

rbison vignette - wrapper to the USGS BISON API

About the package

rbison is an R package to search and retrieve data from the USGS BISON service. **rbison** wraps R code around the BISON API to allow you to talk to the BISON database from R.

BISON has occurrence data for the US only.

BISON is a node of the Global Biodiversity Information Facility (GBIF) - i.e., you can get data that's available in BISON via GBIF instead if you want.

Info

See [here](#) for API docs for the BISON API.

Quick start

Install rbison

```
# install.packages('devtools'); library(devtools); install_github('rbison',  
# 'ropensci')  
library(rbison)  
library(sp)  
library(plyr)  
library(httr)  
library(rjson)  
library(gridExtra)  
library(mapproj)  
library(ggplot2)  
library(maps)  
library(rgeos)  
library(rgdal)
```

Notice that the function **bisonmap** automatically selects the map extent to plot for you, being one of the contiguous lower 48 states, or the lower 48 plus AK and HI, or a global map

If some or all points outside the US, a global map is drawn, and throws a warning. You may want to make sure the occurrence lat/long coordinates are correct.

get data

```
out <- bison(species = "Helianthus annuus", count = 10)
```

inspect summary

```
out$summary
```

```
##   total observation fossil specimen literature unknown living centroid
## 1  4388           13    102     1267       1106    1892      8        1
```

map occurrences

```
head(out$counties)
```

```
##   record_id total      county_name      state
## 1    20041     3 Dickinson County    Kansas
## 2    54103     1   Wetzel County West Virginia
## 3    40149     1 Washita County    Oklahoma
## 4    54105     1    Wirt County West Virginia
## 5    29025     1 Caldwell County    Missouri
## 6    40143     2    Tulsa County    Oklahoma
```

All points within the US (including AK and HI)

get data

```
out <- bison(species = "Bison bison", count = 600)
```

inspect summary

```
out$summary
```

```
##   total observation fossil specimen unknown centroid
## 1   956           32    157     718     49        1
```

map occurrences

```
bisonmap(out, tomap = "state")
```

All points within the contiguous 48 states

get data

```
out <- bison(species = "Aquila chrysaetos", count = 600)
```

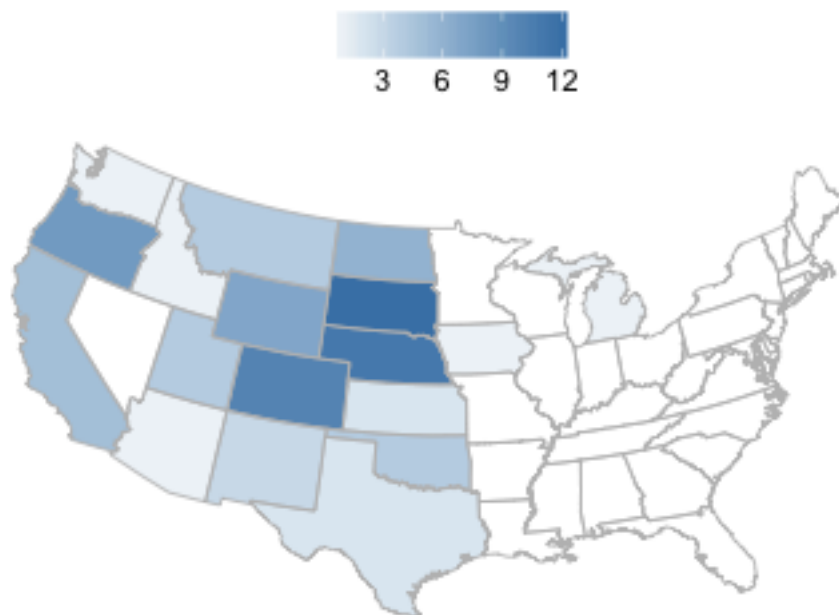


Figure 1: plot of chunk six

inspect summary

`out$summary`

```
## total observation fossil specimen literature unknown centroid
## 1 52626          50896      105        799          118      708          1
```

map occurrences

```
bisonmap(out, tomap = "points")
```

With any data returned from a bison call, you can choose to plot county or state level data

Counties - using last data call for Aquila

```
bisonmap(out, tomap = "county")
```

