

Package ‘rppo’

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Title Access the Global Plant Phenology Data Portal

URL <https://github.com/ropensci/rppo>

BugReports <https://github.com/ropensci/rppo/issues>

Version 1.0

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Description An R interface to the Global Plant Phenology Data Portal,
which is accessible online at <<https://www.plantphenology.org/>>.

Depends R (>= 3.4.0)

License GPL-2

Encoding UTF-8

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Suggests testthat, knitr, rmarkdown, covr

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rppo-package

Access the Global Plant Phenology Data Portal

Description

Access data from the global plant phenology data portal (PPO data portal) and phenology terms from the Plant Phenology Ontology (PPO)

Details

rppo enables users to query the global plant phenology data portal (PPO data portal), which is visible online at <http://plantphenology.org/>. The PPO data portal is an aggregation of phenology data from several different data sources. Currently it contains USA-NPN, NEON, and PEP725 data sources. The PPO data portal harvests data using the ppo-data-pipeline, with code available at <https://github.com/biocodellc/ppo-data-pipeline/>. All phenological terms in the data portal are aligned using the Plant Phenology Ontology (PPO), available at <https://github.com/PlantPhenoOntology/ppo>.

Two functions are contained in the **rppo**: [ppo_terms](#) allows users to discover present and absent phenological stages while [ppo_data](#) enables users to query the PPO data portal. The **rppo** package source code is available at <https://github.com/ropensci/rppo>.

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See Also

Useful links:

- <https://github.com/ropensci/rppo>
- Report bugs at <https://github.com/ropensci/rppo/issues>

ppo_data

*Access Data From the Global Plant Phenology Data Portal***Description**

Access data from the global plant phenology data portal (PPO data portal)

Usage

```
ppo_data(genus = NULL, specificEpithet = NULL, termID = NULL,
         fromYear = NULL, toYear = NULL, fromDay = NULL, toDay = NULL,
         bbox = NULL, limit = NULL)
```

Arguments

genus	(string) a plant genus name
specificEpithet	(string) a plant specific epithet
termID	(string) A single termID from the plant phenology ontology. See the ppo_terms function for more information.
fromYear	(integer) return data from the specified year
toYear	(integer) return data up to and including the specified year
fromDay	(integer) return data starting from the specified day
toDay	(integer) return data up to and including the specified day
bbox	(string) return data within a bounding box. Format is lat, long, lat, long and is structured as a string. Use this website: http://boundingbox.klokantech.com/ to quickly grab a bbox (set format on bottom left to csv and be sure to switch the order from long, lat, long, lat to lat, long, lat, long).
limit	(integer) limit returned data to a specified number of records

Details

The ppo_data function returns a list containing the following information: a readme file, citation information, a data frame with data, an integer with the number of records returned and a status code. The function is called with parameters that correspond to values contained in the data itself which act as a filter on the returned record set.

Value

Return value containing a list with the following components:

- 'data': A data frame containing data
- 'readme': A string with information about the return package
- 'citation': A string with citation information
- 'number_possible': An integer with total possible results
- 'status_code': An integer with status code returned from server

Examples

```
r1 <- ppo_data(genus = "Quercus", termID='obo:PPO_0002313', limit=10)
r2 <- ppo_data(fromDay = 1, toDay = 100, bbox="37,-120,38,-119", limit=10)
my_data_frame <- r2$data
```

ppo_terms

Access Terms From the Plant Phenology Ontology

Description

Access present and absent terms from the Plant Phenology Ontology

Usage

```
ppo_terms(present = FALSE, absent = FALSE)
```

Arguments

present (boolean) If TRUE then return all "present" phenological stages
absent (boolean) IF TRUE then return all "absent" phenological stages.

Details

The `ppo_terms` function returns terms from the Plant Phenology Ontology (PPO). The function only accepts parameters for "present" or "absent" terms. The response populates a data frame with: termID, label, description, and URI. Use the termID values in submitting termID values to the `ppo_data` function. The label and description fields are extracted from the Plant Phenology Ontology and are useful in determining the proper term to query on. The URI field contains a link to the term itself which is useful for determining superclass and subclass relationships for each term. For more information on the PPO ontology itself, we suggest loading the PPO <https://github.com/PlantPhenoOntology/ppo> with protege <https://protege.stanford.edu/>

Value

data.frame

Examples

```
presentTerms <- ppo_terms(present = TRUE)
absentTerms <- ppo_terms(absent = TRUE)
```

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