Package ‘GIFT’

December 19, 2024

Type Package

Title Access to the Global Inventory of Floras and Traits (GIFT)

Version 1.3.3

Description Retrieving regional plant checklists, species traits and distributions, and environmental data from the Global Inventory of Floras and Traits (GIFT). More information about the GIFT database can be found at <`https://gift.uni-goettingen.de/about`> and the map of available floras can be visualized at <`https://gift.uni-goettingen.de/map`>. The API and associated queries can be accessed according the following scheme: <`https://gift.uni-goettingen.de/api/extended/index2.0.php?query=env_raster`>.

Depends R (>= 3.5.3)

License GPL (>= 2)

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LazyData true

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RoxygenNote 7.3.2

Suggests covr, ggplot2, kableExtra, knitr, patchwork, testthat (>= 3.0.0), RColorBrewer, rmarkdown, rnaturalearth, rnaturalearthdata, scales

Config/testthat/edition 3

URL `https://github.com/BioGeoMacro/GIFT`, `https://biogeomacro.github.io/GIFT/`

BugReports `https://github.com/BioGeoMacro/GIFT/issues`

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

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Contents

`GIFT_checklists` *GIFT checklists*

Description

Retrieve GIFT checklists that fulfill specific criteria.

Usage

```
GIFT_checklists(
  taxon_name = "Tracheophyta",
  complete_taxon = TRUE,
  floristic_group = c("all", "native", "endemic", "naturalized")[2],
  complete_floristic = TRUE,
  geo_type = c("All", "Mainland", "Island")[1],
  ref_excluded = NULL,
```

```
  suit_geo = FALSE,
  shp = NULL,
  coordinates = NULL,
  overlap = "centroid_inside",
  remove_overlap = FALSE,
  area_threshold_island = 0,
  area_threshold_mainland = 100,
  overlap_threshold = 0.1,
  by_ref_ID = FALSE,
  taxonomic_group = TRUE,
  namesmatched = FALSE,
  list_set_only = FALSE,
  GIFT_version = "latest",
  api = "https://gift.uni-goettingen.de/api/extended/"
)
```

Arguments

`taxon_name`	Character string corresponding to the taxonomic group of interest.
`complete_taxon`	logical stating you want to retrieve checklists that only contain the exhaustive list of the `taxon_name` argument or as well incomplete lists.
`floristic_group`	Character among the following options: `all`, `native`, `endemic`, `naturalized`.
`complete_floristic`	logical stating you want to retrieve checklists that only contain the exhaustive list of the `floristic_group` argument or as well incomplete lists.
`geo_type`	Character string, either `Mainland`, `Island` or `All`. `Island` gets you to Island, Island Group & Island Part. `Mainland` gets you to Mainland & Island/Mainland. `All` gets you all types.
`ref_excluded`	A vector listing potential ref_IDs that shall be ignored when assembling the set of regions and checklists fulfilling the given criteria. Checklists from these references will not be returned. NULL by default.
`suit_geo`	logical indicating whether only regions classified as suit_geo should be considered (see details).
`shp`	Shapefile provided by the user.
`coordinates`	Custom set of coordinates. The format is a two columns data.frame, the first one being longitudes and the second being latitudes of the vertices of a polygon. If the data.frame only includes two rows, the function assumes that the values are the four limits (min and max. longitude and latitude) of a bounding box.
`overlap`	A character string defining the criteria to use in order to retrieve checklists. Available options are `centroid_inside`, `extent_intersect`, `shape_intersect` and `shape_inside`. For example, `extent_intersect` means that every polygon from GIFT for which the extent intersects the provided shape/coordinates will be retrieved.
`remove_overlap`	a logical stating whether you want to retrieve checklists that overlap or not.

`area_threshold_island`	A number stating from which surface the smallest overlapping polygon is kept. By default set to 0 square kilometer (meaning that by default the smallest islands will be conserved).
`area_threshold_mainland`	When two polygons overlap, the smallest or the biggest one can be kept. When the surface of the smallest polygon exceeds this number, the smallest polygon is kept. Otherwise, we keep the bigger one. Set by default 100 square-kilometers.
`overlap_threshold`	A number ranging from 0 to 1, indicating at what percentage of overlap, partially overlapping polygons should be kept.
`by_ref_ID`	logical indicating whether the removal of overlapping regions shall be applied by *ref_ID* only. Note that regions overlapping with other regions from the same resource will be removed even if there are other references available for those regions.
`taxonomic_group`	logical. When set to `TRUE`, two additional columns (*family* and *tax_group*) are available in the checklists.
`namesmatched`	logical. `FALSE` by default, set to `TRUE` if you want the original species name as they came in the references as well as details on the taxonomic harmonization.
`list_set_only`	logical stating whether you only want the metadata or if you also want to retrieve the species lists.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.
`api`	character string defining from which API the data will be retrieved.

Details

Here is the detail of each data.frame and their columns:

ref_ID - Identification number of each reference.
type- What type the source is.
subset- What information regarding the status of species is available.
native_indicated- Whether native status of species is available in the source.
natural_indicated - Whether naturalized status of species is available in the source.
end_ref - Whether endemism information is available in the source.
restricted - Whether the access to this reference is restricted.
taxon_ID- Identification number of species.
list_ID - Identification number of each list.
end_list - Whether endemism information is available in the list.
entity_ID- Identification number of the polygon of the list.
geo_entity - Name of the location.
suit_geo - Is the polygon suitable.
entity_class - Type of polygon.
entity_type - Name of the location.
taxon_name - Name of the group of taxa available.

For the second data frame with the species, each column refers to:

ref_ID - Identification number of each reference.
list_ID - Identification number of each list
work_ID - Identification number of each species name, after taxonomic harmonization.
genus_ID - Identification number of each genus, after taxonomic harmonization.
species - Species name, after taxonomic harmonization.
questionable - Whether the species occurrence is questionable.
native - Whether the species is native.
quest_native - Whether the native information is questionable.
naturalized - Whether the species is naturalized.
endemic_ref - Whether the species is endemic within the reference.
quest_end_ref - Whether the endemic_ref information is questionable.
endemic_list - Whether the species is endemic within the list.
quest_end_list - Whether the endemic_list information is questionable.
cons_status - Conservation status of the species.
family - Family of the species.
tax_group - Taxonomic group of the species.

