndrome 2	categorial	anemochorous, anthropochorous, autochorous, endozoochorous, epizoochorous, hydrochorous, myrmecochorous, unspecialized, zoochorous	3003
3.4.1	Reproduction	Reproduction_sexual	Reproduction sexual 1	categorial	dioecious, monoecious, bisexual	2699
3.5.1	Reproduction	Reproduction_asexual	Reproduction asexual 1	categorial	present, absent	1703
3.5.2	Reproduction	Reproduction_asexual	Reproduction asexual 2	categorial	above-ground, below-ground	12
3.6.1	Reproduction	Pollination syndrome	Pollination syndrome 1	categorial	wind, water, insect, bird, bat, other	4511
3.6.2	Reproduction	Pollination syndrome	Pollination syndrome 2	categorial	wind, water, bee, beetle, ant, butterfly, moth, fly, insect, bird, bat, other	4014

3.7.1	Reproduction	Flowering time	Flowering start	categorial	Jan, Feb, Mar, Apr, May, Jun, Jul, Aug, Sep, Oct, Nov, Dec, variable	7013
3.7.2	Reproduction	Flowering time	Flowering end	categorial	Jan, Feb, Mar, Apr, May, Jun, Jul, Aug, Sep, Oct, Nov, Dec, variable	6102
3.8.1	Reproduction	Fruiting time	Fruiting start	categorial	Jan, Feb, Mar, Apr, May, Jun, Jul, Aug, Sep, Oct, Nov, Dec, variable	514
3.8.2	Reproduction	Fruiting time	Fruiting end	categorial	Jan, Feb, Mar, Apr, May, Jun, Jul, Aug, Sep, Oct, Nov, Dec, variable	512
3.9.1	Reproduction	Seeds_per_fruit	Seeds per fruit	categorial	0, 1-10, 11-100, 101-1000, >1000	783
4.1.1	Physiology	Specific Leaf Area (SLA)	SLA min	numeric	cm^2/g	252
4.1.2	Physiology	Specific Leaf Area (SLA)	SLA max	numeric	cm^2/g	252
4.1.3	Physiology	Specific Leaf Area (SLA)	SLA mean	numeric	cm^2/g	2304
4.10.1	Physiology	Carnivory	Carnivory	categorial	carnivorous, non-carnivorous	1769
4.2.1	Physiology	Photosynthetic pathway	Photosynthetic pathway	categorial	C3, C4, CAM	31534
4.3.1	Physiology	Stem specific density (SSD)	SSD min	numeric	mg/cm^3	371
4.3.2	Physiology	Stem specific density (SSD)	SSD max	numeric	mg/cm^3	371
4.3.3	Physiology	Stem specific density (SSD)	SSD mean	numeric	mg/cm^3	1094
4.4.3	Physiology	Leaf size	Leaf size mean	numeric	cm^2	1708
4.5.1	Physiology	Nitrogen fixer	Nitrogen fix 1	categorial	yes, no	10143
4.6.1	Physiology	Leaf length	Leaf length min	numeric	cm	5787
4.6.2	Physiology	Leaf length	Leaf length max	numeric	cm	6581
4.6.3	Physiology	Leaf length	Leaf length mean	numeric	cm	132
4.7.1	Physiology	Leaf width	Leaf width min	numeric	cm	5203
4.7.2	Physiology	Leaf width	Leaf width max	numeric	cm	5791
4.7.3	Physiology	Leaf width	Leaf width mean	numeric	cm	132
4.8.3	Physiology	Leaf thickness	Leaf thickness mean	numeric	mm	134
4.9.1	Physiology	Leaf dry matter content (LDMC)	LDMC min	numeric	mg/g	483
4.9.2	Physiology	Leaf dry matter content (LDMC)	LDMC max	numeric	mg/g	483
4.9.3	Physiology	Leaf dry matter content (LDMC)	LDMC mean	numeric	mg/g	483
5.1.1	Genetics	Chromosome number	Chromosome number	text		730
6.1.1	Ecology	Elevational range	Elevational range min	numeric	m AMSL	53024
6.1.2	Ecology	Elevational range	Elevational range max	numeric	m AMSL	54767
6.1.3	Ecology	Elevational range	Elevational range mean	numeric	m AMSL	8170
6.2.1	Ecology	Bedrock	Bedrock 1	text		290
6.3.1	Ecology	Habitat	Habitat 1	text		35542

Table S 2. Links between parent traits and derived traits used in the hierarchical trait derivation in GIFT.

