Package 'expowo'

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Type Package

Title Data Mining of Plant Diversity and Distribution

Version 2.0

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Description Produces diversity estimates and species lists with associated global distribution for any vascular plant family and genus from 'Plants of the World Online' database <https://powo.science.kew.org/>, by interacting with the source code of each plant taxon page. It also creates global maps of species richness, graphics of species discoveries and nomenclatural changes over time.

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Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

Depends R (>= 3.5.0)

Imports RColorBrewer, dplyr, magrittr, data.table, ggplot2, rnaturalearth, sp, sf, utils, R.utils, flora, tibble, cowplot, plyr, PupillometryR, scales, viridisLite

Suggests covr, knitr, rmarkdown, testthat (>= 3.0.0)

URL <https://dboslab.github.io/expowo/>,

<https://github.com/dboslab/expowo>

BugReports <https://github.com/DBOSlab/expowo/issues>

Config/testthat/edition 3

NeedsCompilation no

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Repository CRAN

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R **topics documented:**

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accGraph	*Create graphics of species discoveries accumulation and nomenclatural changes*

Description

Produces graphics of the dynamics of species description and historical nomenclature changes within any family or genus provided. It is designed to create graphics based on the dataframe resulted from powoSpecies. The graph type can be selected by two arguments (spp_acc and spp_changes) and then multiple graphs for any different taxonomic groups within the input data can be produced automatically in a single run.

Usage

```
accGraph(inputdf = NULL,
         verbose = TRUE,
         spp_acc = TRUE,
         spp_changes = TRUE,
         spp_changes_col = NULL,
         genus_plots = TRUE,
         save = FALSE,
         dir = "results_accGraph",
         filename = "cumulative_discovery_",
         format = "pdf")
```

Arguments

inputdf	A dataframe generated using powoSpecies function using the argument synonyms set as TRUE and containing the genus and species column and the associated information about the protologue of each species. The species name must be binomial, i.e. must contain both the genus name and specific epithet.
verbose	Logical, if FALSE, a message showing each step during the POWO search will not be printed in the console in full.
spp_acc	Logical. Setting to FALSE means that you do not want to create individual accumulation graphs for each genus present in your dataset. The default is TRUE.
spp_changes	Logical. Setting to FALSE means that you do not want to create a violin plot with all data provided. The default is TRUE.
spp_changes_col	
	Define the name of a column in the main input data for which the species changes will be considered. For example, if densities and jitters should be presented for each genus in the same graphic, then set spp_changes_col = "genus". If you are plotting the dynamics of nomenclatural changes across the entire dataset in a single density graphic, then you must add a new column in your input data containing the same character inside all rows. In this case, ensure that you also keep genus_plots = TRUE.
genus_plots	Logical. If FALSE, a single density and jitter plot graphic will be produced for the entire input data. The default is TRUE, which will result in a graphic where multiple densities and jitters will be created inside the graphic, depending on the chosen column.
save	Logical, if TRUE, the search results will be saved on disk.
dir	Pathway to the computer's directory, where the file will be saved provided that the argument save is set up in TRUE. The default is to create a directory named **results_accGraph** and the search results will be saved within a subfolder named after the current date.
filename	Name of the output file to be saved. The default is to create a file entitled **cumulative_discovery_**.
format	A character vector related to the file format of the graph to be saved. The default is "pdf" to save the output in Portable Document Format (.pdf), but you can also choose "jpg" to save in Joint Photographic Experts Group (.jpg), "tiff" to save in Tag Image File Format (.tiff) or "png" to save in Portable Network Graphics (.png).

Value

Objects of class c("gg", "ggplot") and saves the output on disk.

Author(s)

Debora Zuanny & Domingos Cardoso

See Also

megaGen

topGen

powoSpecies

powoFam

powoGenera

powoMap

Examples

```
## Not run:

library(expowo)

accGraph(inputdf = "output",
         verbose = TRUE,
         spp_acc = TRUE,
         spp_changes = TRUE,
         spp_changes_col = "genus",
         genus_plots = TRUE,
         save = FALSE,
         dir = "results_accGraph",
         filename = "cumulative_discovery_Cyperaceae",
         format = "pdf")

## End(Not run)
```

---

angioData   *List of Angiosperm species*

Description

Complete list of all non-hybrid species and associated data of Lecythidaceae, Aristolochiaceae, Martyniaceae, Cabombaceae, and Begoniaceae, as retrieved from POWO database in November 2022 using the expowo's function powoSpecies.