While the arguments `taxon_name` in combination with `complete_taxon` = TRUE and `floristic_group` in combination with `complete_floristic` = TRUE make sure to only get back checklists for regions for which GIFT has lists aiming at covering both the entire taxonomic group and floristic subset (for example native vascular plants), it does not mean that the checklists are complete (include all species). We therefore flagged regions in GIFT for which the combination of all checklists is obviously incomplete as `suit_geo` = `0`. This has however only been done only for native angiosperms and the assessment has been subjective. Set `suit_geo` = TRUE if you only want to consider regions classified as `suit_geo`.

Value

List with two data frames: the checklist with species and the list of ID.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_checklists_raw()`

Examples

```
data("western_mediterranean")
ex <- GIFT_checklists(shp = western_mediterranean,
```

```
overlap = "centroid_inside", taxon_name = "Angiospermae",
list_set_only = TRUE) # set to FALSE to get species composition
```

GIFT_checklists_conditional

GIFT checklists meta data

Description

Retrieve meta data of GIFT checklists for regions that are covered by checklists jointly fulfilling specific criteria.

Usage

```
GIFT_checklists_conditional(
  taxon_name = "Tracheophyta",
  floristic_scope = c("all", "native", "native and naturalized",
   "native and historically introduced", "endangered", "endemic", "naturalized",
    "other subset")[1:4],
  ref_excluded = NULL,
 type_ref = c("Account", "Catalogue", "Checklist", "Flora", "Herbarium collection",
    "Key", "Red list", "Report", "Species Database", "Survey"),
  entity_class = c("Island", "Island/Mainland", "Mainland", "Island Group",
    "Island Part"),
  native_indicated = FALSE,
  natural_indicated = FALSE,
  end_ref = FALSE,
  end_list = FALSE,
  suit_geo = FALSE,
  complete_taxon = TRUE,
  GIFT_version = "latest",
  api = "https://gift.uni-goettingen.de/api/extended/",
  list_set = NULL,
  taxonomy = NULL
)
```

Arguments

`taxon_name`	Character string corresponding to the taxonomic group of interest.
`floristic_scope`	A vector listing floristic scopes of the references to be considered. Options are: `all`, `native`, `native and naturalized`, `native and historically introduced`, `endangered`, `endemic`, `naturalized`, `other subset`.
`ref_excluded`	A vector listing potential ref_IDs that shall be ignored when assembling the set of regions and checklists fulfilling the given criteria. Checklists from these references will not be returned. `NULL` by default.

`type_ref`	Character, options are `Account`, `Catalogue`, `Checklist`, `Flora`, `Herbarium collection`, `Key`, `Red list`, `Report`, `Species Database`, `Survey`.
`entity_class`	Character, options are `Island`, `Island/Mainland`, `Mainland`, `Island Group`, `Island Part`.
`native_indicated`	Logical, whether only lists where native status is available should be retrieved.
`natural_indicated`	Logical, whether only lists where natural status is available should be retrieved.
`end_ref`	Logical, whether only lists where endemism at the reference level is available should be retrieved.
`end_list`	Logical, whether only lists where endemism at the list level is available should be retrieved.
`suit_geo`	logical indicating whether only regions classified as suit_geo should be considered (see details).
`complete_taxon`	Logical, default `TRUE`.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.
`api`	character string defining from which API the data will be retrieved.
`list_set`	list_set `NULL` by default. If not, it has to be the list table (see `GIFT_lists()`). Used internally in `GIFT_checklists()` to avoid downloading the table of lists many times.
`taxonomy`	default `NULL`. If not, it has to be the taxonomy table (see `GIFT_taxonomy()`).

Details

Here is what each column refers to:

ref_ID - Identification number of each reference.
type - What type the source is.
subset - What information regarding the status of species is available.
native_indicated - Whether native status of species is available in the source.
natural_indicated - Whether naturalized status of species is available in the source.
end_ref - Whether endemism information is available in the source.
restricted - Whether the access to this reference is restricted.
taxon_ID - Identification number of species.
list_ID - Identification number of each list.
end_list - Whether endemism information is available in the list.
entity_ID - Identification number of the polygon of the list.
geo_entity - Name of the location.
suit_geo - Is the polygon suitable.
entity_class - Type of polygon.
entity_type - Name of the location.
taxon_name - Name of the group of taxa available.

Value

A data frame with 16 columns.

References

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

Weigelt, P, König, C, Kreft, H. GIFT - A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_checklists_raw()`

Examples

```
ex <- GIFT_checklists_conditional(taxon_name = "Embryophyta",
floristic_scope = c("all", "native", "native and naturalized",
"native and historically introduced", "endangered",
"endemic", "naturalized", "other subset")[7],
type_ref = c("Account", "Catalogue", "Checklist","Flora",
"Herbarium collection", "Key", "Red list", "Report", "Species Database",
 "Survey"),
 entity_class = c("Island", "Island/Mainland", "Mainland", "Island Group",
 "Island Part"),
 native_indicated = FALSE, natural_indicated = FALSE, end_ref = FALSE,
 end_list = FALSE, suit_geo = TRUE, complete_taxon = TRUE,
 list_set = NULL, taxonomy = NULL)
```

`GIFT_checklists_raw` *GIFT checklists*

Description

Raw checklists, to combine with other functions.

Usage

```
GIFT_checklists_raw(
  ref_ID = NULL,
  list_ID = NULL,
  namesmatched = FALSE,
  taxon_name = "Tracheophyta",
  floristic_group = "all",
  list_set = NULL,
```

```
  taxonomy = NULL,
  GIFT_version = "latest",
  api = "https://gift.uni-goettingen.de/api/extended/"
)
```

Arguments

`ref_ID`	A vector defining the IDs of the references to retrieve. `NULL` by default.
`list_ID`	A vector defining the IDs of the lists to retrieve. `NULL` by default. These lists are retrieved in addition to the lists contained in the references in `ref_ID`.
`namesmatched`	Logical. `FALSE` by default, set to `TRUE` if you want the original species name as they came in the references as well as details on the taxonomic harmonization.
`taxon_name`	Character string corresponding to the taxonomic group of interest.
`floristic_group`	Character string among these options: `all`, `native`, `naturalized`, `endemic_list`, `endemic_ref`.
`list_set`	`NULL` by default. If not, it has to be the list table (see `GIFT_lists()`). Used internally in `GIFT_checklists()` to avoid downloading the table of lists many times.
`taxonomy`	`NULL` by default. If not, it has to be the taxonomy table (see `GIFT_taxonomy()`). Used internally in `GIFT_checklists()` to avoid downloading the taxonomy table many times.#'
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.
`api`	character string defining from which API the data will be retrieved.

