

# R Python, and Ruby clients for GBIF species occurrence data

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## Abstract

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10 Background. The number of individuals of each species in a given location forms the basis for many  
11 sub-fields of ecology and evolution. Data on individuals, including which species, and where they're  
12 found, can be used for a large number of research questions. Global Biodiversity Information Facility  
13 (hereafter, GBIF) is the largest of these. Programmatic clients for GBIF would make research dealing  
14 with GBIF data much easier.

15 Methods. We have developed clients to access GBIF data for each of the R, Python, and Ruby  
16 programming languages: `rgbif`, `pygbif`, `gbifrb`.

17 Results. For all clients we describe their design and utility, and demonstrate many use cases.

Discussion. Programmatic access to GBIF will facilitate more open and reproducible science. We hope  
that all scientists using GBIF data will do so with one of these two clients.

## 18 **Introduction**

19 Perhaps the most fundamental element in many fields of ecology is the individual organism. The number  
20 of individuals of each species in a given location forms the basis for many sub-fields of ecology and  
21 evolution. Some research questions necessitate collecting new data, while others can easily take advantage  
22 of existing data. In fact, some ecology fields are built largely on existing data, e.g., macro-ecology  
23 (Brown, 1995; Beck et al., 2012).

24 Data on individuals, including which species, and where they're found, can be used for a large number of  
25 research questions. Biodiversity records have been used for a suite of other use cases: validating habitat  
26 suitability models with real occurrence data (Ficetola et al., 2014); ancestral range reconstruction  
27 (Ferretti et al., 2015; María Mendoza et al., 2015); development of invasive species watch lists (Faulkner  
28 et al., 2014); evaluating risk of invasive species spread (Febbraro et al., 2013); and effects of climate  
29 change on future biodiversity (Brown et al., 2015).

30 In addition to wide utility, this data is important for conservation. Biodiversity loss is one of the greatest  
31 challenges of our time (Pimm et al., 2014), and some have called this the sixth great mass extinction  
32 (Ceballos et al., 2015). Given this challenge there is a great need for data on specimen records, whether  
33 collected from live sightings in the field or specimens in museums.

## 34 **Global Biodiversity Information Facility**

35 There are many online services that collect and maintain specimen records. However, Global Biodiversity  
36 Information Facility (hereafter, GBIF, <http://www.gbif.org>) is the largest collection of biodiversity  
37 records globally, currently with 820 million records, roughly 5.9 million taxa, 36,000 datasets from  
38 1,300 publishers (as of 2016-02-09). Many large biodiversity warehouses such as iNaturalist (<http://www.inaturalist.org>), VertNet (<http://vertnet.org>), and USGS's Biodiversity Information Serving  
39 Our Nation (BISON; <http://bison.usgs.ornl.gov>) all feed into GBIF.

41 The most important organizational level in GBIF occurrence data is the occurrence record. The  
42 fields in a record vary, but include information about taxonomy (kingdom, phylum, genus, species  
43 names) and their identifiers, dataset metadata, and locality information including geospatial position.  
44 Going upstream, each record is part of a dataset, where each dataset is submitted by an organization,  
45 organizations are organized into nodes, datasets are published through institutions (which may be  
46 hosted at another organization), and a network is a group of datasets (managed by GBIF).

Each occurrence record has some taxonomic name associated with it, which itself is linked to a lot of other taxonomic data - including a master taxonomic backbone that integrates taxonomies across many taxonomic authorities.

The organization of GBIF matters because you can navigate GBIF data through these hierarchical organizational levels - it helps to be familiar with the terminology and how each group relates to another.

## The clients

Although we discuss libraries for R, Python, and Ruby here, we focus mostly on the R library `rgbif` as it has seen the most developer and user attention, and is the most mature.

### *rgbif*

Herein, we describe the `rgbif` software package (Chamberlain et al.) for working with GBIF data in the R programming environment (R Core Team, 2014). R is a widely used language in academia, as well as non-profit and private sectors. Importantly, R makes it easy to execute all steps of the research process, including data management, data manipulation and cleaning, statistics, and visualization. Thus, an R client for getting GBIF data is a powerful tool to facilitate reproducible research.