Usage

```
data(angioData)
```

Format

```
data.frame
```

| angioGenera | *List of Angiosperm genera* |

Description

Complete list of all genera and associated data of Lecythidaceae, Aristolochiaceae, Begoniaceae, Martyniaceae, Dipterocarpaceae, and Fagaceae, as retrieved from POWO database in January 2023 using the expowo's function powoGenera.

Usage

```
data(angioGenera)
```

Format

```
data.frame
```

| botregions | *Countries and associated classification of botanical divisions* |

Description

Countries and associated classification of botanical divisions according to the World Geographical Scheme for Recording Plant Distributions.

Usage

```
data(botregions)
```

Format

```
data.frame
```

Source

https://www.tdwg.org/standards/wgsrpd/

get_year_pubs   *Secondary function to transform data generated with powoSpecies*

Description

Produces a spreadsheet with extra data about the publication, adding the corrected year of publication and the counting of synonyms of each species. It is an optional function to be used after run expowo's `powoSpecies` and to use as input data in the expowo's `accGraph`.

Usage

```
get_year_pubs(inputdf = NULL,
              verbose = TRUE,
              save = FALSE,
              dir = "results_POWO_with_year_pubs",
              filename = "POWO_with_year_pubs")
```

Arguments

inputdf	A dataframe generated using `powoSpecies` function with the argument synonyms set as `TRUE` and containing the genus and species column and the associated information about the protologue of each species. The species name must be binomial, i.e. must contain both the genus name and specific epithet.
verbose	Logical, if `FALSE`, a message showing each step during the POWO search will not be printed in the console in full.
save	Logical, if `TRUE`, the transformed input POWO database will be saved on disk.
dir	Pathway to the computer's directory, where the file will be saved provided that the argument save is set up in `TRUE`. The default is to create a directory named **results_POWO_with_year_pubs** and the search results will be saved within a subfolder named after the current date.
filename	Name of the output file to be saved. The default is to create a file entitled **POWO_with_year_pubs**.

Value

Objects of class dataframe and saves the output on disk.

Author(s)

Debora Zuanny & Domingos Cardoso

See Also

[megaGen](#)

[powoSpecies](#)

[powoFam](#)

    [powoGenera](#)

    [accGraph](#)

Examples

```
## Not run:

library(expowo)

output <- powoSpecies(family = "Fabaceae",
                      genus = NULL,
                      synonyms = TRUE,
                      country = NULL,
                      save = FALSE,
                      dir = "Fabaceae_results_powoSpecies",
                      filename = "Fabaceae_spp")


output_year_pubs <- get_year_pubs(inputdf = output,
                                  verbose = TRUE,
                                  save = FALSE,
                                  dir = "results_POWO_with_year_pubs",
                                  filename = "POWO_with_year_pubs")

## End(Not run)
```

---

megaGen   *Extract megadiverse genera of any plant family*

Description

Produces a CSV file listing all mega-diverse genera for any plant family at Plants of the World Online (POWO) based on a provided numeric value as the threshold to be considered mega-diverse. Frodin (2004) suggests 500 species as the threshold.

Usage

```
megaGen(family,
        thld = 500,
        verbose = TRUE,
        save = FALSE,
        dir = "results_megaGen",
        filename = "output")
```

Arguments

`family`	Either one family name or a vector of multiple families that is present in POWO.
`thld`	A defined threshold of species number for a genus to be considered megadiverse. The default value is 500 based on Frodin (2004).
`verbose`	Logical, if `FALSE`, a message showing each step during the POWO search will not be printed in the console in full.
`save`	Logical, if `TRUE`, the search results will be saved on disk.
`dir`	Pathway to the computer's directory, where the file will be saved provided that the argument `save` is set up in `TRUE`. The default is to create a directory named **results_megaGen** and the search results will be saved within a subfolder named after the current date.
`filename`	Name of the output file to be saved. The default is to create a file entitled **output**.

Value

A table with the following fields: family, genus, authors, scientific_name, species_number (counting of species within each genus), kew_id (each genus code within Kew's databases), powo_uri (URI to access each genus in POWO).