Details

Here is what each column refers to:

ref_ID - Identification number of each reference
list_ID - Identification number of each list
orig_ID - Identification number of each species name, unchanged from the sources
name_ID - Identification number of each reference
genus - Genus of each species
species_epithet - Epithet of each species
subtaxon - If needed, subtaxon of the species
author - Name of the author who described the species
matched - Whether a match was found when using a taxonomic backbone
epithetscore - Matching score for the epithet
overallscore - Matching score for the overall species name
resolved - Whether the species name was resolved
service - Service used for the taxonomic harmonization
work_ID - Identification number of each species name, after taxonomic harmonization
genus_ID - Identification number of each genus, after taxonomic harmonization
species - Species name, after taxonomic harmonization

questionable - Whether the species occurrence is questionable
native - Whether the species is native
quest_native - Whether the native information is questionable
naturalized - Whether the species is naturalized
endemic_ref - Whether the species is endemic within the reference
quest_end_ref - Whether the endemic_ref information is questionable
endemic_list- Whether the species is endemic within the list
quest_end_list - Whether the endemic_list information is questionable
cons_status - Conservation status of the species

Value

A data frame with 15 or 29 columns (depending on namesmatched). This data frame contains the species checklist for a given reference/list.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_checklists()`

Examples

```
ex <- GIFT_checklists_raw(list_ID = c(1,5))
```

`GIFT_coverage` *Taxonomic and trait coverage per geographic region and taxonomic group in GIFT*

Description

Retrieve taxonomic or trait coverage (for a given trait) of all species, native species, naturalized species and endemic species per taxonomic group and geographic region combination. This function works with taxonomic groups above the genus level.

Usage

```
GIFT_coverage(
  what = "taxonomic_coverage",
  taxon_name = "Embryophyta",
  trait_ID = "1.1.1",
  GIFT_version = "latest",
  api = "https://gift.uni-goettingen.de/api/extended/"
)
```

Arguments

`what`	character indicating whether `taxonomic_coverage` or `trait_coverage` shall be retrieved.
`taxon_name`	Name of the taxonomic group you want to retrieve coverage for. See `GIFT_taxonomy()` for options. The function accepts family names and higher taxonomic groups.
`trait_ID`	Identification number of the trait you want to retrieve coverage for. See `GIFT_traits_meta()` for details.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.
`api`	character string defining from which API the data will be retrieved.

Details

The output has 9 columns:

entity_ID - Identification number of GIFT polygons
total - taxonomic or trait coverage for all species
total_rst - taxonomic or coverage for all species considering restricted resources
native - taxonomic or trait coverage for native species
native_rst - taxonomic or trait coverage for native species considering restricted resources
naturalized - taxonomic or trait coverage for naturalized species
naturalized_rst - taxonomic or trait coverage for naturalized species considering restricted resources
endemic_min - taxonomic or trait coverage for endemic species
endemic_min_rst - taxonomic or trait coverage for endemic species considering restricted resources

In the case of taxonomic coverage, a ’1’ means that species composition data is available for the given combination of taxonomic group and geographic region while ’NA’ means that no data is available. This can differ depending on whether restricted data in GIFT is considered or not (columns with or without _rst at the end).

In the case of trait coverage, the proportion of species of a given taxonomic group with information on the defined trait is reported per geographic region.

Value

A data frame with either taxonomic or trait coverage per GIFT polygon.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43. https://doi.org/10.1111/jbi.13623

See Also

`GIFT_traits_meta()`

Examples

```
ex <- GIFT_coverage(what = "taxonomic_coverage", taxon_name = "Angiospermae")
ex2 <- GIFT_coverage(what = "trait_coverage", taxon_name = "Angiospermae",
trait_ID = "1.2.1")
```

`GIFT_env` *Environmental data for GIFT checklists*

Description

Retrieve environmental data associated to each GIFT checklists. Sources of environmental variables can come from raster layers or from shape files (miscellaneous). Users need to define what variables they are interested in and then ask for a set of summary statistics (in case of raster layers).

Usage

```
GIFT_env(
  entity_ID = NULL,
  miscellaneous = if (is.null(rasterlayer)) "area" else NULL,
  rasterlayer = NULL,
  sumstat = "mean",
  GIFT_version = "latest",
  api = "https://gift.uni-goettingen.de/api/extended/"
)
```

Arguments

`entity_ID`	A vector defining the ID of the lists to retrieve. `NULL` by default, in that case, every list from GIFT is retrieved.

`miscellaneous`	character vector or list specifying the miscellaneous data to retrieve. . A list of all miscellaneous layers for which precomputed information exists in the database can be viewed in the output table returned by `GIFT_env_meta_misc()`.
`rasterlayer`	character vector or list specifying the raster data to retrieve. A list of all raster layers for which precomputed information exists in the database can be viewed in the output table returned by `GIFT_env_meta_raster()`.
`sumstat`	Vector or list indicating the desired summary statistics out of `c("min", "q05", "q10", "q20", "q25", "q30", "q40", "med", "q60", "q70", "q75", "q80", "q90", "q95", "max", "mean", "sd", "modal", "unique_n", "H", "n")` used to aggregate the information coming from the raster layers. If `sumstat` is a vector, the same summary statistics are used for all raster layers. If `sumstat` is a list, the first element defines the summary statistics for the first raster layer, the second for the second and so on. **Important note** Some summary statistics may not be informative depending on the environmental layer you ask for. For example, it is not relevant to retrieve the mean of soil classes for a polygon. The mode or Shannon index are more suitable in that case.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.
`api`	character string defining from which API the data will be retrieved.

Details

The columns of the data.frame are the following:

entity_ID - Identification number of the polygon
geo_entity - Name of the polygon
The other columns relate to the environmental variables the user asked for.

Value

A data frame with the environmental values per polygon (entity_ID).

