

## rgbif tutorial

*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(scientificname = x,  
  coordinatestatus = TRUE))
```

```
[[1]]
```

```
[1] 26
```

```
[[2]]
```

```
[1] 573
```

```
[[3]]
```

```
[1] 945
```

### 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
1	46913	40	41	-67	-66	44
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

```
dat <- occurrencelist(scientificname = "Accipiter erythronemius", coordinatestatus = TRUE,
  maxresults = 10)
gbifdata(dat)
```

	taxonName	occurrenceID	country	decimallatitude
1	Accipiter erythronemius	699199198	Argentina	-25.911
2	Accipiter erythronemius	621073310	Argentina	-27.352
3	Accipiter erythronemius	621073311	Argentina	-27.352
4	Accipiter erythronemius	699199204	Argentina	-25.861
5	Accipiter erythronemius	621073312	Argentina	-27.352
6	Accipiter erythronemius	699199195	Argentina	-25.861
7	Accipiter erythronemius	213206174	W. Colombia	3.767
8	Accipiter erythronemius	352220558	Argentina	-31.133
9	Accipiter erythronemius	699417490	Guyana	5.267
10	Accipiter erythronemius	686297260	Guyana	5.267
	decimallongitude	catalogNumber	earliestDateCollected	
1	-54.36	38199	<NA>	
2	-65.60	42229	<NA>	
3	-65.60	42228	<NA>	
4	-54.52	38015	<NA>	
5	-65.60	42227	<NA>	
6	-54.52	39196	<NA>	
7	-76.75	Skin-470489	<NA>	
8	-59.02	YPM ORN 065671	1961-04-30	
9	-60.73	3998	2001-04-03	
10	-60.73	93439	2001-04-03	
	latestDateCollected			
1	<NA>			
2	<NA>			
3	<NA>			
4	<NA>			
5	<NA>			
6	<NA>			
7	<NA>			
8	1961-04-30			
9	2001-04-03			
10	2001-04-03			

Search for many species and make a map

```
splist <- c("Accipiter erythronemius", "Junco hyemalis", "Aix sponsa")
out <- occurrence_list_many(splist, coordinate_status = TRUE, max_results = 20)
gbifmap_list(out)
```

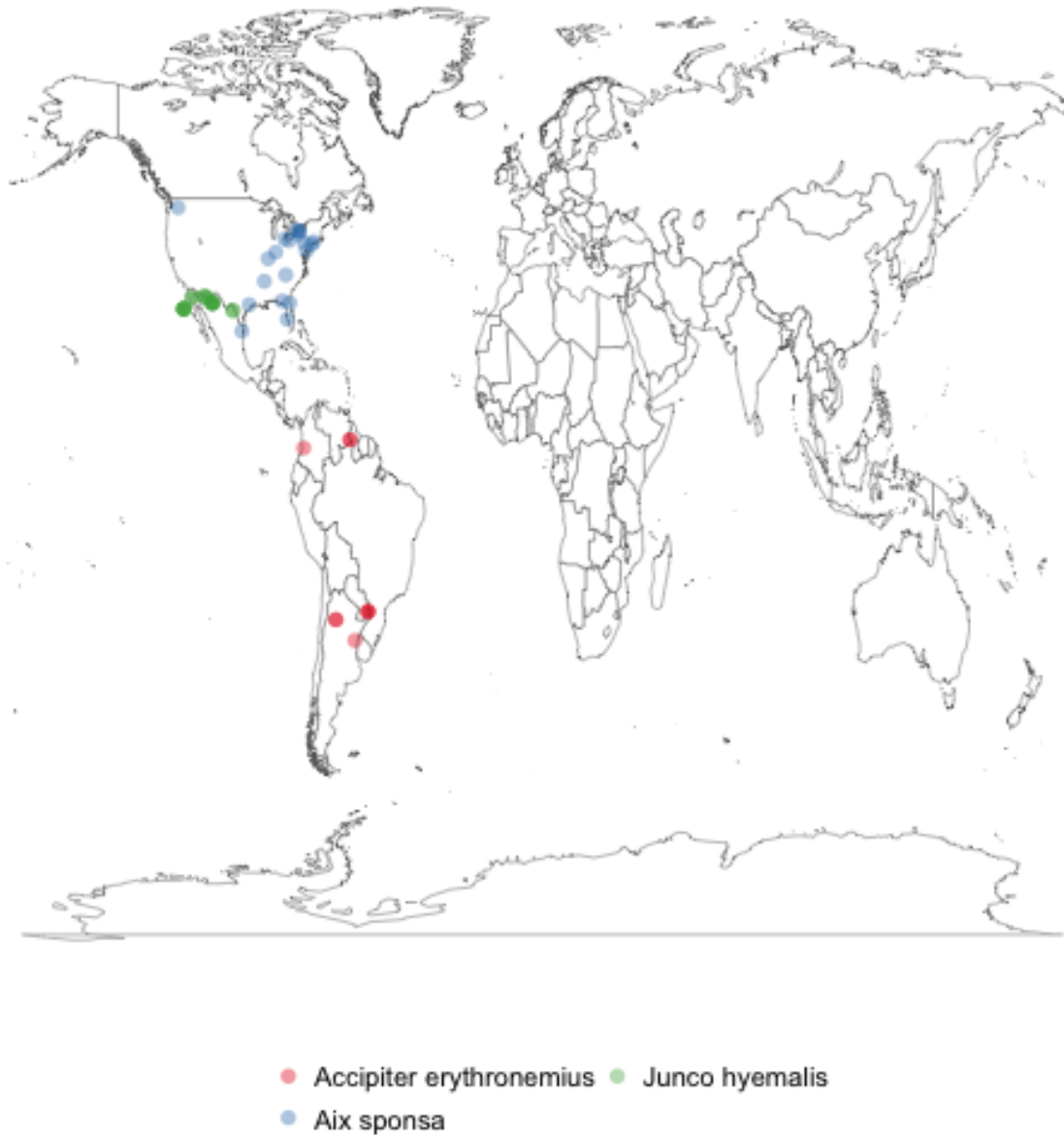


Figure 1: plot of chunk occurrence\_list\_many

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

A simple example