Author(s)

Debora Zuanny & Domingos Cardoso

See Also

POWOcodes

Examples

```
## Not run:

library(expowo)

megaGen(family = "Cyperaceae",
        thld = 500,
        save = FALSE,
        dir = "results_megaGen",
        filename = "Cyperaceae_big_genera")

## End(Not run)
```

POWOcodes *Complete list of vascular plant families and associated URI addresses*

Description

Complete list of the vascular plants (APG IV-based families of flowering plants, gymnosperm and pteridophytes) and associated URI addresses as retrieved with the function get_pow of the package taxize.

Usage

```
data(POWOcodes)
```

Format

```
data.frame
```

---

powoFam *Extract species number of any plant family*

Description

Produces a CSV file listing the number of species and genera within the target botanical families of vascular plants available at Plants of the World Online (POWO).

Usage

```
powoFam(family,
        verbose = TRUE,
        save = FALSE,
        dir = "results_powoFam",
        filename = "output")
```

Arguments

family	Either one family name or a vector of multiple families that is present in POWO.
verbose	Logical, if FALSE, a message showing each step during the POWO search will not be printed in the console in full.
save	Logical, if TRUE, the search results will be saved on disk.
dir	Pathway to the computer's directory, where the file will be saved provided that the argument save is set up in TRUE. The default is to create a directory named **results_powoFam** and the searched results will be saved within a subfolder named after the current date.
filename	Name of the output file to be saved. The default is to create a file entitled **output**.

Value

A table with the following fields: family, genus_number (counting of genera within the specified plant family), species_number (countig of species within each genus), kew_id (the family code used in Kew's database), powo_uri (the URI to access the family in POWO).

Author(s)

Debora Zuanny & Domingos Cardoso

See Also

[megaGen](#)

[topGen](#)

[powoGenera](#)

[powoSpecies](#)

[powoMap](#)

[POWOcodes](#)

Examples

```
## Not run:
library(expowo)

powoFam(family = "Lecythidaceae",
        save = FALSE,
        dir = "results_powoFam",
        filename = "Lecythidaceae_spp_number")

## End(Not run)
```

---

powoGenera   *Extract list of genera for any plant family*

Description

Produces a CSV file listing all genera with associated number of accepted species and geographical distribution for any vascular plant family at Plants of the World Online (POWO).

Usage

```
powoGenera(family,
           genus = NULL,
           hybrid = FALSE,
           country = NULL,
           verbose = TRUE,
```

```
rerun = FALSE,
save = FALSE,
dir = "results_powoGenera",
filename = "output")
```

Arguments

`family`	Either one family name or a vector of multiple families that is present in POWO.
`genus`	Either one genus name or a vector of multiple genera that is present in POWO. If any genus name is not provided, then the function will search all accepted genera known for the target family.
`hybrid`	Logical, if `TRUE`, the search results will include hybrid genera.
`country`	Either one country name or a vector of multiple countries. If country names are provided, then the function will return only the genera that are native to such countries, according to POWO.
`verbose`	Logical, if `FALSE`, a message showing each step during the POWO search will not be printed in the console in full.
`rerun`	Logical, if `TRUE`, a previously stopped search will continue from where it left off, starting with the last retrieved taxon. Please ensure that the 'filename' argument exactly matches the name of the CSV file saved from the previous search, and that the previously saved CSV file is located within a subfolder named after the current date. If it is not, please rename the date subfolder accordingly."
`save`	Logical, if `TRUE`, the search results will be saved on disk.
`dir`	Pathway to the computer's directory, where the file will be saved provided that the argument `save` is set up in `TRUE`. The default is to create a directory named **results_powoGenera** and the search results will be saved within a subfolder named after the current date.
`filename`	Name of the output file to be saved. The default is to create a file entitled **output**.

Value

A table with the following fields: family, genus, authors, scientific_name, publication (information about the protologue of the genus), species_number, native_to_country (original distribution according to political country), native_to_botanical_countries (original distribution according to botanical country), introduced_to_country (exotic distribution according to political country), introduced_to_botanical_countries (exotic distribution according to botanical country), kew_id (genus code within Kew's databases), powo_uri (URI to access each genus in POWO).