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623

See Also

`GIFT_env_meta_misc()` and `GIFT_env_meta_raster()`

Examples

```
ex <- GIFT_env(entity_ID = c(1,5),
               miscellaneous = c("perimeter", "biome"),
               rasterlayer = c("mn30_grd", "wc2.0_bio_30s_01"),
               sumstat = list(c("mean", "med"), "max"))
```

`GIFT_env_meta_misc` *Metadata for the environmental miscellaneous variables in GIFT*

Description

Retrieve the metadata of all miscellaneous environmental layers accessible in GIFT.

Usage

```
GIFT_env_meta_misc(
  api = "https://gift.uni-goettingen.de/api/extended/",
  GIFT_version = "latest"
)
```

Arguments

`api`	character string defining from which API the data will be retrieved.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.

Details

Here is what each column refers to:

dataset - Name of the source dataset.
variable - Name of the environmental layer.
description- Description.
unit - Unit.
num - Whether the environmental layer is numeric or not.
ref_long - Full reference to cite when using an environmental layer.

Value

A data frame with 6 columns.

References

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

Weigelt, P, König, C, Kreft, H. GIFT - A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_env()`

Examples

```
ex <- GIFT_env_meta_misc()
```

`GIFT_env_meta_raster` *Metadata for the environmental rasters in GIFT*

Description

Retrieve the metadata of every environmental raster accessible in GIFT.

Usage

```
GIFT_env_meta_raster(
  api = "https://gift.uni-goettingen.de/api/extended/",
  GIFT_version = "latest"
)
```

Arguments

`api`	character string defining from which API the data will be retrieved.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.

Details

Here is what each column refers to:

dataset - Name of the source dataset
layer_name - Name of the environmental layer
layer - Full name
description - Description
unit - Unit
coord_system - Coordinate system
resolution - Resolution
extent - Extent
version - Version of the source
ref_long - Full reference to cite when using an environmental layer

Value

A data frame with 10 columns.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_env()`

Examples

```
ex <- GIFT_env_meta_raster()
```

`GIFT_lists` *Metadata for checklists available in GIFT*

Description

Retrieves the metadata of each checklist within GIFT.

Usage

```
GIFT_lists(
  api = "https://gift.uni-goettingen.de/api/extended/",
  GIFT_version = "latest"
)
```

Arguments

`api`	character string defining from which API the data will be retrieved.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.

Details

Here is what each column refers to:

ref_ID - Identification number of each reference.
Columns *type* and *subset* indicate what information can be found in each reference. Similarly, *native_indicated*, *natural_indicated* and *end_ref* indicate respectively whether native, naturalized and endemic species were stated in the reference. *restricted* refers to the availability of the reference, *taxon_ID* to the taxonomic group available in a reference. *list_ID* is the identification number of a checklist within a reference, *entity_ID* of the associated polygon. *geo_entity* associates a name to this identification number. *suit_geo* indicates whether the checklist is suitable for use, *entity_class* and *entity_unit* give additional details about the polygon.

Value

A data frame with 15 columns.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_checklists()`

Examples

```
ex <- GIFT_lists()
```

`GIFT_no_overlap` *Select non-overlapping regions*

Description

Identify overlapping regions in a set of GIFT regions and choose only non-overlapping regions based on size and overlap criteria

Usage

```
GIFT_no_overlap(
  entity_IDs = NULL,
  area_threshold_island = 0,
  area_threshold_mainland = 100,
  overlap_threshold = 0.1,
  geoentities_overlap = NULL,
  api = "https://gift.uni-goettingen.de/api/extended/",
  GIFT_version = "latest"
)
```

Arguments

`entity_IDs`	A vector of IDs of the regions for which we want to check overlap
`area_threshold_island`	A number stating from which surface the smallest overlapping polygon is kept. By default set to 0 square kilometer (meaning that by default the smallest islands will be conserved).
`area_threshold_mainland`	When two polygons overlap, the smallest or the biggest one can be kept. When the surface of the smallest polygon exceeds this number, the smallest polygon is kept. Otherwise, we keep the bigger one. Set by default 100 square-kilometers.
`overlap_threshold`	A number ranging from 0 to 1, indicating at what percentage of overlap, partially overlapping polygons should be kept.
`geoentities_overlap`	A table coming from GIFT indicating the overlap in km^2 between pairs of polygons.
`api`	character string defining from which API the data will be retrieved.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.

Value

A vector of entity_IDs (identification numbers of polygons) non-overlapping.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43. https://doi.org/10.1111/jbi.13623

See Also

`GIFT_checklists()`

Examples

```
ex <- GIFT_no_overlap(entity_IDs = c(10071, 12078)) # Andalusia and Spain.
# We get Andalusia because it is smaller than Spain and larger than 100 km²
ex2 <- GIFT_no_overlap(entity_IDs = c(10071, 12078),
area_threshold_mainland = 100000) # since Andalusia is smaller than
# 100,000 km² large, the larger entity (Spain) is chosen here.
```

`GIFT_overlap` *Spatial overlap between GIFT polygons and external polygons*

Description

Calculate the spatial overlap between GIFT polygons and shapefiles coming from other resources

Usage

```
GIFT_overlap(
  resource = "glonaf",
  GIFT_version = "latest",
  api = "https://gift.uni-goettingen.de/api/extended/"
)
```

Arguments

`resource`	A character string indicating from which resource the spatial overlap is calculated. Available options are `glonaf` and `gmba`. glonaf stands for Global Naturalized Alien Flora and gmba for Global Mountain Biodiversity Assessment.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.
`api`	character string defining from which API the data will be retrieved.

Details

The columns of the data.frame are the following:

entity_ID - Identification number of the GIFT polygon
glonaf_ID (or *gmba_ID*) - Identification number of the polygon from the other resource
overlap12 - Spatial overlap in percentage between GIFT polygon and the external polygon
overlap21 - The other way around

Value

A data frame with the spatial overlap.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_lists()`

Examples

```
glonaf <- GIFT_overlap(resource = "glonaf")
gmba <- GIFT_overlap(resource = "gmba")
```

`GIFT_phylogeny` *Phylogeny of the species in GIFT*

Description

Retrieve a phylogeny of the plant species available in GIFT. The phylogeny table is not available for GIFT_version 1.0, 2.0, 2.1 and 2.2.

