

# Package ‘expowo’

February 22, 2023

**Type** Package

**Title** Data Mining of Plant Diversity and Distribution for R

**Version** 1.0

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**Description** Produces diversity estimates and species lists with associated global distribution for any angiosperm 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, and creates global maps of species richness.

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.2.3

**Depends** R (>= 3.5.0)

**Imports** RColorBrewer, dplyr, magrittr, data.table, ggplot2, rnatuarearth, sp, sf, utils

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

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

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

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**NeedsCompilation** no

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**Repository** CRAN

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**R topics documented:**

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angioData	<i>List of Angiosperm species</i>
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**Description**

Complete list of all non-hybrid species and associated data of Lecythidaceae, Aristolochiaceae, Martyniaceae, Cabombaceae and Begoniaceae as retrieved from POWO database with the function powoSpecies of this package gathered at Nov 2022.

**Usage**

```
data(angioData)
```

**Format**

Dataframe

---

angioGenera	<i>List of Angiosperm genera</i>
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**Description**

Complete list of all genera and associated data of Lecythidaceae, Aristolochiaceae, Begoniaceae, Martyniaceae, Dipterocarpaceae, and Fagaceae as retrieved from POWO database with the function powoGenera of this package gathered at Jan 2023.

**Usage**

```
data(angioGenera)
```

**Format**

Dataframe

---

botregions	<i>Countries and associated classification of botanical divisions</i>
------------	---

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**Description**

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

**Usage**

```
data(botregions)
```

**Format**

Table in .csv format

**Source**

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

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megaGen	<i>Extract megadiverse genera from POWO</i>
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**Description**

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

**Usage**

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

**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) in Taxon.
verbose	Logical, if FALSE, the search results will not be printed in the console in full.
save	Logical, if FALSE, the searched results will not 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 <b>results_megaGen</b> and the searched results will be saved within a subfolder named by the current date.
filename	Name of the output file to be saved. The default is to create a file entitled <b>output</b> .

**Value**

Table in .csv format.

**Author(s)**

Debora Zuanny & Domingos Cardoso

**See Also**

[POWOCodes](#)

**Examples**

```
library(expowo)

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

---

POWOCodes

*Complete list of angiosperm families and associated URI addresses*

---

**Description**

Complete list of the APG IV-based families of flowering plants and associated URI addresses as retrieved with the function `get_pow` of the package `taxize`.

**Usage**

```
data(POWOCodes)
```

**Format**

Dataframe

---

powoFam

*Extract species number of any plant family from POWO*

---

## Description

Produces a CSV file listing the number of species within the target botanical families of flowering plants available at [Plants of the World Online \(POWO\)](#).

## Usage

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

## Arguments

family	Either one family name or a vector of multiple families that is present in POWO.
verbose	Logical, if FALSE, the search results will not be printed in the console in full.
save	Logical, if FALSE, the search results will not 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 <b>results_powoFam</b> and the searched results will be saved within a subfolder named by the current date.
filename	Name of the output file to be saved. The default is to create a file entitled <b>output</b> .

## Value

Table in .csv format.

## Author(s)

Debora Zuanny & Domingos Cardoso

## See Also

[megaGen](#)  
[topGen](#)  
[powoGenera](#)  
[powoSpecies](#)  
[powoMap](#)  
[POWOcodes](#)

## Examples

```
library(expowo)

powoFam(family = "Lecythidaceae",
        verbose = TRUE,
        save = FALSE,
        dir = "results_powoFam/",
        filename = "Lecythidaceae_spp_number")
```

---

powoGenera

*Extract list of genera from POWO*

---

## Description

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

## Usage