Trait ID parent	Trait parent	Trait value parent	Trait ID child	Trait child	Trait value child
3.6.2	Pollination syndrome 2	ant	3.6.1	Pollination syndrome 1	insect
3.6.2	Pollination syndrome 2	wind	3.6.1	Pollination syndrome 1	wind
3.6.2	Pollination syndrome 2	water	3.6.1	Pollination syndrome 1	water
3.6.2	Pollination syndrome 2	bee	3.6.1	Pollination syndrome 1	insect
3.6.2	Pollination syndrome 2	beetle	3.6.1	Pollination syndrome 1	insect
3.6.2	Pollination syndrome 2	butterfly	3.6.1	Pollination syndrome 1	insect
3.6.2	Pollination syndrome 2	moth	3.6.1	Pollination syndrome 1	insect
3.6.2	Pollination syndrome 2	bird	3.6.1	Pollination syndrome 1	bird
3.6.2	Pollination syndrome 2	bat	3.6.1	Pollination syndrome 1	bat
3.3.2	Dispersal syndrome 2	anemochorous	3.3.1	Dispersal syndrome 1	anemochorous
3.3.2	Dispersal syndrome 2	zoochorous	3.3.1	Dispersal syndrome 1	zoochorous
3.3.2	Dispersal syndrome 2	endozoochorous	3.3.1	Dispersal syndrome 1	zoochorous
3.3.2	Dispersal syndrome 2	epizoochorous	3.3.1	Dispersal syndrome 1	zoochorous
3.3.2	Dispersal syndrome 2	myrmecochorous	3.3.1	Dispersal syndrome 1	zoochorous
3.3.2	Dispersal syndrome 2	autochorous	3.3.1	Dispersal syndrome 1	autochorous
3.3.2	Dispersal syndrome 2	hydrochorous	3.3.1	Dispersal syndrome 1	hydrochorous
3.3.2	Dispersal syndrome 2	anthropochorous	3.3.1	Dispersal syndrome 1	unspecialized
3.3.2	Dispersal syndrome 2	unspecialized	3.3.1	Dispersal syndrome 1	unspecialized
2.3.2	Life form 2	nanophanerophyte	2.3.1	Life form 1	phanerophyte
2.3.2	Life form 2	phanerophyte	2.3.1	Life form 1	phanerophyte
2.3.2	Life form 2	chamaephyte	2.3.1	Life form 1	chamaephyte
2.3.2	Life form 2	hemicryptophyte	2.3.1	Life form 1	hemicryptophyte
2.3.2	Life form 2	geophyte	2.3.1	Life form 1	cryptophyte
2.3.2	Life form 2	hydrophyte	2.3.1	Life form 1	cryptophyte
2.3.2	Life form 2	hydrophyte	1.7.1	Aquatic 1	aquatic
2.3.2	Life form 2	helophyte	2.3.1	Life form 1	cryptophyte
2.3.2	Life form 2	therophyte	2.3.1	Life form 1	therophyte
2.3.1	Life form 1	chamaephyte	1.2.2	Growth form 2	subshrub
2.3.1	Life form 1	hemicryptophyte	1.2.2	Growth form 2	herb
2.3.1	Life form 1	cryptophyte	1.2.2	Growth form 2	herb
2.3.1	Life form 1	therophyte	1.2.2	Growth form 2	herb
1.4.2	Climber 2	vine	1.4.1	Climber 1	obligatory
1.4.2	Climber 2	vine	1.1.1	Woodiness 1	non-woody
1.4.2	Climber 2	liana	1.4.1	Climber 1	obligatory
1.4.2	Climber 2	liana	1.1.1	Woodiness 1	woody
1.4.2	Climber 2	self-supporting	1.4.1	Climber 1	self-supporting
1.3.2	Epiphyte 2	holoepiphyte	1.3.1	Epiphyte 1	obligatory
1.3.2	Epiphyte 2	hemiepiphyte	1.3.1	Epiphyte 1	obligatory
1.3.2	Epiphyte 2	prim hemiepiphyte	1.3.1	Epiphyte 1	obligatory
1.3.2	Epiphyte 2	sec hemiepiphyte	1.3.1	Epiphyte 1	obligatory
1.3.2	Epiphyte 2	facultative	1.3.1	Epiphyte 1	facultative
1.3.2	Epiphyte 2	terrestrial	1.3.1	Epiphyte 1	terrestrial
1.2.2	Growth form 2	herb	1.2.1	Growth form 1	herb
1.2.2	Growth form 2	graminoid	1.2.1	Growth form 1	herb
1.2.2	Growth form 2	forb	1.2.1	Growth form 1	herb
1.2.2	Growth form 2	subshrub	1.2.1	Growth form 1	shrub
1.2.2	Growth form 2	shrub	1.2.1	Growth form 1	shrub
1.2.2	Growth form 2	tree	1.2.1	Growth form 1	tree
1.2.2	Growth form 2	palm	1.2.1	Growth form 1	other
1.2.2	Growth form 2	other	1.2.1	Growth form 1	other
1.2.1	Growth form 1	herb	1.1.1	Woodiness 1	non-woody
1.2.1	Growth form 1	shrub	1.1.1	Woodiness 1	woody
1.2.1	Growth form 1	tree	1.1.1	Woodiness 1	woody
2.1.1	Lifecycle 1	biennial	1.2.2	Growth form 2	herb
2.1.1	Lifecycle 1	annual	1.2.2	Growth form 2	herb
2.3.1	Life form 1	phanerophyte	1.1.1	Woodiness 1	woody
3.6.2	Pollination syndrome 2	insect	3.6.1	Pollination syndrome 1	insect
3.6.2	Pollination syndrome 2	other	3.6.1	Pollination syndrome 1	other
3.6.2	Pollination syndrome 2	fly	3.6.1	Pollination syndrome 1	insect
1.5.1	Parasite 1	obligatory	1.3.2	Epiphyte 2	terrestrial
3.16.1	Fruit type 1	achene	3.17.1	Dehiscence 1	indehiscent
3.16.1	Fruit type 1	berry	3.17.1	Dehiscence 1	indehiscent
3.16.1	Fruit type 1	drupe	3.17.1	Dehiscence 1	indehiscent
3.16.1	Fruit type 1	capsule	3.17.1	Dehiscence 1	dehiscent
3.16.1	Fruit type 1	baccate	3.17.1	Dehiscence 1	indehiscent
3.16.1	Fruit type 1	drupe	3.17.1	Dehiscence 1	indehiscent
3.16.1	Fruit type 1	lomentum	3.17.1	Dehiscence 1	indehiscent
3.16.1	Fruit type 1	nut	3.17.1	Dehiscence 1	indehiscent
3.16.1	Fruit type 1	pod	3.17.1	Dehiscence 1	dehiscent
3.16.1	Fruit type 1	siliqua	3.17.1	Dehiscence 1	dehiscent
3.16.1	Fruit type 1	utricle	3.17.1	Dehiscence 1	indehiscent

