METHODS AND TOOLS

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

Patrick Weigelt | Christian König | Holger Kreft

Abstract

Aim: To understand how functional 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. Range maps only exist for a small subset of all plant species and digitally available point-occurrence information is biased both geographically and taxonomically. Floras and checklists represent an alternative, yet rarely used potential source of information. They contain highly curated information about the species composition of a clearly defined area, and 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.

Location: Global.

Taxon: Land plants (Embryophyta).

Methods: GIFT integrates plant distributions from regional Floras and checklists with functional traits, phylogenetic information, and region-level geographic, environmental and socio-economic data. It 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.

Results: GIFT 1.0 holds species lists for 2,893 regions across the whole globe including ~315,000 taxonomically standardized species names (i.e. 80% of all known land plant species) and ~3 million species-by-region occurrences. Based on a hierarchical and taxonomical derivation scheme, GIFT contains 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.).

Main conclusions: 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 with 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. cacti in Barthlott et al., 2015; conifers in Farjon & Filer, 2013) or regions (e.g. woody plants of China in Fang, Wang, & Tang, 2011; Europe in Tutin et al., 1964–1980). 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. König, Weigelt, & Kreft, 2017; Morueta-Holme et al., 2013; Weigelt et al., 2015).

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, Weigelt, & Kreft, 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 of all plant species at comparatively coarse spatial grains (e.g. BIEN for the Americas; Enquist, Condit, Peet, Schildhauer, & Thiers, 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. Kattge, Diaz, et al., 2011; RBG Kew, 2008) 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 (Figure 1). As such, the database architecture, workflows and data of GIFT facilitate a wide array of macroecological and biogeographical analyses and may help to extend 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.

CONTENT AND STRUCTURE OF GIFT

2.1 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 labour-intensive to convert into structured data. These resources, however, are increasingly being made digitally available (e.g. Acevedo-Rodríguez & Strong, 2007; Zuloaga, Morrone, & Belgrano, 2004) 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 Figure 2). All this information is linked to metadata on the included literature references, species lists, traits and geographic entities (white boxes in Figure 2). Semi-automated workflows allow a fast and reliable integration of new datasets and provide extensive curated and derived information (blue boxes in Figure 2): (i) taxonomic match-up with taxonomic resources and name standardization (Section 2.3), (ii) taxon placement according to a taxonomic backbone and phylogeny (Section 2.4), (iii) trait standardization and hierarchical and taxonomic trait derivation (Section 2.5), (iv) calculation of regional summary statistics like species richness or trait coverage (Section 2.6) and (v) extraction and computation of geographic, environmental and socio-economic regional characteristics (Section 2.6). 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).

2.2 | Checklists

GIFT currently contains 3,826 species lists referring to 2,893 different geographic regions which are based on 429 original checklist data sources (Figure 2, Appendix 1). 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 list of all data references is available in Appendix 1 and on the GIFT website http://gift.uni-goettingen.de. Publications based on GIFT are requested to cite the checklist resources the analyses are based upon (e.g in Weigelt, Steinbauer, Cabral, & Kreft, 2016). Checklists and inventories stem from publicly available sources as well as from unpublished sources with restricted access (4.2%). Metadata of 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 (Figure 2, “species occurrences”).

FIGURE 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 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 [Colour figure can be viewed at wileyonlinelibrary.com]
FIGURE 2  Simplified structure of the Global Inventory of Floras and Traits database. Metadata 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) [Colour figure can be viewed at wileyonlinelibrary.com]
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 as binary variables whether the occurrence and the different kinds of floristic status information are questionable or doubtful according to the literature source. 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 (Figure 2). Routines to export checklists from GIFT and their metadata as Darwin Core (Wieczorek et al., 2014, 2012) and Humboldt Core (Guralnick, Walls, & Jetz, 2018) archives, respectively, are currently being developed to allow easy integration with other kinds of distribution data (e.g. point occurrences from GBIF).

### 2.3 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. 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. IPNI, 2012; Mabberley, 2008). 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 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 (Figure 2). The taxonomic standardization in GIFT is thus 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.

### 2.4 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 are 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 group.

All seed plant species are linked to a global phylogeny with 353,185 terminal taxa (Smith & Brown, 2018). 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.

2.5 Functional traits

Species in GIFT are linked to functional trait information from currently 155 original resources. Most trait data come from 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. BGCI, 2017; Zotz, 2013). The range of functional traits currently covered by GIFT reflects different aspects of plant morphology, life history, reproduction, physiology, genetics and ecology (Table S1). 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. Enquist et al., 2016; Kattge, Díaz, et al., 2011).