Usage

```
GIFT_phylogeny(
  clade = "Tracheophyta",
  as_tree = TRUE,
  return_work_ID = FALSE,
  work_ID_subset = NULL,
  api = "https://gift.uni-goettingen.de/api/extended/",
  GIFT_version = "latest"
)
```

Arguments

`clade`	Character string indicating the taxonomic group of interest corresponding to the node labels in the phylogeny.
`as_tree`	Logical, whether you want the phylogeny to be returned as a phylogenetic tree (`TRUE`) or in a table (`FALSE`). `TRUE` by default.
`return_work_ID`	Logical, whether you want to retrieve the species' names or their identification number (work_ID) in the GIFT database. `FALSE` by default.
`work_ID_subset`	A vector of work_ID to prune the phylogenetic tree. `NULL` by default.
`api`	character string defining from which API the data will be retrieved.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.

Details

Here is what each column refers to:

taxon_label - Name of the taxonomic group
work_ID - Standardized species name IDs for the species at the tips of the tree
edge_length - Edge length
lft - Left border of a given taxon in the Newick sequence
rgt - Right border of a given taxon in the Newick sequence

Value

A data frame with 5 columns or a tree object.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16– 43. https://doi.org/10.1111/jbi.13623

See Also

`GIFT_checklists()`

Examples

```
ex <- GIFT_phylogeny(clade = "Tracheophyta", as_tree = FALSE)
```

`GIFT_references` *Metadata for references available in GIFT*

Description

Retrieve the metadata of every reference accessible in GIFT.

Usage

```
GIFT_references(
  api = "https://gift.uni-goettingen.de/api/extended/",
  GIFT_version = "latest"
)
```

Arguments

`api`	character string defining from which API the data will be retrieved.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.

Details

Here is what each column refers to:

ref_ID - Identification number of the reference
ref_long - Full reference for the reference
geo_entity_ref - Name of the location
type - What type the source is
subset - What information regarding the status of species is available
taxon_ID - Identification number of the group of taxa available
taxon_name - Name of the group of taxa available
checklist - Is the source a checklist
native_indicated - Whether native status of species is available in the source
natural_indicated - Whether naturalized status of species is available in the source
end_ref - Whether endemism information is available in the source
traits - Whether trait information is available in the source
restricted - Whether the access to this reference is restricted
proc_date - When the source was processed

Value

A data frame with 14 columns.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_checklists()`

Examples

```
ex <- GIFT_references()
```

`GIFT_regions` *Metadata for GIFT regions*

Description

Retrieves miscellaneous information for GIFT regions.

Usage

```
GIFT_regions(
  api = "https://gift.uni-goettingen.de/api/extended/",
  GIFT_version = "latest"
)
```

Arguments

`api`	character string defining from which API the data will be retrieved.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.

Details

Here is the detail of each column:

entity_ID - Identification number of GIFT polygons
geo_entity - Name of GIFT polygons
suit_geo - Whether the polygon is suitable
entity_class - Class of the polygon
entity_type - Type of the polygon
TDWG_lvl3_ID - Whether the polygon is a TDWG region (see https://www.tdwg.org/)
country - Whether the polygon is a country

Value

A data frame with 7 columns.

References

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

Weigelt, P, König, C, Kreft, H. GIFT - A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_env_meta_misc()`

Examples

```
ex <- GIFT_regions()
```

`GIFT_richness` *Species richness per geographic region and taxonomic group in GIFT*

Description

Retrieve species richness of all species, native species, naturalized species and endemic species per taxonomic group and geographic region combination.

Usage

```
GIFT_richness(
  taxon_name = "Embryophyta",
  GIFT_version = "latest",
  api = "https://gift.uni-goettingen.de/api/extended/"
)
```

Arguments

`taxon_name`	Taxonomic group to retrieve species richness for.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.
`api`	character string defining from which API the data will be retrieved.

Details

The output has 5 columns:

entity_ID - Identification number of the geographic region
total - total species richness
native - number of native species
naturalized - number of naturalized species
endemic_min - number of endemic species

The number of endemic species is a conservative count not counting occurrences of species which go back to infraspecific taxa.

Value

A data frame with species richness values for different floristic subsets per geographic region in GIFT.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_traits_meta()`

Examples

```
ex <- GIFT_richness(taxon_name = "Angiospermae")
```

`GIFT_shapes` *Shape files of GIFT regions*

Description

Get shapefile of GIFT regions for selected regions.

Usage

```
GIFT_shapes(
  entity_ID = NULL,
  api = "https://gift.uni-goettingen.de/api/extended/",
  GIFT_version = "latest"
)
```

Arguments

`entity_ID`	A vector defining the IDs of the regions.
`api`	character string defining from which API the data will be retrieved.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.

Details

Here is the detail of each column:

entity_ID - Identification number of the polygon
geo_entity - Name of the polygon
point_x - Longitude of the centroid of the polygon
point_y - Latitude of the centroid of the polygon
area - Area in km2 of the polygon
x_min - Minimum longitude of the polygon
x_max - Maximum longitude of the polygon
y_min - Minimum latitude of the polygon
y_max - Maximum latitude of the polygon
entity_class - Class of the polygon
entity_type - Type of the entity
polygon_source - Source of the polygon
geometry - Geometry column from sf

Value

A spatial data.frame with 13 columns.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_env()`

Examples

```
ex <- GIFT_shapes(entity_ID = c(677, 200))
plot(sf::st_geometry(ex), col = ex$entity_ID)
```

`GIFT_spatial` *Spatial selection of GIFT checklists*

Description

Retrieve checklists overlapping with a shape file or a set of coordinates.

Usage

```
GIFT_spatial(
  shp = NULL,
  coordinates = NULL,
  overlap = "centroid_inside",
  entity_ID = NULL,
  GIFT_version = "latest",
  api = "https://gift.uni-goettingen.de/api/extended/"
)
```

Arguments

`shp`	Shapefile provided by the user. Its Coordinate Reference System (CRS) must be set to WGS84 (EPSG code 4326).
`coordinates`	Custom set of coordinates. The format is a two columns data.frame, the first one being longitudes and the second being latitudes of the vertices of a polygon. If the data.frame only includes two rows, the function assumes that the values are the four limits (min and max. longitude and latitude) of a bounding box.
`overlap`	A character string defining the criteria to use in order to retrieve checklists. Available options are `centroid_inside`, `extent_intersect`, `shape_intersect` and `shape_inside`. For example, `extent_intersect` means that every polygon from GIFT for which the extent intersects the provided shape/coordinates will be retrieved.
`entity_ID`	Constrain the list of regions to be received by a predefined set of entity_IDs. E.g. this list could come from GIFT_checklists_conditional().
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.
`api`	character string defining from which API the data will be retrieved.