Table S 3. Groups of physical geographical, environmental and socio-economic variables in GIFT. Metrics of datasets of type miscellaneous are calculated based on the regions polygons and eventually additional resources cited under "References". For resources of type raster, summary statistics (15 quantiles including minimum, median and maximum, mean, standard deviation, mode, number of unique values, Shannon diversity and number of cells) are calculated for all raster cells that fall into a region or are crossed by its border. Please revisit the original publications of the raster resources for more information.

Dataset	Type	Reference
Accessibility to cities	Raster	Weiss *et al.* 2018
Archipelago	Miscellaneous	
Area of ice cover today and during last glacial maximum	Miscellaneous	Ehlers *et al.* 2011
Area of region and largest included landmass	Miscellaneous	
Biome	Miscellaneous	Dinerstein *et al.* 2017
Canopy height	Raster	Simard *et al.* 2011
Centroid latitude and longitude coordinates	Miscellaneous	
Chelsa 1.2 bioclimatic variables	Raster	Karger *et al.* 2017
Consensus land cover	Raster	Tuanmu & Jetz 2014
Distance to nearest mainland	Miscellaneous	Weigelt *et al.* 2013
GDP from satellite	Raster	Ghosh *et al.* 2010
Geographic extent of region and largest included landmass	Miscellaneous	
Global aridity and potential evapotranspiration	Raster	Zomer *et al.* 2008
Global cloud cover	Raster	Wilson & Jetz 2016
Global gridded soil information	Raster	Hengl *et al.* 2017
Global habitat heterogeneity	Raster	Tuanmu & Jetz 2015
Global multi-resolution terrain elevation data	Raster	USGS 2011
Global soil water balance	Raster	Trabucco & Zomer 2010
Gridded population of the world 4	Raster	Doxsey-Whitfield *et al.* 2015
Human footprint	Raster	Venter *et al.* 2016
Last glacial maximum mainland connection, area and number of landmass entities	Miscellaneous	Weigelt *et al.* 2016, Weatherall *et al.* 2015
Last of the wild human influence	Raster	WCS & CIESIN 2005a, 2005b
MODIS gross and net primary productivity	Raster	Zhao & Running 2010
Number of landmass entities comprised by region	Miscellaneous	
Past climate change velocity	Raster	Weigelt *et al.* 2013, Hijmans *et al.* 2005
Species richness at nearest mainland	Miscellaneous	Weigelt *et al.* 2013, Kreft & Jetz 2007
Surrounding landmass proportion	Miscellaneous	Weigelt *et al.* 2013
Takhtajan floristic region	Miscellaneous	Takhtajan 1986
TDWG region	Miscellaneous	Brummitt 2001
Tree density	Raster	Crowther *et al.* 2015
WorldClim 1.4 last glacial maximum climate	Raster	Hijmans *et al.* 2005
WorldClim 2.0 bioclimatic variables	Raster	Fick & Hijmans 2017

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Appendix S 1. Literature resources used to assemble the species checklist and trait data in GIFT.

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