```
powoGenera(family, genus = NULL, country = NULL,
            verbose = TRUE, save = FALSE, dir, filename)
```

## 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 are present in POWO. If any genus name is not provided, then the function will search all accepted genera known for the target family.
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, the searched results will not be printed in the console in full.
save	Logical, if FALSE, the searched results will not 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 <b>results_powoGenera</b> and the searched results will be saved within a subfolder named by the current date.
filename	Name of the output file to be saved. The default is to create a file entitled <b>output</b> .

## Value

Table in .csv format.

**Author(s)**

Debora Zuanny & Domingos Cardoso

**See Also**

[megaGen](#)

[topGen](#)

[powoSpecies](#)

[powoFam](#)

[POWOCodes](#)

**Examples**

```
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")
```

---

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 <code>powoSpecies</code> .
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 <b>World Geographical Scheme</b> for Recording Plant Distributions. If the species distribution is given with botanical subdivisions, then you must also change the argument <code>botctrs</code> to TRUE. If the distribution is described only by political country names, then set <code>botctrs</code> 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, the map creation steps will not be printed in the console in full.
save	Logical. If FALSE, the global maps will not be saved on disk.



vir_color	A character vector with the name or code of any of the color palettes from <b>Viridis</b> package.
bre_color	A character vector with the name or code of any of the color palettes from <b>RColorBrewer</b> package.
leg_title	A character vector to be displayed in the output map as a legend. Default is to create a title called <b>SR</b> , 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 <code>save</code> is set up in TRUE. The default is to create a directory named <b>results_powoMap/</b> and the search results will be saved within a subfolder named by the current date.
filename	Name of the output file to be saved. The default is to create a file entitled <b>global_richness_map</b> .
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 list of species distribution from POWO*

---

## Description

Produces a CSV file listing the geographical distribution of all target species of flowering plants available at [Plants of the World Online \(POWO\)](#).

## Usage

```

powoSpDist(family, species = NULL,
           verbose = TRUE, save = FALSE, dir, filename)

```

**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 are 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, the search results will not be printed in the console in full.
save	Logical, if FALSE, the search results will not 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 <b>results_powoSpDist</b> and the search results will be saved within a subfolder named by the current date.
filename	Name of the output file to be saved. The default is to create a file entitled <b>output</b> .

**Value**

Table in .csv format.

**Author(s)**

Debora Zuanny & Domingos Cardoso

**See Also**

[POWOCodes](#)

**Examples**

```
library(expowo)

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

---

powoSpecies

*Extract list of species from POWO*

---

**Description**

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

**Usage**

```
powoSpecies(family, genus = NULL, hybridssp = FALSE, country = NULL,
            verbose = TRUE, save = FALSE, dir, filename)
```

**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 are 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.
hybridssp	Logical, if TRUE, the search results will include hybrid species.
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, the search results will not be printed in the console in full.
save	Logical, if FALSE, the search results will not 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 <b>results_powoSpecies</b> and the search results will be saved within a subfolder named by the current date.
filename	Name of the output file to be saved. The default is to create a file entitled <b>output</b> .

**Value**

Table in .csv format.

**Author(s)**

Debora Zuanny & Domingos Cardoso

**See Also**

[megaGen](#)  
[topGen](#)  
[powoFam](#)  
[powoGenera](#)  
[POW0codes](#)

**Examples**

```
library(expowo)

powoSpecies(family = "Martyniaceae",
            hybridssp = FALSE,
            country = c("Argentina", "Brazil", "French Guiana"),
```

```

verbose = TRUE,
save = FALSE,
dir = "results_powoSpecies/",
filename = "Martyniaceae_spp")

```

---

topGen

*Extract the top most species-rich genera*


---

### Description

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

### Usage

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

### 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, the search results will not be printed in the console in full.
save	Logical, if FALSE, the search results will not 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 <b>results_topGen</b> and the searched results will be saved within a subfolder named by the current date.
filename	Name of the output file to be saved. The default is to create a file entitled <b>output</b> .

### Value

Table in .csv format.

### Author(s)

Debora Zuanny & Domingos Cardoso

### See Also

[POWOCodes](#)

**Examples**

```
library(expowo)

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

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