Value

A data frame with 3 columns: *entity_ID* the identification number of a polygon, *geo_entity_ref* its name, and *coverage* which indicates the percentage of overlap between the provided shape and the different polygons of GIFT.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16– 43. https://doi.org/10.1111/jbi.13623

See Also

`GIFT_checklists()`

Examples

```
# With a shapefile
data("western_mediterranean")
ex <- GIFT_spatial(shp = western_mediterranean, overlap = "centroid_inside")

# With a shapefile coming from GIFT
spain <- GIFT_shapes(entity_ID = 10071)
```

```
ex_spain <- GIFT_spatial(shp = spain)

# With a point
custom_point <- cbind(9.9, 51)
ex2 <- GIFT_spatial(coordinates = custom_point,
overlap = "extent_intersect")

# With an extent
custom_extent <- cbind(c(-13, -18), c(27.5, 29.3))
ex3 <- GIFT_spatial(coordinates = custom_extent,
overlap = "extent_intersect")

# With a custom polygon
custom_polygon <- cbind(c(-18, -16.9, -13, -13, -18, -18),
c(29.3, 33, 29.3, 27.5, 27.5, 29.3))
ex4 <- GIFT_spatial(coordinates = custom_polygon,
overlap = "extent_intersect")

#With a linestring
custom_linestring <- rbind(c(9.9, 51), c(2.35, 48.9))
custom_linestring <- sf::st_as_sf(as.data.frame(custom_linestring),
coords = c("V1", "V2"))
custom_linestring <- dplyr::summarise(custom_linestring,
geometry = sf::st_combine(geometry))
sf::st_crs(custom_linestring) <- sf::st_crs(western_mediterranean)
ex5 <- GIFT_spatial(shp = custom_linestring, overlap = "extent_intersect")
```

`GIFT_species` *Species list in GIFT*

Description

Retrieve the whole set of plant species available in GIFT.

Usage

```
GIFT_species(
  api = "https://gift.uni-goettingen.de/api/extended/",
  GIFT_version = "latest"
)
```

Arguments

`api`	character string defining from which API the data will be retrieved.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.

Details

Here is what each column refers to:

work_ID - Identification number of the species
genus_ID - Identification number of the genus
work_genus - Genus name after taxonomic harmonization
work_species - Species name after taxonomic harmonization
work_author - Author who described the species (after taxonomic harmonization)

Value

A data frame with 5 columns.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_checklists()`

Examples

```
ex <- GIFT_species()
```

`GIFT_species_distribution`

GIFT species distribution

Description

Retrieve the distribution of one species from GIFT checklists.

Usage

```
GIFT_species_distribution(
  genus = "Fagus",
  epithet = "sylvatica",
  namesmatched = FALSE,
  remove_overlap = FALSE,
  area_th_island = 0,
  area_th_mainland = 100,
  overlap_th = 0.1,
  by_ref_ID = FALSE,
  aggregation = FALSE,
  GIFT_version = "latest",
  api = "https://gift.uni-goettingen.de/api/extended/"
)
```

Arguments

`genus`	Character string corresponding to the genus of the species of interest.
`epithet`	Character string corresponding to the epithet of the species of interest.
`namesmatched`	Logical `FALSE` by default, set to TRUE if you want to look for the species not only in the standardized species names but also in the original species names as they came in the original resources.
`remove_overlap`	a logical stating whether you want to retrieve checklists that overlap or not. `FALSE` by default.
`area_th_island`	A number stating from which surface the smallest overlapping polygon is kept. By default set to 0 square kilometer (meaning that by default the smallest islands will be conserved).
`area_th_mainland`	When two polygons overlap, the smallest or the biggest one can be kept. When the surface of the smallest polygon exceeds this number, the smallest polygon is kept. Otherwise, we keep the bigger one. Set by default 100 square-kilometers.
`overlap_th`	A number ranging from 0 to 1, indicating at what percentage of overlap, partially overlapping polygons should be kept.
`by_ref_ID`	logical indicating whether the removal of overlapping regions shall be applied by ref_ID only. Note that regions overlapping with other regions from the same resource will be removed even if there are other references available for those regions.
`aggregation`	A logical stating whether you want to aggregate in a simpler way the floristic status of species per entity_ID. For example, two lists associated to the same entity_ID could describe a species both as native and non-native. In that case, the aggregation would consider the species to be native. Reverse for naturalized and alien.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.
`api`	character string defining from which API the data will be retrieved.

Details

Here is the detail of each data.frame and their columns: *ref_ID* - Identification number of the reference
list_ID - Identification number of the list
entity_ID - Identification number of the polygon
name_ID - Identification number of the genus before taxonomic harmonization
cf_genus - Whether the genus name is uncertain
cf_species - Whether the species' epithet is uncertain
aff_species - Species' epithet uncertain
questionable - Whether the species name is questionable
native - Is the species native
quest_native - Is the native status questionable
naturalized - Is the species naturalized
endemic_ref - Is the species endemic at the reference level
quest_end_ref - Is the endemic_ref status questionable
endemic_list - Is the species endemic at the list level
quest_end_list - Is the endemic_list status questionable
genus - Genus name before taxonomic harmonization
species_epithet - Epithet before taxonomic harmonization
subtaxon - Subtaxon name before taxonomic harmonization
author - Author who described the species before taxonomic harmonization
matched - Is the species name matched in the taxonomic backbone
epithetscore - Matching score for the epithet
overallscore - Overall matching score for the species
resolved - Is the species name resolved in the taxonomic backbone
synonym -Is the species a synonym in the taxonomic backbone
matched_subtaxon -Is the sub-species name matched in the taxonomic backbone
accepted - Is the species name accepted in the taxonomic backbone
service - Service use for the taxonomic harmonization
work_ID -Identification number of the species after taxonomic harmonization
taxon_ID -Identification number of the taxonomic group
work_genus - Identification number of the genus after taxonomic harmonization
work_species_epithet - Identification number of the species epithet after taxonomic harmonization
work_species - Species name (after taxonomic harmonization)
work_author - Author who described the species (after taxonomic harmonization)

Value

A data frame with 33 columns.