Author(s)

Debora Zuanny & Domingos Cardoso

See Also

megaGen

topGen

[powoSpecies](#)

[powoFam](#)

[POWOcodes](#)

Examples

```
## Not run:
library(expowo)

powoGenera(family = "Lecythidaceae",
           verbose = TRUE,
           save = FALSE,
           dir = "results_powoGenera",
           filename = "Lecythidaceae_genera")

powoGenera(family = "Lecythidaceae",
           genus = "Bertholletia",
           country = c("Argentina", "Brazil", "French Guiana"),
           verbose = TRUE,
           save = FALSE,
           dir = "results_powoGenera",
           filename = "Lecythidaceae_search")

## End(Not run)
```

---

powoMap   *Create global maps of species richness*

Description

Produces global-scale maps of species richness at political country and botanical country levels. Despite being originally designed to create maps for all input data of any specified taxonomic group (genus or family) from the search results with powoSpecies, the function is also useful for any dataframe-formatted input data that has at least a column with species and one or two columns with associated distribution in the countries and/or botanical regions. Multiple richness maps for any different taxonomic groups within the input data can be produced automatically in a single run by just specifying a column name with the associated taxonomic classification.

Usage

```
powoMap(inputdf = NULL,
        botctrs = FALSE,
        distcol = NULL,
        taxclas = NULL,
        verbose = TRUE,
        save = FALSE,
        vir_color = "viridis",
```

```
            bre_color = NULL,
            leg_title = "SR",
            dpi = 600,
            dir = "results_powoMap",
            filename = "global_richness_map",
            format = "jpg")
```

Arguments

inputdf	A dataframe with a species column and the associated global distribution at country or botanical country level. The species name must be as a binomial, i.e. must contain both the genus name and specific epithet, but the authorship is optional. Each species must be as a single row with its corresponding full distribution in all countries and/or botanical regions within a single cell of their respective columns, where the country names or botanical regions are separated by a comma. This is, for example, the standard dataframe from the search results with the function powoSpecies.
botctrs	Logical. If TRUE, the species richness maps will be created according to the botanical country subdivisions of the world. Also, a WGSRPD folder including the level 3 shapefile and the associated Brummitt's (2001) book fully describing the World Geographical Scheme for Recording Plant Distributions will be downloaded into the working directory. If you do not remove this folder or rename any of the contents, then the function will not download the same folder again. The default is FALSE.
distcol	Column name with the full global distribution data for each species at political country level or the level 3 of botanical subdivision of the World Geographical Scheme for Recording Plant Distributions. If the species distribution is given with botanical subdivisions, then you must also change the argument botctrs to TRUE. If the distribution is described only by political country names, then set botctrs to FALSE.
taxclas	A character vector with the column name for the corresponding taxonomic classification of each species in any higher taxonomic level. If provided, the function will produce, in a single run, all global richness maps for every distinct group within the input data. The default is NULL, then the function will generate only one global species richness map for the entire input data.
verbose	Logical. If FALSE, a message showing the map creation steps will not be printed in the console in full.
save	Logical, if TRUE, the global maps will be saved on disk.
vir_color	A character vector with the name or code of any of the color palettes from Viridis package.
bre_color	A character vector with the name or code of any of the color palettes from RColorBrewer package.
leg_title	A character vector to be displayed in the output map as a legend. Default is to create a title called **SR**, an acronym for species richness.
dpi	One number in the range of 72-4000 referring to the image resolution in the format of dots per inch in the output file. Default is to create an output with 600 dpi.

dir   Pathway to the computer's directory, where the map file will be saved provided
                 that the argument save is set up in TRUE. The default is to create a directory
                 named **results_powoMap** and the search results will be saved within a subfolder
                 named after the current date.

filename   Name of the output file to be saved. The default is to create a file entitled
                 global_richness_map.

format   A character vector related to the file format of the global map to be saved. The
                 default is "jpg" to save the output in Joint Photographic Experts Group (.jpg),
                 but you can also choose "pdf" to save in Portable Document Format (.pdf), "tiff"
                 to save in Tag Image File Format (.tiff) or "png" to save in Portable Network
                 Graphics (.png).

Value

One or a list of objects of class c("gg", "ggplot").

