

rgbif vignette - Search and retrieve data from the Global Biodiversity Information Facility (GBIF)

About the package

rgbif is an R package to search and retrieve data from the Global Biodiversity Information Facility (GBIF). rgbif wraps R code around the [GBIF API](#) to allow you to talk to GBIF from R.

Install rgbif and dependencies

```
install.packages("devtools")
library(devtools)
install_github("rgbif", "ropensci", ref = "newapi")
```

Load rgbif and dependencies

```
library(rgbif)
library(XML)
library(RCurl)
library(plyr)
library(ggplot2)
library(maps)
```

Get number of occurrences for a set of search parameters

Search by type of record, all observational in this case

```
occ_count(basisOfRecord = "OBSERVATION")
```

```
[1] 286071783
```

Records for Puma concolor with lat/long data (georeferenced) only

```
occ_count(nubKey = 2435099, georeferenced = TRUE)
```

```
[1] 2541
```

All georeferenced records in GBIF

```
occ_count(georeferenced = TRUE)
```

```
[1] 3.55e+08
```

Records from Denmark

```
occ_count(country = "DENMARK")
```

```
[1] 8628822
```

Records from France

```
occ_count(hostCountry = "FRANCE")
```

```
[1] 17272175
```

Number of records in a particular dataset

```
occ_count(datasetKey = "9e7ea106-0bf8-4087-bb61-dfe4f29e0f17")
```

```
[1] 4591
```

All records from 2012

```
occ_count(year = 2012)
```

```
[1] 31483292
```

Records for a particular dataset, and only for preserved specimens

```
occ_count(datasetKey = "8626bd3a-f762-11e1-a439-00145eb45e9a", basisOfRecord = "PRESERVED_SPECIMEN")
```

```
[1] 550849
```

Get possible values to be used in taxonomic rank arguments in functions

```
taxrank()
```

```
[1] "kingdom"      "phylum"     "class"        "order"  
[5] "family"       "genus"        "species"      "infraspecific"
```

Search for taxon information

Search for a genus

```
head(name_lookup(query = "Cnaemidophorus", rank = "genus", return = "data"))
```

	key	nubKey	parentKey	parent	kingdom	phylum	clazz
1	116755723	1858636	110614854	Pterophoridae	Animalia	Arthropoda	Insecta
2	1858636	1858636	8863	Pterophoridae	Animalia	Arthropoda	Insecta
3	125802004	1858636	125793784	Pterophoridae	<NA>	<NA>	Insecta
4	124531302	1858636	NA	<NA>	<NA>	<NA>	<NA>
5	126862804	1858636	126783981	Pterophoridae	Animalia	Arthropoda	Insecta
6	115123697	1858636	NA	<NA>	<NA>	<NA>	<NA>

	order	family	genus	kingdomKey	phylumKey	classKey
1	Lepidoptera	Pterophoridae	Cnaemidophorus	116630539	116762374	116686069
2	Lepidoptera	Pterophoridae	Cnaemidophorus	1	54	216
3	Lepidoptera	Pterophoridae	Cnaemidophorus	NA	NA	125831175
4	<NA>	<NA>	Cnaemidophorus	NA	NA	NA
5	Lepidoptera	Pterophoridae	Cnaemidophorus	126774927	126774928	126775138
6	<NA>	<NA>	Cnaemidophorus	NA	NA	NA

	orderKey	familyKey	genusKey	canonicalName	authorship	nameType
1	116843281	110614854	116755723	Cnaemidophorus	Wallengren, 1862	WELLFORMED
2	797	8863	1858636	Cnaemidophorus	Wallengren, 1862	WELLFORMED
3	125810165	125793784	125802004	Cnaemidophorus	Wallengren, 1862	WELLFORMED
4	NA	NA	124531302	Cnaemidophorus		WELLFORMED
5	126775421	126783981	126862804	Cnaemidophorus		WELLFORMED
6	NA	NA	115123697	Cnaemidophorus		WELLFORMED

	rank	numOccurrences
1	GENUS	0
2	GENUS	0
3	GENUS	0
4	GENUS	0
5	GENUS	0
6	GENUS	0

Search for the class mammalia

```
name_lookup(class = "mammalia")
```

Error: unused argument (class = "mammalia")

