Package ‘chromer’

August 29, 2016

Title  Interface to Chromosome Counts Database API
Version  0.1
Date  2014-12-01
Description  A programmatic interface to the Chromosome Counts Database (http://ccdb.tau.ac.il/). This package is part of the rOpenSci suite (http://ropensci.org)
Depends  R (>= 2.15)
Imports  dplyr, httr, data.table
Suggests  testthat, roxygen2
URL  http://www.github.com/ropensci/chomer
BugReports  http://www.github.com/ropensci/chomer/issues/new
License  CC0
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NeedsCompilation  no
Repository  CRAN
Date/Publication  2015-01-13 10:27:09

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Description

This package is a R based interface to the Chromosome Counts Database (CCDB). Currently, this consists of just one function `chrom_counts`, which queries the database using the taxa supplied. The function `summarize_counts` cleans and processes the data.

References


Usage

```r
chrom_counts(taxa, rank = c("species", "genus", "family", "majorGroup"),
full = FALSE, foptions = list())
```

Arguments

taxa  Taxonomic name(s) to query. Can be either a single name, a vector of multiple names or a list. If supplying multiple names, these must all be of the same rank.

rank  Rank to query.

full  Logical. Whether to return full records. Defaults to FALSE which returns only partial records. Partial records includes the resolved name as well as the gametophytic (n) and sporophytic (2n) counts.

foptions  additional options to be passed to `httr::GET`
Details
When using the API to query for species, both matched names and resolved names are searched. This means that all records for potential synonyms will be returned as well. Currently species binomials must be specified by either 'genus species' (i.e., space between genus and species) or 'genus_species'.

To search for subspecies (subsp.) or varieties (var.), you can use search terms like: "Solanum acaule var. albicans".

Searching for "Solanum acaule" will return all subspecies and varieties.

Currently the only acceptable search terms when specifying "majorGroup" are "Angiosperms", "Gymnosperms", "Pteridophytes", or "Bryophytes".

Value
A data.frame containing all records matched by query

Examples
```
## Not run:

## Get all counts for genus Castilleja
chrom_counts("Castilleja", "genus")

## Get all counts for both Castilleja and Lachemilla
chrom_counts(c("Castilleja", "Lachemilla"), "genus")

## Get all counts for Castilleja miniata
chrom_counts("Castilleja miniata", "species")

## Get all counts for only Castilleja miniata subsp. elata
chrom_counts("Castilleja miniata subsp. elata", "species")

## Note that searching for "Castilleja miniata" will return
## all subspecies and varieties

## Get all counts for the Orobanchaceae
chrom_counts("Orobanchaceae", "family")
```

## End(Not run)

summarize_counts

Summarize chromosome counts from API call

Description
This function processes and cleans the data returned from the API call for use in downstream analysis.
summarize_counts

Usage

summarize_counts(counts)

Arguments

counts A 'chrom.counts' object inherited from chrom_counts.

Details

The results from the API call are a bit messy and difficult to use for downstream analyses. This function cleans up the data in three ways. First, it combines aggregates and summarizes all records from each species. Second, many of the counts are combined with text characters (e.g., "#-#", "c.#", and "#, #, "). This function uses regular expressions to pull out all and any numeric values from these strings. Third, some of the records are gametophytic (n) counts and others are from sporophytes (2n); the function simply divides the sporophytic counts in half so that all measurements are on a common scale.

IMPORTANT: Use this function with caution. Parsing the counts programmatically may be useful but it may generate erroneous results in some cases if input is in an odd format. For example, if the count is "#+-#", the function will return both the first and second # as valid counts. Given the creativity(?) of researchers in entering data, it is hard to predict all possible ways that the counts may be represented. Therefore, some manual checking will probably be necessary.

Value

A data.frame containing the resolved binomial, the count type (gametophytic or sporophytic), the counts, the inferred gametophytic count (for sporophytic records) and the number of records supporting each count.

Examples

## Not run:

## Get all counts for genus Castilleja
res <- chrom_counts("Castilleja", "genus")

## summarize the results
summarize_counts(res)

## End(Not run)
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