## rgbif tutorial

[1] 573

[[3]] [1] 945

Note: this vignette works with the current version on CRAN that works with the old GBIF API.

The rgbif package interacts with the API services of the Global Biodiversity Information Facility GBIF. GBIF currently holds 377,177,914 indexed records, ~10K datasets, and 419 publishers (i.e., dataset submitters).

This tutorial will go through three use cases to demonstrate the kinds of things possible in rgbif.

- Counts taxon concept records matching a range of filters.
- Returns summary counts of occurrence records by one-degree cell.
- occurrencelist searches for taxon concept records matching a range of filters.
- densitylist gets density of occurrence records by one-degree cell.
- Search by taxon to retrieve number of records in GBIF.

## Install and load package from GitHub

```
install.packages("rgbif")
library(rgbif)
```

Counts taxon concept records matching a range of filters.

```
occurrencecount(scientificname = "Helianthus annuus", coordinatestatus = TRUE,
    year = 2005, maxlatitude = 20)

[1] 138

Count many taxa
lapply(c("Helianthus debilis", "Abies procera", "Astragalus"), function(x) occurrencecount(scientificnate coordinatestatus = TRUE))

[[1]]
[1] 26
[[2]]
```

Return summary counts of occurrence records by one-degree cell for a single taxon, country, dataset, data publisher or data network

```
out <- densitylist(originisocountrycode = "CA")
head(gbifdata(out))

cellid minLatitude maxLatitude minLongitude maxLongitude count</pre>
```

```
1 46913
              40
                       41
2 46914
              40
                       41
                                 -66
                                           -65
                                                519
3 46915
             40
                       41
                                 -65
                                           -64
                                                475
4 46916
              40
                       41
                                 -64
                                           -63
                                                432
5 46917
              40
                       41
                                 -63
                                           -62
                                                55
6 46918
              40
                       41
                                 -62
                                           -61
                                                143
```

Occurrencelist searches for taxon concept records matching a range of filters.

A simple example

		taxonName	occurrenceID	country	decimalLatitude
1	Accipiter	erythronemius	352220558	Argentina	-31.133
2	-	erythronemius	213206174	•	3.767
3	Accipiter	erythronemius	699199195	Argentina	-25.861
4	Accipiter	erythronemius	699199198	Argentina	-25.911
5	Accipiter	erythronemius	621073311	Argentina	-27.352
6	Accipiter	erythronemius	621073312	Argentina	-27.352
7	Accipiter	erythronemius	621073310	Argentina	-27.352
8	Accipiter	erythronemius	699199204	Argentina	-25.861
9	Accipiter	erythronemius	699417490	Guyana	5.267
10	Accipiter	erythronemius	686297260	Guyana	5.267
	${\tt decimalLongitude}  {\tt catalogNumber\ earliestDateCollected}$				
1		-59.02 YPM OR	N 065671	1961-0	04-30
2		-76.75 Ski	n-470489		<na></na>
3		-54.52	39196		<na></na>
4		-54.36	38199		<na></na>
5		-65.60	42228		<na></na>
6		-65.60	42227		<na></na>
7		-65.60	42229		<na></na>
8		-54.52	38015		<na></na>
9		-60.73	3998	2001-0	04-03
10		-60.73	93439	2001-0	04-03
	latestDate	eCollected			
1	:	1961-04-30			
2		<na></na>			
3		<na></na>			
4		<na></na>			
5		<na></na>			
6		<na></na>			
7		<na></na>			
8		<na></na>			
9	2	2001-04-03			
10	2	2001-04-03			

Search for many species and make a map

```
splist <- c("Accipiter erythronemius", "Junco hyemalis", "Aix sponsa")
out <- occurrencelist_many(splist, coordinatestatus = TRUE, maxresults = 20)
gbifmap_list(out)</pre>
```

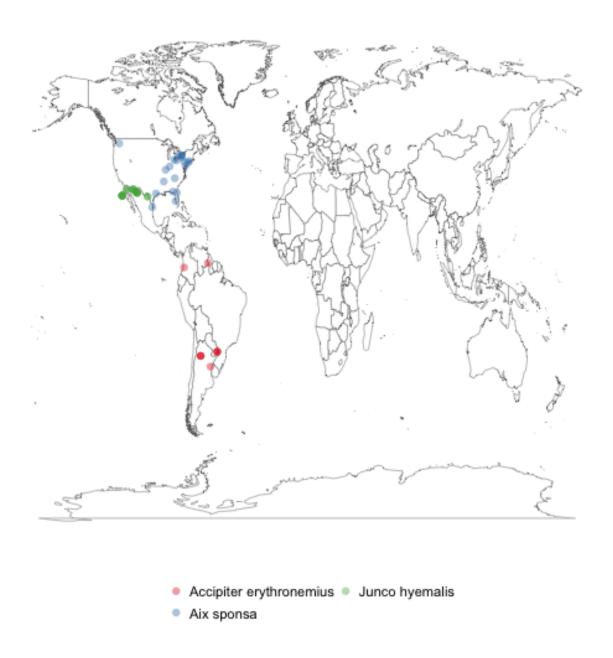


Figure 1: plot of chunk occurrencelist\_many

densitylist provides access to records showing the density of occurrence records from the GBIF Network by one-degree cell.

A simple example

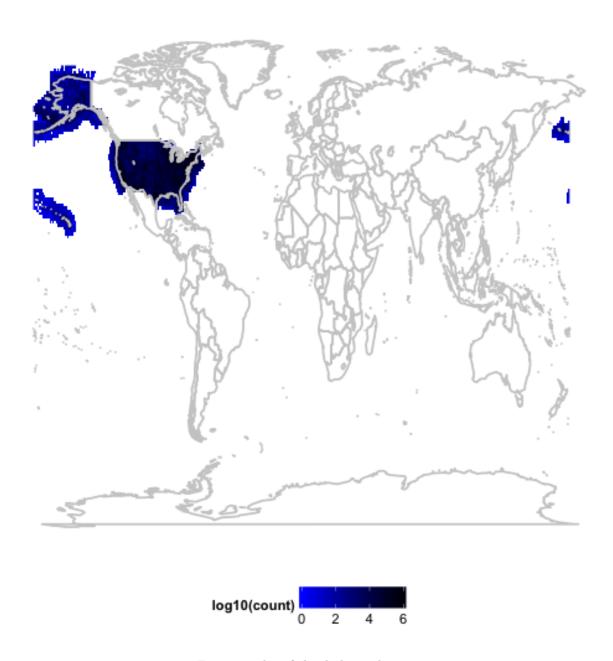


Figure 2: plot of chunk densitylist2

Search by taxon to retrieve number of records in GBIF.

```
taxoncount("Puma concolor")
```

taxoncount("Helianthus annuus")

[1] 142