Look up the species *Helianthus annuus*

```
name_lookup("Helianthus annuus", rank = "species")
```

\$meta

	offset	limit	endOfRecords	count
1	0	20	FALSE	69

\$data

	key	nubKey	parentKey	parent	kingdom
1	116845199	3119195	116853573	Helianthus	Plantae

2	3119195	3119195	3119134	Helianthus	Plantae
3	125790787	3119195	125809269	Helianthus	<NA>
4	106239436	3119195	106239325	Helianthus	Viridiplantae
5	121635316	3119195	124573711	Helianthus	<NA>
6	111449704	3119195	111449703	Helianthus	Plantae
7	108157198	NA	108086589	Asteraceae	Plantae
8	108157199	NA	108086589	Asteraceae	Plantae
9	108157200	NA	108086589	Asteraceae	Plantae
10	115043868	3119195	115091988	Helianthus	Plantae
11	107290518	NA	107290513	Helianthus	Plantae
12	107001935	NA	107105089	Helianthus	Plantae
13	117214133	3119195	117208777	Virus	Virus
14	117075019	3119195	117061550	Helianthus	Plantae
15	110853779	3119195	116128567	Helianthus	Plantae
16	125879180	3119195	126824197	Helianthus	Plantae
17	124780276	3119195	124852643	Helianthus	Plantae
18	100837541	3119195	102425010	Helianthus	Plantae
19	100019171	3119195	100009008	Helianthus	<NA>
20	125587214	3119195	106573315	unclassified phytoplasmas	<NA>
	order		family	genus	kingdomKey
1	Asterales		Asteraceae	Helianthus	116668764
2	Asterales		Asteraceae	Helianthus	6
3	Asterales		Asteraceae	Helianthus	NA
4	Asterales		Asteraceae	Helianthus	106147210
5	<NA>		<NA>	Helianthus	NA
6	<NA>		Compositae	Helianthus	111449174
7	<NA>		Asteraceae	<NA>	115219148
8	<NA>		Asteraceae	<NA>	115219148
9	<NA>		Asteraceae	<NA>	115219148
10	Asterales		Asteraceae	Helianthus	115107585
11	Asterales		Asteraceae	Helianthus	107264512
12	<NA>		Asteraceae	Helianthus	124856107
13	<NA>		<NA>	<NA>	117208777
14	Asterales		Compositae	Helianthus	117067772
15	Asterales		Compositae	Helianthus	116127234
16	Asterales		Asteraceae	Helianthus	126775066
17	Asterales		Compositae	Helianthus	124850847
18	Asterales		Asteraceae	Helianthus	102545045
19	Asterales		Asteraceae	Helianthus	NA
20	Acholeplasmatales	Acholeplasmataceae	Candidatus		NA
	familyKey	genusKey	canonicalName	authorship	nameType
1	116856030	116853573	Helianthus annuus	L.	WELLFORMED SPECIES
2	3065	3119134	Helianthus annuus	L.	WELLFORMED SPECIES
3	125799038	125809269	Helianthus annuus	L.	WELLFORMED SPECIES
4	106237535	106239325	Helianthus annuus		WELLFORMED SPECIES
5	NA	124573711	Helianthus annuus		WELLFORMED SPECIES
6	111442813	111449703	Helianthus annuus	L.	WELLFORMED SPECIES
7	108086589	NA	Helianthus annuus	L.	WELLFORMED SPECIES
8	108086589	NA	Helianthus annuus	L.	WELLFORMED SPECIES
9	108086589	NA	Helianthus annuus	L.	WELLFORMED SPECIES
10	115105473	115091988	Helianthus annuus	L.	WELLFORMED SPECIES
11	107289191	107290513	Helianthus annuus	L.	WELLFORMED SPECIES
12	107079268	107105089	Helianthus annuus	L.	WELLFORMED SPECIES
13	NA	NA	Helianthus annuus	L.	WELLFORMED SPECIES

```

14 117068545 117061550 Helianthus annuus      L. WELLFORMED SPECIES
15 116128511 116128567 Helianthus annuus      L. WELLFORMED SPECIES
16 126781795 126824197 Helianthus annuus      L. WELLFORMED SPECIES
17 124852489 124852643 Helianthus annuus      L. WELLFORMED SPECIES
18 102234418 102425010 Helianthus annuus      Linnaeus WELLFORMED SPECIES
19 100025154 100009008 Helianthus annuus      Linnaeus WELLFORMED SPECIES
20 106039581 106155719 Helianthus annuus      SCINAME SPECIES
  numOccurrences      phylum      clazz phylumKey      classKey
1              0      <NA>      <NA>      NA      NA
2              0 Magnoliophyta Magnoliopsida      49      220
3              0      <NA>      <NA>      NA      NA
4              0 Streptophyta      <NA> 106171079      NA
5              0      <NA>      <NA>      NA      NA
6              0 Spermatophyta Dicotyledones 111449175 111449177
7              0      <NA>      <NA>      NA      NA
8              0      <NA>      <NA>      NA      NA
9              0      <NA>      <NA>      NA      NA
10             0 Magnoliophyta Magnoliopsida 115107589 115107444
11             0 Magnoliophyta Magnoliopsida 107240291 107240313
12             0      <NA>      <NA>      NA      NA
13             0      <NA>      <NA>      NA      NA
14             0 Spermatophyta Magnoliopsida 117080124 117074792
15             0 Magnoliophyta Magnoliopsida 116127951 116128467
16             0 Tracheophyta Magnoliopsida 126775067 126775068
17             0 Tracheophyta Magnoliopsida 124851364 124852364
18             0 Magnoliophyta Magnoliopsida 102545123 101741810
19             0      <NA> Equisetopsida      NA 100023390
20             0 Tenericutes      Mollicutes 106355900 106136190