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 (Garnier et al., 2017; Pérez-Harguindeguy et al., 2013) (Figure 3) using defined categorical levels (categorical traits) and units of measurement (numerical traits) (Table S1). 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 logical imputation, which makes use of logical relationships among many functional traits based on their definitions (Figure 3). For example, the value “tree” in the trait growth form implies the value “woody” in the trait woodiness. As such, logical imputation increases the amount of trait information in GIFT and 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 (Figure S1). A tabular version of the graph is stored in the database for modifications (Table S2). A similar derivation approach is implemented for taxonomic groups that are uniform with respect to a particular trait (taxonomic trait derivation).

**FIGURE 3** Trait processing in the Global Inventory of Floras and Traits (GIFT). Original trait records entering GIFT are subjected to three processing steps: (i) Trait values are standardized with respect to language, terminology and measurement unit. (ii) Additional trait values are derived hierarchically for traits that are logically nested (colored rows under “derived traits”, see also Figure S1), and taxonomically for species that belong to taxonomic groups that are uniform with respect to a particular trait. (iii) 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) [Colour figure can be viewed at wileyonlinelibrary.com]
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.

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) (Figure 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 (Schrödt et al., 2015) and aggregation techniques (Kattge, Ogle, et al., 2011) in the future.

### 2.6 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. We assemble spatial polygons for these regions from the Biodiversity Information Standards Working Group (TDWG, 2007), the GADM database of Global Administrative Areas (Hijmans et al., 2009), single island polygons isolated from GADM (see Weigelt, Jetz, & Kreft, 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 (Figure S2). 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 (Figure S3, Table S3). Specifically, this includes (i) characteristics based on the spatial polygon itself like its area, centroid coordinates and geographic extent, (ii) 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 (iii) miscellaneous metrics calculated from additional spatial resources like biogeographic region affinity (Takhtajan, 1986) or island isolation (Weigelt & Kreft, 2013) (Figure S3c).

For families and higher taxonomic groups, we 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 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.

### 2.7 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.

### 3 CURRENT STATE

#### 3.1 Geographic coverage

Initially, GIFT started with the collection of Floras and checklists for oceanic islands and many 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 islands have clearly defined geographic boundaries. As such, they have attracted much scientific interest in the past, leading to a high availability of island Floras and checklists (Frodin, 2001). GIFT therefore offers a very comprehensive overview over the floristic composition of 1,845 of the world’s islands, which has already led to several studies on island biodiversity patterns and their determinants (e.g. Cabral, Weigelt, Kissling, & Kreft, 2014; Lenzner,
Weigelt, Kreft, Beierkuhnlein, & Steinbauer, 2017; Taylor, Weigelt, König, Zotz, & Kreft, 2019; Weigelt et al., 2013; Weigelt et al., 2015; Weigelt et al., 2016). More recently, GIFT has been expanded to mainland floras, currently covering 1,048 regions, to support comparative analyses of continental and insular floras (e.g. Karger et al., 2019; König et al., 2017; Razanajatovo et al., 2019) and extensive studies of global plant diversity (e.g. Delavaux et al., 2019).

In total, GIFT 1.0 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 regions 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 (Figure 4a). 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 km$^2$) 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 (Figure 4, Table 1) and floristic status (Figure S4), 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 (Figure 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. BGCI, 2017; WCSP, 2012), many mainland regions in GIFT are relatively large (mean area = 170,287 km$^2$, median = 30,454 km$^2$), especially in comparison to an average island (3,265 km$^2$; Figure S2). 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).

### 3.2 Taxonomic coverage

GIFT 1.0 includes 324,136 taxonomically standardized species from all major groups of land plants (Embryophyta), 277,580 of which

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**FIGURE 4** Spatial coverage of checklist data stored in the Global Inventory of Floras and Traits 1.0. (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 km$^2$ are plotted as points [Colour figure can be viewed at wileyonlinelibrary.com]
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 $C_{\text{mean}} = 0.03$, $p = 0.142$; Abouheif, 1999), i.e. it exhibits no detectable bias towards certain clades (Figure 5). The 324,136 species names in total derive from 717,117 unstandardized original names (after genus name correction and

| Taxonomic group     | Regions | Names    | Species  | Species resolved | Trait records |
|---------------------|---------|----------|----------|------------------|---------------|
| Embryophyta         | 53      | 717,117  | 324,136  | 277,580          | 2,307,100     |
| Tracheophyta        | 2,062   | 714,781  | 322,002  | 275,610          | 2,306,973     |
| Pteridophyta        | 2,079   | 24,241   | 11,888   | 8,408            | 54,772        |
| Gymnospermae        | 2,211   | 4,031    | 1,151    | 1,051            | 12,352        |
| Angiospermae        | 2,218   | 686,509  | 308,963  | 266,151          | 2,239,849     |
| Orchidaceae         | 2,478   | 64,508   | 28,155   | 27,029           | 192,332       |
| Asteraceae          | 2,218   | 58,492   | 27,755   | 24,450           | 167,300       |
| Fabaceae            | 2,218   | 46,999   | 21,000   | 18,416           | 145,895       |
| Poaceae             | 2,431   | 38,464   | 12,368   | 11,215           | 130,492       |
| Rubiaceae           | 2,431   | 29,485   | 14,260   | 13,545           | 96,684        |
| Lamiaceae           | 2,431   | 18,120   | 7,882    | 7,560            | 61,708        |
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.