States - using last data call for Aquila

```
bisonmap(out, tomap = "state")
```



Figure 2: plot of chunk nine

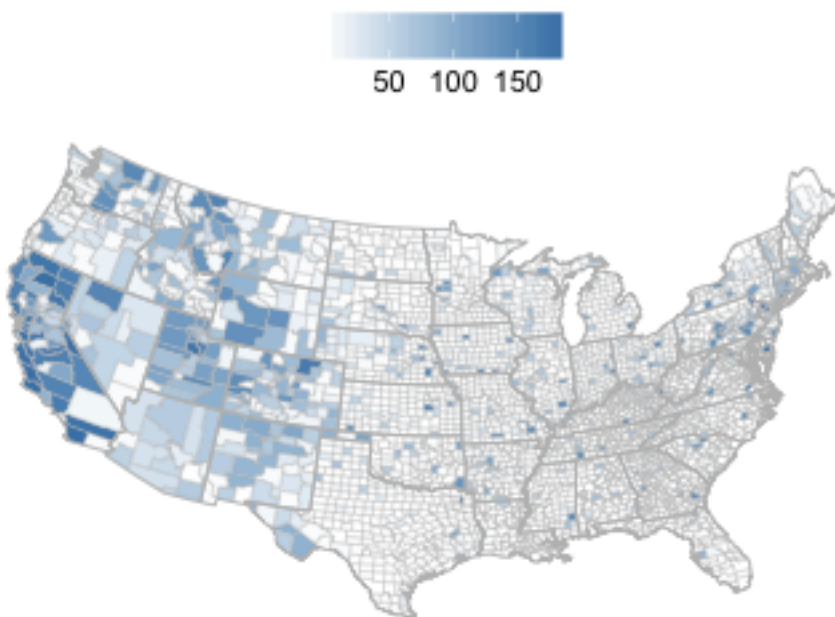


Figure 3: plot of chunk ten

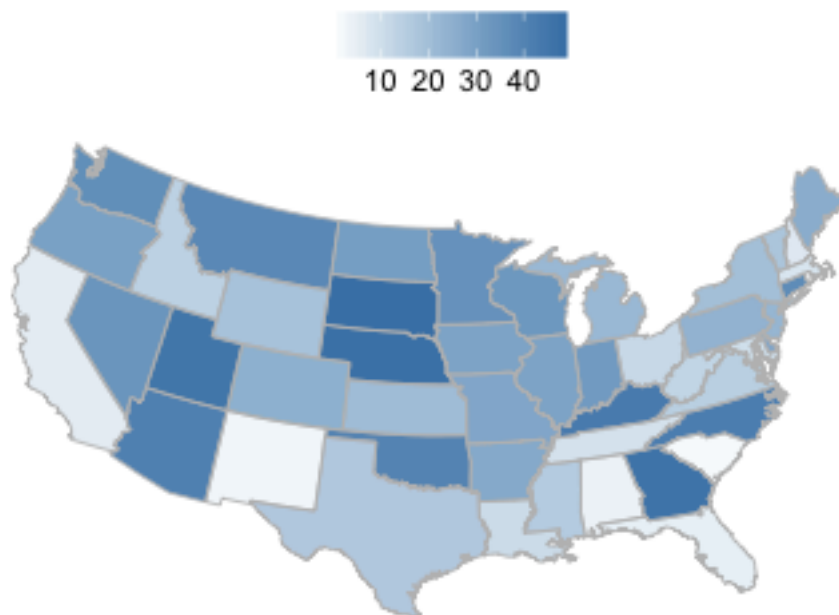


Figure 4: plot of chunk eleven

Constrain search with county IDs or bounding boxes

Constrain search to a certain county. Check out [this site](#) to get state and county fips codes. Fips codes are like so: First two digits are the state code - last three are the county code. For example the *06* in 06037 is the state of California, and the *037* is the Los Angeles county.

```
out <- bison(species = "Helianthus annuus", countyFips = "06037")
```

```
# Inspect summary
out$summary
```

```
##      total observation fossil specimen literature unknown centroid
## 1      24              1       3        12             1         7         1
```

```
# By default, the query only returned 10 records
head(out$points)
```

```
##           name decimalLongitude decimalLatitude occurrenceID
## 1 Helianthus annuus          -118.4           33.39    1032095838
## 2 Helianthus annuus          -118.3           34.20     45597818
## 3 Helianthus annuus          -118.0           34.00    225207520
## 4 Helianthus annuus          -118.0           34.00    225206595
## 5 Helianthus annuus          -118.0           34.00    225207727
## 6 Helianthus annuus          -118.0           34.00    225207562
```

```
##               provider      basis
## 1      USDA PLANTS Database Literature
## 2 University of California, Davis      Unknown
## 3 Consortium of California Herbaria    Specimen
## 4 Consortium of California Herbaria    Specimen
## 5 Consortium of California Herbaria    Specimen
## 6 Consortium of California Herbaria    Specimen
##                                     common_name geo
## 1 sunflower, annual sunflower, common sunflower, wild sunflower Yes
## 2 sunflower, annual sunflower, common sunflower, wild sunflower Yes
## 3 sunflower, annual sunflower, common sunflower, wild sunflower Yes
## 4 sunflower, annual sunflower, common sunflower, wild sunflower Yes
## 5 sunflower, annual sunflower, common sunflower, wild sunflower Yes
## 6 sunflower, annual sunflower, common sunflower, wild sunflower Yes
```