```

```

$facets
NULL

```

Get data for a single occurrence. Note that data is returned as a list, with slots for metadata and data, or as a hierarchy, or just data.

Just data

```
occ_get(key = 773433533, return = "data")
```

```

      name      key longitude latitude
1 Helianthus annuus L. 773433533      -117      32.85

```

Just taxonomic hierarchy

```
occ_get(key = 773433533, return = "hier")
```

```

      name      key      rank
1      Plantae      6 kingdom
2 Magnoliophyta      49 phylum
3 Magnoliopsida     220 clazz

```

```

4      Asterales      414  order
5      Asteraceae     3065 family
6      Helianthus 3119134 genus
7 Helianthus annuus L. 3119195 species

```

All data, or leave return parameter blank

```
occ_get(key = 773433533, return = "all")
```

\$hierarch

```

      name      key  rank
1      Plantae      6 kingdom
2      Magnoliophyta  49 phylum
3      Magnoliopsida 220 clazz
4      Asterales    414 order
5      Asteraceae   3065 family
6      Helianthus 3119134 genus
7 Helianthus annuus L. 3119195 species

```

\$data

```

      name      key longitude latitude
1 Helianthus annuus L. 773433533      -117      32.85

```

Get many occurrences. `occ_get` is vectorized

```
occ_get(key = c(773433533, 101010, 240713150, 855998194, 49819470), return = "data")
```

```

      name      key longitude latitude
1      Helianthus annuus L. 773433533      -117.00      32.85
2      Platyodoras costatus (Linnaeus, 1758) 101010      -70.07      -4.35
3      Pelosina 240713150      163.58      -77.57
4      Sciurus vulgaris Linnaeus, 1758 855998194      12.04      58.41
5      Phlogophora meticulosa Linnaeus, 1758 49819470      13.28      55.72

```

Maps

Static map using the `ggplot2` package

Make a map of **Puma concolor** occurrences

```

key <- name_backbone(name = "Puma concolor", kingdom = "plants")$speciesKey
dat <- occ_search(taxonKey = key, return = "data", limit = 300, minimal = FALSE)
gbifmap(input = dat)