3.3 | 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 S1) such as woodiness (234,214 species) or 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 complementary 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, Díaz, et al., 2011]) 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 (Figure 6a). 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 (Figure 6). Life-form sensu Raunkiær (1907), for example, is widely available throughout Europe, but rarely reported for species in other regions of the world (Figure 6d). Likewise, plant height and seed mass exhibit uneven geographical coverage distributions, with highest coverage in Australia, South Africa and Europe (Figure 6c,e).

The taxonomic coverage of trait information in GIFT has small, yet significant phylogenetic signal ($C_{mean} = 0.21$, $p < 0.001$, Figure S5a). That means 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 (Figure S5b–e). For example, plant height is very well-covered for the graminid clade (leftmost group within the monocots, Figure S5c), and Raunkiær life-form is particularly well-covered in gymnosperms and monocots (Figure S5d).

3.4 | Web interface

An updated overview of 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.

4 | 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 (Figure 1) facilitates moving global plant diversity research beyond using species richness as a proxy for biodiversity (Barthlott, Mutke, Rafiqpoor, Kier, & Kreft, 2005; Kreft & Jetz, 2007). Examining the drivers of taxonomic, functional and phylogenetic diversity and turnover (König et al., 2017; Lamanna et al., 2014; Qian, Swenson, & Zhang, 2013; Tuomisto, 2010; Weigelt et al., 2015) 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 (Vièlle, Reich, Pacala, Enquist, & Kattge, 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 (Butler et al., 2017; Engemann et al., 2016; Moles et al., 2014; Reichstein, Bahn, Mahecha, Kattge, & Baldocchi, 2014), 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 biogeographical 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 biogeographical patterns (Weigelt et al., 2016). Naturalized alien species and their traits help to understand the role of humans in changing plant assemblages and may
FIGURE 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 km$^2$ are plotted as points [Colour figure can be viewed at wileyonlinelibrary.com]
teach us how new habitats and regions are colonized (e.g. Delavaux et al., 2019; Razanajatovo et al., 2019). Knowledge on the composition of native versus alien floras (see www.glnaf.org; van Kleunen et al., 2015; Pýšek et al., 2017) facilitates addressing 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 (Figure 1). Having near-global and full taxonomic coverage of distribution data (Figure 4) and several functional traits (Table S1), 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 (e.g. FitzJohn et al., 2014; König, Weigelt, Schrader, et al., 2019; Scheffer et al., 2014). 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 (König, Weigelt, Schrader, et al., 2019; Meyer et al., 2016). 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 (Barbet-Massin, Jiguet, Albert, & Thuiller, 2012; Lobo et al., 2010). 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, Weigelt, Taylor, et al., 2019; Taylor et al., 2019). Defining the regional species pool or inferring the floristic status may not only be useful 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, allows 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, Weigelt, Schrader, et al., 2019). 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 by the end of 2019 to 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 facilitate 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 (Brueheide 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 deviations 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, Jones, Quicke, & Hortal, 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 of alternative resources. In addition, the outlined database framework can serve as an example for other taxa with insufficient 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.

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DATA AVAILABILITY STATEMENT

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 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 macroecological and biogeographical analyses (https://github.com/BiGeoMacro/GIFT-export). Once these tools have reached a status that allows easy handling of the complex content of the database, accounting for data restrictions of the original sources and evaluation of potential biases, GIFT will become publicly available, at the latest by 2025. 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 significant amounts of trait data (e.g. on 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 users 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/).

ORCID

Patrick Weigelt https://orcid.org/0000-0002-2485-3708
Christian König https://orcid.org/0000-0003-0585-5983
Holger Kreft https://orcid.org/0000-0003-4471-8236

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**BIOSKETCHES**

**Patrick Weigelt** is fascinated by the distribution of plant life on earth. He combines large databases and tools from ecoinformatics to study the past and present drivers and mechanisms that shaped today’s plant diversity patterns among island and mainland systems.

**Christian König** is a quantitative ecologist working at the interface between biodiversity research and data science. He is particularly interested in understanding the mechanisms underlying large-scale patterns in taxonomic, functional and phylogenetic diversity.

**Holger Kreft** is interested in biogeographical and ecological patterns from local to global scales, particularly gradients of species richness and endemism. His research includes analyses of plant and vertebrate diversity, and island and conservation biogeography.

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.

**SUPPORTING INFORMATION**

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

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**APPENDIX 1**

**LITERATURE RESOURCES USED TO ASSEMBLE THE SPECIES CHECKLIST AND TRAIT DATA IN GIFT**

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