Author(s)

Debora Zuanny & Domingos Cardoso

See Also

[megaGen](#)

[topGen](#)

[powoSpecies](#)

[powoFam](#)

[powoGenera](#)

Examples

```
## Not run:
library(expowo)

mapspdist <- powoSpecies(family = "Martyniaceae",
                         hybridspp = FALSE,
                         country = NULL,
                         verbose = TRUE,
                         save = FALSE,
                         dir = "results_powoSpecies",
                         filename = "Martyniaceae_spp")

# To create multiple maps for each genus within the input data according to
# political countries.
powoMap(inputdf = mapspdist,
        botctrs = FALSE,
        distcol = "native_to_country",
        taxclas = "genus",
        verbose = FALSE,
        save = FALSE,
```

```
                vir_color = "viridis",
                bre_color = NULL,
                leg_title = "SR",
                dpi = 600,
                dir = "results_powoMap",
                filename = "global_richness_country_map",
                format = "jpg")

# To create multiple maps for each genus within the input data according to
# botanical country subdivisions.
powoMap(inputdf = mapspdist,
        botctrs = TRUE,
        distcol = "native_to_botanical_countries",
        taxclas = "genus",
        verbose = FALSE,
        save = FALSE,
        vir_color = "viridis",
        bre_color = NULL,
        leg_title = "SR",
        dpi = 600,
        dir = "results_powoMap",
        filename = "global_richness_botcountry_map",
        format = "jpg")

## End(Not run)
```

---

powoSpDist   *Extract distribution of any plant species*

Description

Produces a CSV file listing the geographical distribution at country and botanical subdivisions of all target species of vascular plants at Plants of the World Online (POWO).

Usage

```
powoSpDist(family,
           species = NULL,
           verbose = TRUE,
           save = FALSE,
           dir = "results_powoSpDist",
           filename = "output")
```

Arguments

family   Either one family name or a vector of multiple families that is present in POWO.

species   Either one non-hybrid species name or a vector of multiple species that is present
             in POWO. If any species name is not provided, then the function will search any
             species from all accepted genera known for the target family.

verbose	Logical, if FALSE, a message showing each step during the POWO search will not be printed in the console in full.
save	Logical, if TRUE, the search results will be saved on disk.
dir	Pathway to the computer's directory, where the file will be saved provided that the argument save is set up in TRUE. The default is to create a directory named **results_powoSpDist** and the search results will be saved within a subfolder named after the current date.
filename	Name of the output file to be saved. The default is to create a file entitled **output**.

Value

A table with the following fields: family, genus, species, taxon_name, authors, scientific_name, native_to_country (original distribution according to political country), native_to_botanical_countries (original distribution according to botanical country), introduced_to_country (exotic distribution according to political country), introduced_to_botanical_countries (exotic distribution according to botanical country), kew_id (each species code within Kew's databases), powo_uri (URI to access each species in POWO).

Author(s)

Debora Zuanny & Domingos Cardoso

See Also

[POWOcodes](#)

Examples

```
## Not run:
library(expowo)

powoSpDist(family = "Lecythidaceae",
           species = "Lecythis pisonis",
           save = FALSE,
           dir = "results_powoSpDist",
           filename = "L_pisonis_distribution")

## End(Not run)
```

---

powoSpecies   *Extract list of species for any plant genus and family*

Description

Produces a CSV file listing all accepted species and associated geographical distribution from any target genus or family of vascular plants at Plants of the World Online (POWO).

Usage

```
powoSpecies(family,
            genus = NULL,
            hybrid = FALSE,
            synonyms = FALSE,
            country = NULL,
            verbose = TRUE,
            rerun = FALSE,
            save = FALSE,
            dir = "results_powoSpecies",
            filename = "output")
```

Arguments

`family`	Either one family name or a vector of multiple families that is present in POWO.
`genus`	Either one genus name or a vector of multiple genera that is present in POWO. If any genus name is not provided, then the function will search any species from all accepted genera known for the target family.
`hybrid`	Logical, if `TRUE`, the search results will include hybrid species.
`synonyms`	Logical, if `TRUE`, the search results will include synonyms.
`country`	Either one country name or a vector of multiple countries. If country names are provided, then the function will return only the species that are native to such countries, according to POWO.
`verbose`	Logical, if `FALSE`, a message showing each step during the POWO search will not be printed in the console in full.
`rerun`	Logical, if `TRUE`, a previously stopped search will continue from where it left off, starting with the last retrieved taxon. Please ensure that the 'filename' argument exactly matches the name of the CSV file saved from the previous search, and that the previously saved CSV file is located within a subfolder named after the current date. If it is not, please rename the date subfolder accordingly."
`save`	Logical, if `TRUE`, the search results will be saved on disk.
`dir`	Pathway to the computer's directory, where the file will be saved provided that the argument `save` is set up in `TRUE`. The default is to create a directory named **results_powoSpecies** and the search results will be saved within a subfolder named after the current date.
`filename`	Name of the output file to be saved. The default is to create a file entitled **output**.