```
out <- densitylist(originisocountrycode = "US")
gbifmap_dens(out)
```

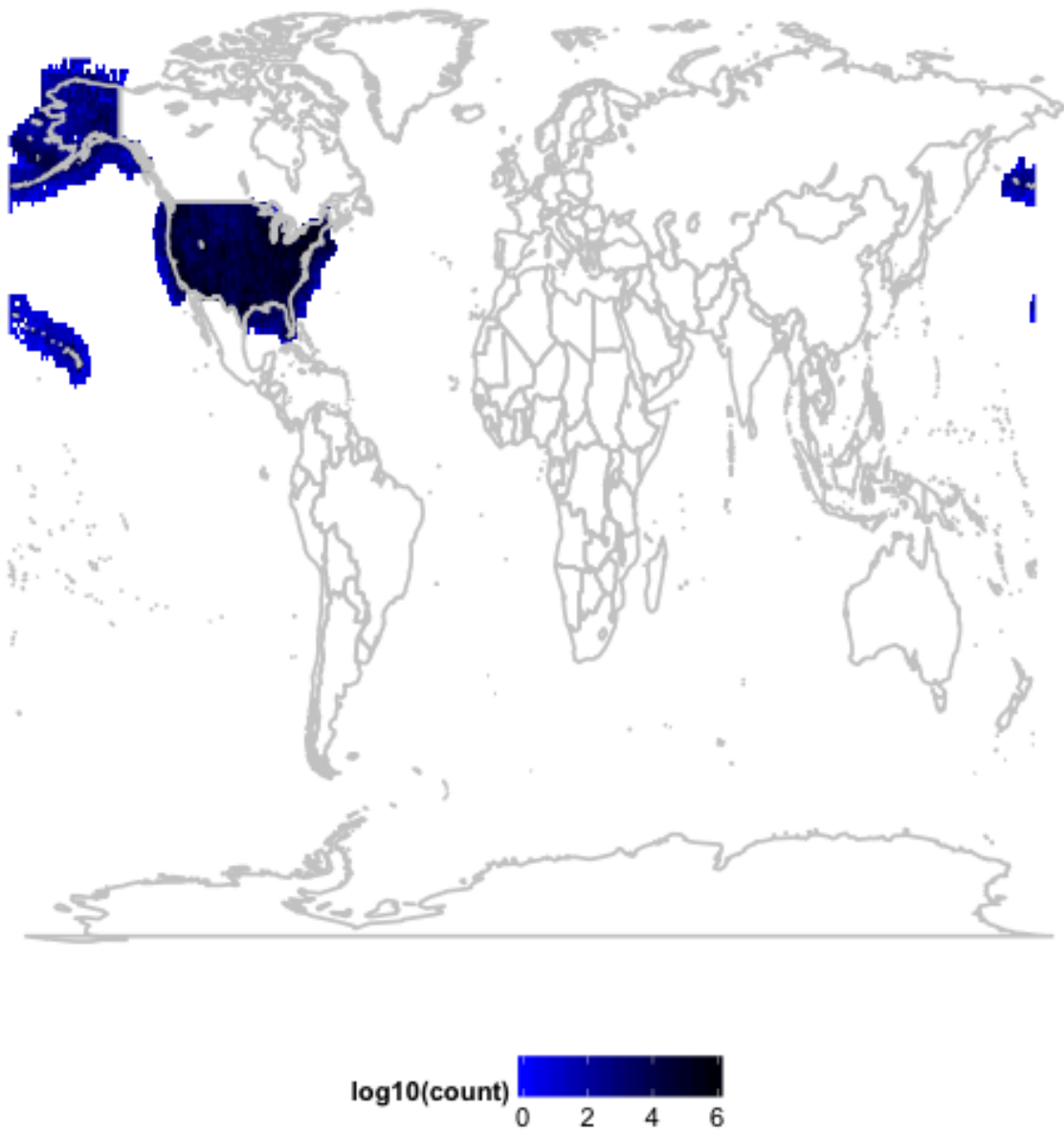


Figure 2: plot of chunk densitylist2

Search by taxon to retrieve number of records in GBIF.

```
taxoncount("Puma concolor")

[1] 91

taxoncount("Helianthus annuus")
```

[1] 142