Package ‘rbison’

February 20, 2015

Title R Interface to the USGS BISON API

Description Interface to the USGS BISON API, a database for species occurrence data on the web. Data comes from species in the United States, from participating data providers. This package focuses mostly on getting data from BISON, via taxonomic and location based queries. A simple function is provided to help visualize data.

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URL https://github.com/ropensci/rbison

BugReports https://github.com/ropensci/rbison/issues

LazyLoad yes

LazyData yes

VignetteBuilder knitr

Imports plyr, httr, mapproj, ggplot2, grid, gridExtra, maptools, sp, dplyr, jsonlite

Suggests knitr, testthat, taxize

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R topics documented:

rbison-package .......................................................... 2
all_states ............................................................... 2
bison ................................................................. 3
bisonmap ............................................................. 4
bison_datause ....................................................... 5
rbisson-package

rbisson is an interface to the USGS Bison API.

Description

To get started, see the vignette in vignette(package="rbisson")

Details

See http://bison.usgs.ornl.gov/doc/api.jsp for API docs for the BISON API.

To cite rbisson, do citation(package='rbisson')

Use the following format to cite data retrieved from BISON:


For example:


Author(s)

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all_states

Data for a states map

Description

Data for a states map
Search for and collect data from the USGS Bison API.

Description

Search for and collect data from the USGS Bison API.

Usage

bison(species = NULL, type = "scientific_name", tsn = NULL, 
      start = NULL, count = 10, countyFips = NULL, county = NULL, 
      state = NULL, aoi = NULL, aoibbox = NULL, params = NULL, 
      what = "all", ...)

Arguments

species (character) A species name.

(type (character) Type, one of scientific_name or common_name.

(tsn (numeric) Specifies the TSN to query by. If you supply a tsn it doesn’t make 
      sense to supply a species name as well. Example:162003.

start (numeric) Record to start at.

(count (numeric) Number of records to return.

(countyFips (character) Specifies the county fips code to geographically constrain the search 
      to one county. Character must be supplied as a number starting with zero may 
      lose the zero. Eg: "49015".

(county (character) County name. As codes are a pain in the ass, you can put in the 
      county name here instead of specifying a countyFips entry, and bison will at- 
      tempt to look up the countyFips code. (character)

(state (characte) Specifies the state name to geographically constrain the search. Ex- 
      ample: Tennessee.

(ai (character) Specifies a WKT (Well-Known Text) polygon to geographically constrain the search. Eg.: c(-111.06 38.84, -110.80 39.377, -110.20 39.17, -110.20 38.90, 
      -110.63 38.67, -111.06 38.84), which calls up the occurrences within the spec- 
      ified area. Check out the Wikipedia page here http://en.wikipedia.org/ 
      wiki/Well-known_text for an in depth look at the options, terminology, etc. 
      (character)

( aoibbox (character) Specifies a four-sided bounding box to geographically constrain the search (us- 
      ing format: minx, miny, maxx, maxy). The coordinates are Spherical Mercator 
      with a datum of WGS84. Example: -111.31,38.81,-110.57,39.21 (character)

(params (character) String of parameters, one of providerID, resourceId, basisOfRecord, 
      catalogNumber, year, computedStateFips, hierarchy_homonym_string, TSNs, 
      recordedBy, occurrenceID, collectorNumber, provider, ownerInstitutionCollectionCode, eventDate, providedScientificName, scientificName, ITISscientific- 
      Name, providedCommonName, ITIScommonName, kingdom, ITIStsn, centroid,
higherGeographyID, computedCountyFips, providedCounty, calculatedCounty, stateProvince, calculatedState, countryCode. See examples.

what
What to return? One of 'all', 'summary', 'points', 'counties', 'states', 'raw', or 'list'. All data is returned from the BISON API, but this parameter lets you select just the parts you want, and the rest is discarded before returning the result to you.

Further args passed on to httr::GET. See examples.

See Also

bison_solr bison_tax

Examples

bison(species="Bison bison", count=50, what='summary')
bison(species="Bison bison", count=50, what='points')

Description

Make map to visualize BISON data.

Usage

bisonmap(input = NULL, tomap = "points", geom = geom_point, jitter = NULL, customize = NULL)

## S3 method for class 'bison'
bisonmap(input = NULL, tomap = "points", geom = geom_point, jitter = NULL, customize = NULL)

## S3 method for class 'bison_solr'
bisonmap(input = NULL, tomap = "points", geom = geom_point, jitter = NULL, customize = NULL)

Arguments

input         Input bison object.
tomap         One of points (occurrences), county (counts by county), or state (counts by state).
geom          geom_point or geom_jitter, not quoted.
jitter        jitter position, see ggplot2 help.
customize     Pass in more to the plot.
Value

Map (using ggplot2 package) of points on a map.