Value

A table with the following fields: family, genus, species, taxon_name, authors, scientific_name, publication (information about the protologue of the species), native_to_country (original distribution according to political country), native_to_botanical_countries (original distribution according to botanical country), introduced_to_country (exotic distribution according to political country), introduced_to_botanical_countries (exotic distribution according to botanical country), kew_id (each species code within Kew's databases), powo_uri (the URI to access each species in POWO).

Author(s)

Debora Zuanny & Domingos Cardoso

See Also

megaGen

topGen

powoFam

powoGenera

POWOcodes

Examples

```
## Not run:
library(expowo)

powoSpecies(family = "Martyniaceae",
            synonyms = TRUE,
            country = c("Argentina", "Brazil", "French Guiana"),
            save = FALSE,
            dir = "Martyniaceae_results_powoSpecies",
            filename = "Martyniaceae_spp")

## End(Not run)
```

---

saveCSV   *Fastly save CSV file within a current date folder*

Description

Uses `fwrite` to fastly write a CSV file within a current date subfolder of a provided specific directory.

Usage

```
saveCSV(df,
        dir = "results",
        filename = "output",
        verbose = TRUE,
        append = FALSE,
        save = TRUE,
        foldername = NULL)
```

Arguments

df	Any input list of same length vectors (e.g. `data.frame` and `data.table`).
dir	Pathway to the computer's directory, where the file will be saved provided that the argument `save` is set up in `TRUE`. The default is to create a directory named **results** and the input `data.frame` will be saved within a subfolder named after the current date.
filename	Name of the output file to be saved. The default is to create a file entitled **output**.
verbose	Logical, if `FALSE`, a message showing the saving process will not be printed in the console in full.
append	Logical, if `TRUE`, the file is opened in append mode and column names (header row) are not written.
save	Logical, if `FALSE`, the input `data.frame` will be not be saved on disk.
foldername	A parameter only for internal use with expowo's main functions. You must keep this always as `NULL`.

Author(s)

Debora Zuanny & Domingos Cardoso

Examples

```
library(expowo)

res <- powoGenera(family = "Lecythidaceae",
                  verbose = TRUE,
                  save = FALSE)

saveCSV(res,
        dir = "results_powoGenera",
        filename = "Lecythidaceae_search",
        append = FALSE)
```

---

topGen	*Extract the top most species-rich genera of any plant family*

Description

Produces a CSV file listing the top most diverse genera of any target botanical family of vascular plants at Plants of the World Online (POWO).

Usage

```
topGen(family,
       limit = 10,
       verbose = TRUE,
       save = FALSE,
       dir = "results_topGen",
       filename = "output")
```

Arguments

`family`	Either one family name or a vector of multiple families that is present in POWO.
`limit`	A defined numerical value to limit the most diverse genera to be selected within each plant family. The default is to select the top ten richest genera.
`verbose`	Logical, if `FALSE`, a message showing each step during the POWO search will not be printed in the console in full.
`save`	Logical, if `TRUE`, the search results will be saved on disk.
`dir`	Pathway to the computer's directory, where the file will be saved provided that the argument `save` is set up in `TRUE`. The default is to create a directory named **results_topGen** and the search results will be saved within a subfolder named after the current date.
`filename`	Name of the output file to be saved. The default is to create a file entitled **output**.

Value

A table with the following fields: family, genus, authors, scientific_name, species_number (counting of species within each genus), kew_id (each genus code within Kew's databases), powo_uri (URI to access each genus in POWO).

Author(s)

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See Also

POWOcodes

Examples

```
## Not run:
library(expowo)

topGen(family = "Lecythidaceae",
       limit = 10,
       save = FALSE,
       dir = "results_topGen",
       filename = "Lecythidaceae_top_ten")

## End(Not run)
```

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