```

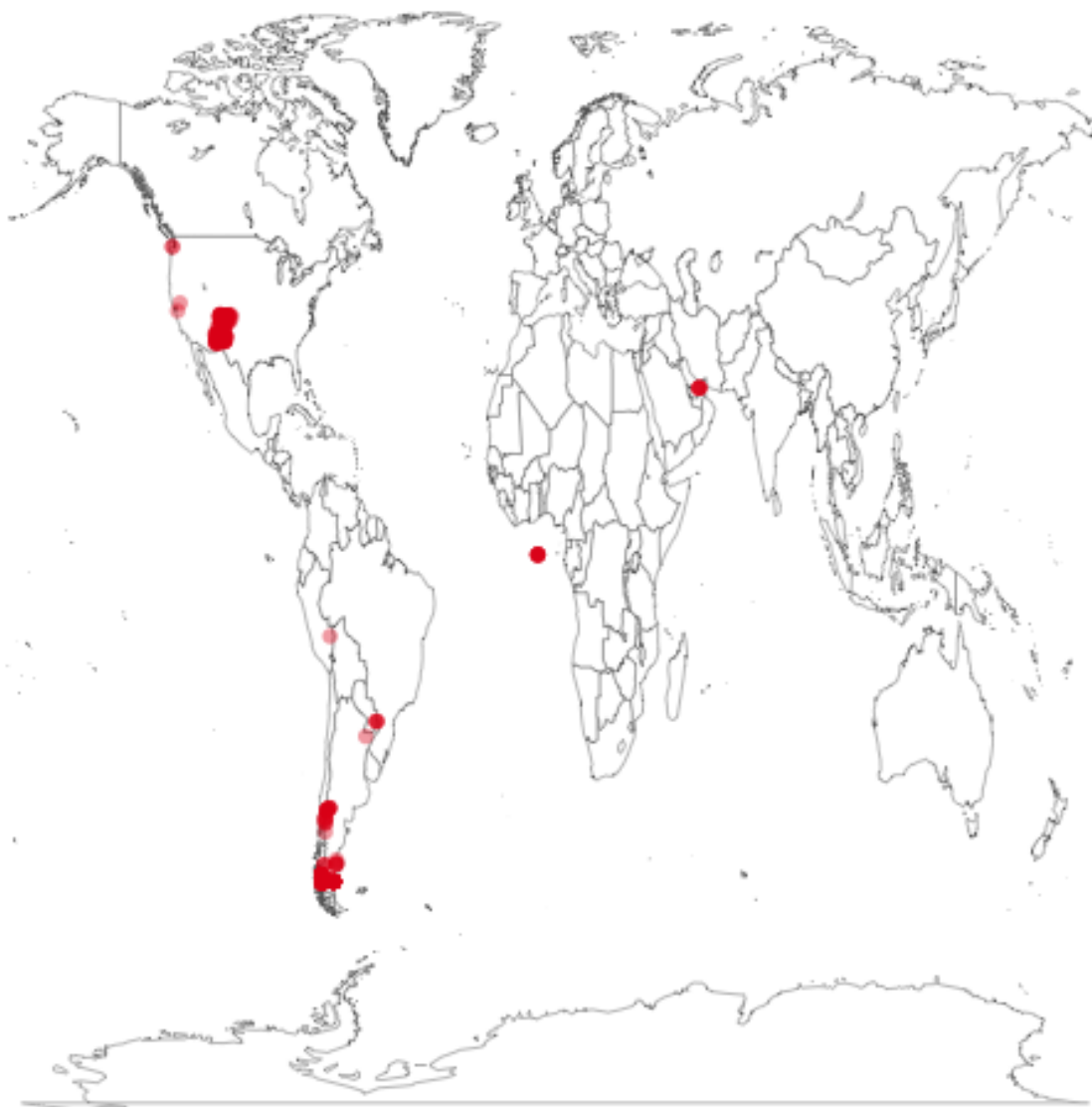


Figure 1: plot of chunk gbifmap1

Interactive map using a geoJSON file with your Github account

```
library(plyr)
splist <- c("Accipiter erythronemius", "Junco hyemalis", "Aix sponsa")
keys <- sapply(splist, function(x) name_backbone(name = x, kingdom = "plants")$speciesKey,
  USE.NAMES = FALSE)
out <- occ_search(keys, georeferenced = TRUE, limit = 50, return = "data")
dat <- ldply(out)
datgeojson <- stylegeojson(input = dat, var = "name", color = c("#976AAE", "#6B944D",
  "#BD5945"), size = c("small", "medium", "large"))
write.csv(datgeojson, "~/my.csv")
togeojson(input = "~/my.csv", method = "web", outfilename = "my")
gist("~/my.geojson", description = "Occurrences of three bird species mapped")
```