Examples

```r
## Not run:
# Using function bison
library("ggplot2")
out <- bison(species="Accipiter", type="scientific_name", count=300)
bisonmap(input=out)
bisonmap(input=out, geom=geom_jitter, jitter=position_jitter(width = 0.3, height = 0.3))

# Using function bison_solr
out <- bison_solr(scientificName='Ursus americanus', rows=200)
bisonmap(out)

## End(Not run)
```

---

**bison_datause**

*Get BISON data use agreement details and examples for how to cite data.*

---

**Description**

Get BISON data use agreement details and examples for how to cite data.

**Usage**

```r
bison_datause()

bison_citation()
```

**References**

http://bison.usgs.ornl.gov/doc/api.jsp#data

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**bison_providers**

*Get information about BISON data providers.*

---

**Description**

Get information about BISON data providers.

**Usage**

```r
bison_providers(details = FALSE, provider_no = NULL, ...)
```
Arguments

details (logical) If TRUE, returns a list of data.frame’s for each provider, including their resource details. If FALSE (default), only coarse grained data returned.
details (numeric) Provider number. If this parameter is provided, details is forced to be FALSE.

Further args passed on to http::GET. See examples in bison

Value

A data.frame or list of data.frame’s

Examples

head(bison_providers())
head(bison_providers(provider_no=131))
out <- bison_providers(details=TRUE)
out$National_Herbarium_of_New_South_Wales

bison_solr

Search for and collect occurrence data from the USGS Bison API using their solr endpoint.

Description

This fxn is somewhat similar to bison, but interacts with the SOLR interface http://bison.usgs.ornl.gov/doc/api.jsp#solr instead of the OpenSearch interface http://bison.usgs.ornl.gov/doc/api.jsp#opensearch, which bison uses.

Usage

bison_solr(decimalLatitude = NULL, decimalLongitude = NULL, year = NULL,
providerID = NULL, resourceID = NULL, pointPath = NULL,
basisOfRecord = NULL, eventDate = NULL, computedCountyFips = NULL,
computedStateFips = NULL, scientificName = NULL,
hierarchy_homonym_string = NULL, TSNs = NULL, recordedBy = NULL,
occurrenceID = NULL, catalogNumber = NULL, ITIScommonName = NULL,
kingdom = NULL, callopts = list(), verbose = TRUE, ...)

Arguments

decimalLatitude

Geographic coordinate that specifies the north south position of a location on the Earth surface.
decimalLongitude

Geographic coordinate that specifies the east-west position of a location on the Earth surface.
year
   The year the collection was taken.

providerID
   (character) Unique identifier assigned by GBIF.

resourceID
   (character) A unique identifier that is a concatenation of the provider identifier and the resource id separated by a comma.

pointPath
   A dynamic field that contains the location in longitude and latitude followed by the basis of record and an optional Geo (Spatial) precision. Geo (Spatial) precision is an added descriptor when the record is a county centroid.

basisOfRecord
   One of these enumerated values: Observation, Germplasm, Fossil, Specimen, Literature, Unknown, or Living.

eventDate
   The date when the occurrence was recorded.

computedCountyFips
   County FIPS code conforming to standard FIPS 6-4 but with leading zeros removed.

computedStateFips
   The normalized case sensitive name. For example q=state_code:"New Mexico" will return all of the occurrences from New Mexico.

scientificName
   The species scientific name that is searchable in a case insensitive way.

hierarchy_homonym_string
   Hierarchy of the accepted or valid species name starting at kingdom. If the name is a taxonomic homonym more than one string is provided separated by ‘;’.

TSNs
   Accepted or valid name is provided. If the name is a taxonomic homonym more than one TSN is provided.

recordedBy
   Individual responsible for the scientific record.

occurrenceID
   Non-persistent unique identifier.

catalogNumber
   Unique key for every record (occurrence/row) within a dataset that is not manipulated nor changed (nor generated, if not provided) during the data ingest.

ITISCommonName
   Common name(s) from ITIS, e.g. "Canada goose"

kingdom
   Kingdom name, from GBIF raw occurrence or BISON provider.

callopts
   Further args passed on to http::GET for HTTP debugging/inspecting. In bison, bison_providers, and bison_stats, ... is used instead of callopts, but ... is used here to pass additional Solr params.

verbose
   Print message with url (TRUE, default).