References

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

`Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and`

```
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_species_lookup()`

Examples

```
ex <- GIFT_species_distribution()
```

`GIFT_species_lookup` *Species list in GIFT*

Description

Retrieve all name matching information for one taxonomic name. All results are returned, where the name is either found in the unstandardized or taxonomically standardized names.

Usage

```
GIFT_species_lookup(
  genus = "",
  epithet = "",
  namesmatched = FALSE,
  api = "https://gift.uni-goettingen.de/api/extended/",
  GIFT_version = "latest"
)
```

Arguments

`genus`	character string defining the genus name to be looked for.
`epithet`	character string defining the specific epithet to be looked for.
`namesmatched`	Logical `FALSE` by default, set to `TRUE` if you want to look for the species not only in the standardized species names but also in the original species names as they came in the original resources.
`api`	character string defining from which API the data will be retrieved.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.

Details

Here is what each column refers to: *orig_ID* - Identification number of the species before taxonomic harmonization
orig_genus - Genus before taxonomic harmonization
name_ID - Identification number of the genus before taxonomic harmonization
cf_genus- Whether the genus name is uncertain
genus- Genus before taxonomic harmonization
cf_species- Whether the species' epithet is uncertain
aff_species- Species' epithet uncertain
species_epithet- Epithet of the species before taxonomic harmonization
subtaxon- Subtaxon of the species before taxonomic harmonization
author- Author who described the species (before taxonomic harmonization)
matched- Is the species matched in the taxonomic backbone
epithetscore- Matching score for the epithet
overallscore- Overall matching score for the species
resolved- Is the species name resolved in the taxonomic backbone
synonym- Is the species name a synonym in the taxonomic backbone
matched_subtaxon- Is the subtaxon matched in the taxonomic backbone
accepted- Is the species name accepted in the taxonomic backbone
service- Service use for the taxonomic harmonization
work_ID- Identification number of the species after taxonomic harmonization
taxon_ID- Identification number of the taxonomic group
work_genus- Identification number of the genus after taxonomic harmonization
work_species_epithet- Identification number of the species epithet after taxonomic harmonization
work_species - Species name (after taxonomic harmonization)
work_author- Author who described the species (after taxonomic harmonization)

Value

A data frame with 19 columns (or 24 if namesmatched = TRUE).

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_checklists()`

Examples

```
ex <- GIFT_species_lookup(genus = "Fagus", epithet = "sylvatica")
```

`GIFT_taxgroup` *Taxonomic group of species*

Description

Assign taxonomic groups of various hierarchical level to species from GIFT (`work_ID`).

Usage

```
GIFT_taxgroup(
  work_ID = NULL,
  taxon_lvl = c("family", "order", "higher_lvl")[1],
  return_ID = FALSE,
  GIFT_version = "latest",
  api = "https://gift.uni-goettingen.de/api/extended/",
  taxonomy = NULL,
  species = NULL
)
```

Arguments

`work_ID`	A vector defining the IDs of the species to retrieve taxonomic groups for. `NULL` by default.
`taxon_lvl`	taxonomic level to retrieve names for. `family` by default. Check `GIFT_taxonomy()` for available levels. In addition to the available levels one can put `higher_lvl` to retrieve the higher level groups "Anthocerotophyta", "Marchantiophyta", "Bryophyta", "Lycopodiophyta", "Monilophyta", "Gymnospermae", and "Angiospermae".
`return_ID`	logical indicating whether to give back taxon_IDs instead of names.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.
`api`	character string defining from which API the data will be retrieved.
`taxonomy`	option to supply taxonomy object here if loaded already to avoid double loading. For internal use within GIFT functions. If `NULL` (default) taxonomy will be loaded within this function.
`species`	option to supply species names object here if loaded already to avoid double loading. For internal use within GIFT functions. If `NULL` (default) species will be loaded within this function.

Value

A vector with the taxonomic group of the species used as input.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_taxonomy()`

Examples

```
ex <- GIFT_taxgroup(work_ID = c(1, 4, 7, 8), taxon_lvl = "family")
```

`GIFT_taxonomy` *Taxonomy of GIFT*

Description

Retrieves the taxonomy of GIFT.

Usage

```
GIFT_taxonomy(
  GIFT_version = "latest",
  api = "https://gift.uni-goettingen.de/api/extended/"
)
```

Arguments

`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.
`api`	character string defining from which API the data will be retrieved.

Details

Here is what each column refers to:

taxon_ID - the identification number of each taxonomic entry.
taxon_name - names describing taxa.
taxon_name - author name for a given taxon.
taxon_lvl - splits every taxon in genus, family, order or superior orders. Taxonomy is a linear sequence of left and right borders for each taxon. This is nested, for example left and right borders of a genus would fall between the left and right borders of the corresponding family.
lft - left border of one taxon in the taxonomic sequence.
rgt - right border of one taxon in the taxonomic sequence.

Value

A data frame with 6 columns.

References

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

Weigelt, P, König, C, Kreft, H. GIFT - A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_checklists()`

Examples

```
ex <- GIFT_taxonomy()
```

`GIFT_traits` *Trait values at the species level*

Description

Retrieve specific trait values.

Usage

```
GIFT_traits(
  trait_IDs = "",
  agreement = 0.66,
  bias_ref = TRUE,
  bias_deriv = TRUE,
  api = "https://gift.uni-goettingen.de/api/extended/",
  GIFT_version = "latest"
)
```

Arguments

`trait_IDs`	a character string indicating which trait you want to retrieve. Traits must belong to the available list of traits.
`agreement`	Percentage of resources that agree on an aggregated trait value, entries below this threshold will be omitted.
`bias_ref`	When FALSE, exclude entries that are only based on a resource that potentially introduces a bias (e.g. a resource only including trees).
`bias_deriv`	When FALSE, exclude entries that are only based on a derivation that potentially introduces a bias (e.g. all phanerophytes being woody but some life forms being ambiguous).
`api`	character string defining from which API the data will be retrieved.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.

Details

Here is the detail of each column:

trait_ID - Identification number of the trait
work_ID - Identification number of the taxonomically harmonized species
species - Species name
trait_value - Value of the trait
agreement - Agreement score between the different sources for that trait value, only for categorical traits
cv - Coefficient of variation for the different sources for that trait value, only for numeric traits
n - Number of sources leading to the trait value
references - ref_ID from which we got the trait information

Value

A long-format data frame with 6 columns: `trait_ID`, `work_ID`, `species`, `trait_value`, `agreement` and `references`.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16– 43. https://doi.org/10.1111/jbi.13623

See Also

`GIFT_traits_meta()`

Examples

