

# Package ‘GIFT’

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**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](https://gift.uni-goettingen.de/api/extended/index2.0.php?query=env_raster).

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**License** GPL (>= 2)

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<https://biogeomacro.github.io/GIFT/>

**BugReports** <https://github.com/BioGeoMacro/GIFT/issues>

**VignetteBuilder** knitr

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GIFT_checklists	<i>GIFT_checklists</i>
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### 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 <i>ref_ID</i> 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 ( <i>family</i> and <i>tax_group</i> ) 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.

<code>type_ref</code>	Character, options are Account, Catalogue, Checklist, Flora, Herbarium collection, Key, Red list, Report, Species Database, Survey.
<code>entity_class</code>	Character, options are Island, Island/Mainland, Mainland, Island Group, Island Part.
<code>native_indicated</code>	Logical, whether only lists where native status is available should be retrieved.
<code>natural_indicated</code>	Logical, whether only lists where natural status is available should be retrieved.
<code>end_ref</code>	Logical, whether only lists where endemism at the reference level is available should be retrieved.
<code>end_list</code>	Logical, whether only lists where endemism at the list level is available should be retrieved.
<code>suit_geo</code>	logical indicating whether only regions classified as <code>suit_geo</code> should be considered (see details).
<code>complete_taxon</code>	Logical, default TRUE.
<code>GIFT_version</code>	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.
<code>api</code>	character string defining from which API the data will be retrieved.
<code>list_set</code>	<code>list_set</code> NULL by default. If not, it has to be the list table (see <a href="#">GIFT_lists()</a> ). Used internally in <a href="#">GIFT_checklists()</a> to avoid downloading the table of lists many times.
<code>taxonomy</code>	default NULL. If not, it has to be the taxonomy table (see <a href="#">GIFT_taxonomy()</a> ).

## 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

<code>ref_ID</code>	A vector defining the IDs of the references to retrieve. NULL by default.
<code>list_ID</code>	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 <code>ref_ID</code> .
<code>namesmatched</code>	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.
<code>taxon_name</code>	Character string corresponding to the taxonomic group of interest.
<code>floristic_group</code>	Character string among these options: <code>all</code> , <code>native</code> , <code>naturalized</code> , <code>endemic_list</code> , <code>endemic_ref</code> .
<code>list_set</code>	NULL by default. If not, it has to be the list table (see <code>GIFT_lists()</code> ). Used internally in <code>GIFT_checklists()</code> to avoid downloading the table of lists many times.
<code>taxonomy</code>	NULL by default. If not, it has to be the taxonomy table (see <code>GIFT_taxonomy()</code> ). Used internally in <code>GIFT_checklists()</code> to avoid downloading the taxonomy table many times. #'
<code>GIFT_version</code>	character string defining the version of the GIFT database to use. The function retrieves by default the latest stable version. If set to <code>beta</code> , the most up-to-date version which is still subject to changes and edits is used.
<code>api</code>	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**

<code>what</code>	character indicating whether <code>taxonomic_coverage</code> or <code>trait_coverage</code> shall be retrieved.
<code>taxon_name</code>	Name of the taxonomic group you want to retrieve coverage for. See <a href="#">GIFT_taxonomy()</a> for options. The function accepts family names and higher taxonomic groups.
<code>trait_ID</code>	Identification number of the trait you want to retrieve coverage for. See <a href="#">GIFT_traits_meta()</a> for details.
<code>GIFT_version</code>	character string defining the version of the GIFT database to use. The function retrieves by default the latest stable version. If set to <code>beta</code> , the most up-to-date version which is still subject to changes and edits is used.
<code>api</code>	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.
<b>Important note</b>	
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<sup>2</sup> 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**

<code>clade</code>	Character string indicating the taxonomic group of interest corresponding to the node labels in the phylogeny.
<code>as_tree</code>	Logical, whether you want the phylogeny to be returned as a phylogenetic tree (TRUE) or in a table (FALSE). TRUE by default.
<code>return_work_ID</code>	Logical, whether you want to retrieve the species' names or their identification number ( <code>work_ID</code> ) in the GIFT database. FALSE by default.
<code>work_ID_subset</code>	A vector of <code>work_ID</code> to prune the phylogenetic tree. NULL by default.
<code>api</code>	character string defining from which API the data will be retrieved.
<code>GIFT_version</code>	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**

<code>api</code>	character string defining from which API the data will be retrieved.
<code>GIFT_version</code>	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	<i>Metadata for GIFT regions</i>
--------------	----------------------------------

---

**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\_lv13\_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**

<code>taxon_name</code>	Taxonomic group to retrieve species richness for.
<code>GIFT_version</code>	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.
<code>api</code>	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**

<code>entity_ID</code>	A vector defining the IDs of the regions.
<code>api</code>	character string defining from which API the data will be retrieved.
<code>GIFT_version</code>	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 km<sup>2</sup> 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 <code>centroid_inside</code> , <code>extent_intersect</code> , <code>shape_intersect</code> and <code>shape_inside</code> . For example, <code>extent_intersect</code> 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 <code>GIFT_checklists_conditional()</code> .
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 <code>beta</code> , 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	<i>Taxonomic group of species</i>
---------------	-----------------------------------

---

### 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**

<code>trait_IDs</code>	a character string indicating which trait you want to retrieve. Traits must belong to the available list of traits.
<code>agreement</code>	Percentage of resources that agree on an aggregated trait value, entries below this threshold will be omitted.
<code>bias_ref</code>	When FALSE, exclude entries that are only based on a resource that potentially introduces a bias (e.g. a resource only including trees).
<code>bias_deriv</code>	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).
<code>api</code>	character string defining from which API the data will be retrieved.
<code>GIFT_version</code>	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	<i>Trait metadata</i>
------------------	-----------------------

---

## 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**

<code>trait_IDs</code>	a character string indicating which traits you want to retrieve. Traits must belong to the available list of traits. See <a href="#">GIFT_traits_meta()</a> .
<code>derived</code>	include logically derived traits.
<code>bias_ref</code>	When FALSE, exclude entries that are only based on a resource that potentially introduces a bias (e.g. a resource only including trees).
<code>bias_deriv</code>	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).
<code>api</code>	character string defining from which API the data will be retrieved.
<code>GIFT_version</code>	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	<i>Traits at the taxonomic level</i>
-----------------	--------------------------------------

---

### 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	<i>Versions of GIFT available</i>
---------------	-----------------------------------

---

**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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