Or specify county by its actual name - probably much easier.

```
out <- bison(species = "Helianthus annuus", county = "Los Angeles")
```

```
# Inspect summary
```

```
out$summary
```

```
## total observation fossil specimen literature unknown centroid
## 1      24           1       3       12           1       7       1
```

```
# By default, the query only returned 10 records
```

```
head(out$points)
```

```
##               name decimalLongitude decimalLatitude occurrenceID
## 1 Helianthus annuus          -118.4           33.39    1032095838
## 2 Helianthus annuus          -118.3           34.20     45597818
## 3 Helianthus annuus          -118.0           34.00    225207520
## 4 Helianthus annuus          -118.0           34.00    225206595
## 5 Helianthus annuus          -118.0           34.00    225207727
## 6 Helianthus annuus          -118.0           34.00    225207562
##               provider      basis
## 1      USDA PLANTS Database Literature
## 2 University of California, Davis      Unknown
## 3 Consortium of California Herbaria    Specimen
## 4 Consortium of California Herbaria    Specimen
## 5 Consortium of California Herbaria    Specimen
## 6 Consortium of California Herbaria    Specimen
##                                     common_name geo
## 1 sunflower, annual sunflower, common sunflower, wild sunflower Yes
## 2 sunflower, annual sunflower, common sunflower, wild sunflower Yes
## 3 sunflower, annual sunflower, common sunflower, wild sunflower Yes
## 4 sunflower, annual sunflower, common sunflower, wild sunflower Yes
## 5 sunflower, annual sunflower, common sunflower, wild sunflower Yes
## 6 sunflower, annual sunflower, common sunflower, wild sunflower Yes
```

bison will help you if you spell the name wrong, or use a partial name. The results are not printed below, but you would get a prompt asking you to pick between the two counties that start with *Los*.

```
bison(species = "Helianthus annuus", county = "Los")
```

Constrain search to a amorphous area. Check out the Wikipedia page [here](#) for an in depth look at the options, terminology, etc.

```
out <- bison(species = "Helianthus annuus", aoi = "POLYGON((-111.06360117772908 38.84001566645886,-110.8

# Inspect summary
out$summary

##    total literature centroid
## 1      1      1      1

# The data
head(out$points)

##           name decimalLongitude decimalLatitude occurrenceID
## 1 Helianthus annuus          -110.7           38.99    1032098012
##           provider      basis
## 1 USDA PLANTS Database Literature
##
##           common_name geo
## 1 sunflower, annual sunflower, common sunflower, wild sunflower Yes
```

Constrain search to a certain aoibbox. An aoibbox uses the format minx, miny, maxx, maxy.

```
out <- bison(species = "Helianthus annuus", aoibbox = "-120.31,35.81,-110.57,40.21")

# Inspect summary
out$summary

##    total observation fossil specimen literature unknown centroid
## 1    149              6      8      33      25      77      1

# The data, by default, the query only returned 10 records
head(out$points)

##           name decimalLongitude decimalLatitude occurrenceID
## 1 Helianthus annuus          -115.0           36.21    320466814
## 2 Helianthus annuus          -111.8           35.83    320466028
## 3 Helianthus annuus          -119.7           36.76    45598447
## 4 Helianthus annuus          -119.7           36.76    45598264
## 5 Helianthus annuus          -111.8           35.84    1032095762
## 6 Helianthus annuus          -115.0           36.20    1032096818
##           provider      basis
## 1 Missouri Botanical Garden Specimen
## 2 Missouri Botanical Garden Specimen
## 3 University of California, Davis Unknown
## 4 University of California, Davis Unknown
## 5 USDA PLANTS Database Literature
## 6 USDA PLANTS Database Literature
##
##           common_name geo
```

1 sunflower, annual sunflower, common sunflower, wild sunflower Yes
2 sunflower, annual sunflower, common sunflower, wild sunflower Yes
3 sunflower, annual sunflower, common sunflower, wild sunflower Yes
4 sunflower, annual sunflower, common sunflower, wild sunflower Yes
5 sunflower, annual sunflower, common sunflower, wild sunflower Yes
6 sunflower, annual sunflower, common sunflower, wild sunflower Yes