```
self_fertilization <- GIFT_traits(trait_IDs = "3.1.1", agreement = 0.66,
bias_ref = FALSE, bias_deriv = FALSE)
```

GIFT_traits_meta *Trait metadata*

Description

Retrieve metadata of the functional traits coming from GIFT.

Usage

```
GIFT_traits_meta(
  api = "https://gift.uni-goettingen.de/api/extended/",
  GIFT_version = "latest"
)
```

Arguments

`api`	Character string corresponding to the API.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the most up-to-date version.

Details

Here is what each column refers to:

Lvl1 - First level of the trait classification
Category - Name of the first level of classification
Lvl2 - Second level of the trait classification
Trait1 - Name of the second level of classification
Lvl3 - Identification number of the trait
Trait2 - Trait name
Units - Trait unit
type - Trait type
comment - Comment
count - How many entries for that traits are in the database

Value

A data frame with 10 columns.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16– 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_traits()`

Examples

```
ex <- GIFT_traits_meta()
```

`GIFT_traits_raw` *Raw trait values*

Description

Retrieve non-aggregated trait values at the level of the bibliographic references and un-standardized species names in GIFT.

Usage

```
GIFT_traits_raw(
  trait_IDs = "",
  derived = TRUE,
  bias_ref = TRUE,
  bias_deriv = TRUE,
  api = "https://gift.uni-goettingen.de/api/extended/",
  GIFT_version = "latest"
)
```

Arguments

`trait_IDs`	a character string indicating which traits you want to retrieve. Traits must belong to the available list of traits. See `GIFT_traits_meta()`.
`derived`	include logically derived traits.
`bias_ref`	When `FALSE`, exclude entries that are only based on a resource that potentially introduces a bias (e.g. a resource only including trees).
`bias_deriv`	When `FALSE`, exclude entries that are only based on a derivation that potentially introduces a bias (e.g. all phanerophytes being woody but some life forms being ambiguous).
`api`	character string defining from which API the data will be retrieved.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.

Details

Here is the detail of each column:

trait_derived_ID - Identification number of the trait record in the database
ref_ID - Identification number of the reference
orig_ID - Identification number of the species, as it came in the source
trait_ID - Identification number of the trait
trait_value - Value of the trait (coded as character, even for continuous trait)
derived - Is the trait value derived from another information (e.g. phanerophytes are woody)
bias_deriv - Is the derivation potentially introducing a bias
bias_ref - Is the resource potentially introducing a bias
name_ID - Identification number of the species before being resolved
cf_genus - Whether the genus name is uncertain
genus - Genus of the species
cf_species - Whether the species' epithet is uncertain
aff_species - Species' epithet uncertain
species_epithet - Epithet of the species
subtaxon - Sub-taxon name
author - Author who described the species
matched - Was the species name matched in the taxonomic backbone
epithetscore - Matching score for the epithet
overallscore - Overall matching score

resolved - Was the species name resolved in the taxonomic backbone
service - Taxonomic backbone used for taxonomic harmonization
work_ID - Identification number of the taxonomically harmonized species
genus_ID - Identification number of the taxonomically harmonized genus
work_genus - Genus name (after taxonomic harmonization)
work_species - Species name (after taxonomic harmonization)
work_author - Name of the author who described the species
geo_entity _ref - Name of the region of the reference
ref_long - Full reference to cite

Value

A data.frame with 28 columns.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16– 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_traits_meta()` and `GIFT_traits()`

Examples

```
succulence <- GIFT_traits_raw(trait_IDs = c("4.10.1"))
```

`GIFT_traits_tax` *Traits at the taxonomic level*

Description

Retrieve specific trait values at a high taxonomic level.

Usage

```
GIFT_traits_tax(
  trait_IDs = "",
  agreement = 0.66,
  bias_ref = TRUE,
```

```
  bias_deriv = TRUE,
  api = "https://gift.uni-goettingen.de/api/extended/",
  GIFT_version = "latest"
)
```

Arguments

`trait_IDs`	a character string indicating which trait you want to retrieve. Traits must belong to the available list of traits.
`agreement`	Percentage of resources that agree on an aggregated trait value, entries below this threshold will be omitted.
`bias_ref`	When `FALSE`, exclude entries that are only based on a resource that potentially introduces a bias (e.g. a resource only including trees).
`bias_deriv`	When `FALSE`, exclude entries that are only based on a derivation that potentially introduces a bias (e.g. all phanerophytes being woody but some life forms being ambiguous).
`api`	character string defining from which API the data will be retrieved.
`GIFT_version`	character string defining the version of the GIFT database to use. The function retrieves by default the `latest` stable version. If set to `beta`, the most up-to-date version which is still subject to changes and edits is used.

Details

Here is the detail of each column:

taxon_ID - Identification number of the taxon
taxon_name - Name of the taxon
agreement - Agreement score between the different sources for that trait value, only for categorical traits
references - Source of the trait values (`ref_ID`)
negative - Does the record indicate the absence of trait value in taxon_ID

and then one column per trait with the respective trait values

Value

A long-format data frame with 7 columns: `taxon_ID`, `taxon_name`, `trait_value`, `agreement`, `references` and `negative`.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_traits_meta()`

Examples

```
ex <- GIFT_traits_tax(trait_IDs = c("1.2.1", "1.4.1"),
bias_ref = FALSE, bias_deriv = FALSE)
```

`GIFT_versions` *Versions of GIFT available*

Description

Returns a table with information on the different versions of the database

Usage

```
GIFT_versions()
```

Details

Here is what each column refers to:

ID - Identification number of the version
version - Version number
description - What were the major updates about

Value

A data frame with 4 columns.

References

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

Weigelt, P, König, C, Kreft, H. GIFT – A Global Inventory of Floras and
Traits for macroecology and biogeography. J Biogeogr. 2020; 47: 16- 43.
https://doi.org/10.1111/jbi.13623
```

See Also

`GIFT_checklists()`

Examples

```
ex <- GIFT_versions()
```

`western_mediterranean` *Shape file of the western Mediterranean basin*

Description

Shape file encompassing the western part of the Mediterranean basin. CRS is WGS84.

Usage

```
data("western_mediterranean")
```

Format

An object of class `"sf"`

Examples

```
data(western_mediterranean)
```

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