... Additional SOLR query arguments. See details.

Details

Some SOLR search parameters:

- **fl** Fields to return in the query
- **rows** Number of records to return
- **sort** Field to sort by, see examples
- **facet** Facet or not, logical
bison_stats

- facet.field Fields to facet by

You can also use highlighting in solr search, but I’m not sure I see a use case for it with BISON data, though you can do it with this function.


**Value**

An object of class bison_solr - which is a list with slots for number of records found (num_found), records, highlight, or facets.

**See Also**

bison_tax

bison

The USGS BISON Solr installation version as of 2014-10-14 was 4.4.

**Examples**

```r
bison_solr(scientificName='Ursus americanus')
```

*bison_stats*  
*Get statistics about BISON downloads.*

**Description**

Get statistics about BISON downloads.

**Usage**

```r
bison_stats(what = "stats", ...)
```

**Arguments**

what (character) One of stats (default), search, downnload, or wms. See Details.  
... Further args passed on to http::GET. See examples in bison

**Details**

For the ’what’ parameter:

- stats - Retrieve all data provider accumulated statistics.  
- search - Retrieve data provider statistics for BISON searches.  
- download - Retrieve data provider statistics for data downloads from BISON.  
- wms - Retrieve data provider statistics for BISON OGC WMS tile requests.
Value

A list of data frame's with names of the list the different data sources

Examples

```r
## Not run:
out <- bison_stats()
out <- bison_stats(what='search')
out <- bison_stats(what='download')
out <- bison_stats(what='wms')
out$Arctos
out$Harvard_University_Herbaria
out$ZooKeys

## End(Not run)
```

bison_tax

Search for and collect taxonomic name data from the USGS Bison API using solr.

Description

See the SOLR documentation here [http://lucene.apache.org/solr/](http://lucene.apache.org/solr/) for other parameters you can use.

The following two methods are possible, as far as I know you can only use one at a time:

- vernacularName The species specific common names that is searchable in a case insensitive way.
- scientificName The species scientific name that is associated with a common name that is searchable in a case insensitive way.

Usage

```r
bison_tax(query = NULL, method = "vernacularName", exact = FALSE,
parsed = TRUE, callopts = list(), ...)
```

Arguments

- **query** Name to search for. If left blank, the first ten results are returned using a more or less random search.
- **method** The field to query by. See description below for details.
- **exact** Exact matching or not. See examples. Defaults to FALSE.
- **parsed** If TRUE (default) creates data.frame of names data output. Otherwise, a list.
- **callopts** Further args passed on to httr::GET for HTTP debugging/inspecting. In bison, bison_providers, and bison_stats, ... is used instead of callopts, but ... is used here to pass additional Solr params.
- **...** Further solr arguments passed in to the query. See examples below.
Value

A list.

See Also

bison_solr bison

Examples

```r
## Not run:
# Some example calls
bison_tax(query="*bear")
bison_tax(query="Helianthus", method="scientificName")

# Exact argument, here nothing found with latter call as 'bear' doesn't exist,
# which makes sense
bison_tax(query="*bear", exact=FALSE)
bison_tax(query="*bear", exact=TRUE)

# Using solr arguments (not all Solr arguments work)
## Return a certain number of rows
bison_tax(query="*bear", method="vernacularName", rows=3)
## Return certain fields
bison_tax(query="*bear", method="vernacularName", fl='vernacularName')

## Curl options
library("httr")
bison_tax(query='*dolphin', callopts=verbose())

## End(Not run)
```

---

### fips

**Fips codes for states and counties**

**Description**

Fips codes for states and counties

---

### is.bison

**Check if object is of class bison**

**Description**

Check if object is of class bison
is.bison.solr

Usage

is.bison(x)

Arguments

x input

is.bison.solr  Check if object is of class bison.solr

Description

Check if object is of class bison.solr

Usage

is.bison.solr(x)

Arguments

x input
Index

*Topic data
  all_states, 2
  fips, 10

*Topic package
  rbison-package, 2

all_states, 2

bison, 3, 6, 8, 10
bison_citation (bison_datause), 5
bison_datause, 5
bison_providers, 5
bison_solr, 4, 6, 10
bison_stats, 8
bison_tax, 4, 8, 9
bisonmap, 4

fips, 10

is.bison, 10
is.bison_solr, 11

rbison (rbison-package), 2
rbison-package, 2