The `rgbif` package is nearly completely written in R (a small Javascript library is included for reading well known text (Herring, 2011)), uses an [MIT license](#) to maximize use everywhere. `rgbif` is developed publicly on GitHub at <https://github.com/ropensci/rgbif>, where development versions of the package can be installed, and bugs and feature requests reported. Stable versions of `rgbif` can be installed from [CRAN](#), the distribution network for R packages. `rgbif` is part of the rOpenSci project (<http://ropensci.org>), a developer network making R software to facilitate reproducible research.

### *pygbif*

`pygbif` (Chamberlain) is a Python library for working with GBIF data in the Python programming environment. Python is a general purpose programming language used widely in all sectors, and for all parts of software development including server and client side use cases. Python is used exclusively in some scientific disciplines (e.g., astronomy), and has partial usage in other disciplines. A Python client for GBIF data is an important tool given the even wider usage of Python than R, though maybe slightly less than R for ecology/biology disciplines.

```
pip install pygbif
```

```
import pygbif
```

74 The `pygbif` library is less mature and complete than the R package. It also uses an [MIT license](#) to  
75 maximize use everywhere. `pygbif` is developed publicly on GitHub at <https://github.com/sckott/pygbif>,  
76 where development versions of the package can be installed, and bugs and feature requests reported.  
77 Stable versions of `pygbif` can be installed from [pypi](#), the distribution network for Python libraries.

78 *gbifrb*

79 `gbifrb` (Chamberlain) is a library for working with GBIF data in the Ruby programming environment.  
80 Like Python, Ruby is a general purpose programming language used widely in all sectors. Unlike  
81 Python, Ruby is not used extensively in scientific disciplines. However, a Ruby client for GBIF data  
82 can be an important tool given how widely Ruby is used for web and web service development.

```
gem install gbifrb
```

```
require 'gbifrb'
```

83 The `gbifrb` library is less mature and complete than the R and Python libraries. It also uses  
84 an [MIT license](#) to maximize use everywhere. `gbifrb` is developed publicly on GitHub at <https://github.com/sckott/gbifrb>, where development versions of the package can be installed, and bugs and  
85 feature requests reported. Stable versions of `gbifrb` can be installed from [Rubygems][gemgbif], the  
86 distribution network for Ruby libraries.  
87

88 *Library interfaces*

89 `rgbif`, `pygbif`, and `gbifrb` are designed following the [GBIF Application Programming Interface](#), or  
90 API. The GBIF API has four major components: registry, taxonomic names, occurrences, and maps. We  
91 also include functions to interface with the OAI-PMH GBIF service; only dataset (registry) information  
92 is available via this service, however. An interface to the GBIF maps API is in development for `rgbif`,  
93 but is non-existent for both `pygbif` and `gbifrb`. All three libraries have a suite of functions dealing  
94 with each of registry, taxonomic, names, and occurrences - we'll go through each in turn describing  
95 design of the user interface and example usage.

## 96 *GBIF headers*

97 With each request `rgbif`, `pygbif`, `gbifrb` make to GBIF's API, we send request headers that tell GBIF  
98 what library the request is coming from, including what version of the library. This helps GBIF know  
99 what proportion of requests are coming from which library, and therefore from R vs. Python vs. Ruby;  
100 this information is helpful for GBIF in thinking about how people are using GBIF data.

## 101 *Registry*

102 The GBIF registry API services are spread across five sets of functions via the main GBIF API:

- 103     • Datasets
- 104     • Installations
- 105     • Networks
- 106     • Nodes
- 107     • Organizations

108 Dataset information in general is available via the OAI-PMH service, functions in `rgbif` prefixed with  
109 `gbif_oai_`, but not available in `pygbif` or `gbifrb` yet.

110 Datasets are owned by organizations. Organizations are endorsed by nodes to share datasets with GBIF.  
111 Datasets are published through institutions, which may be hosted at another organization. A network  
112 is a group of datasets (managed by GBIF). Datasets are the units that matter the most with respect  
113 to registry information, while installations, networks, nodes, and organizations are simply higher level  
114 organizational structure.

## 115 *Datasets*

116 Dataset functions include search, dataset metadata retrieval, and dataset metrics. Searching for datasets  
117 is an important part of the discovery process. One can search for datasets on the GBIF web portal.  
118 However, programmatic searching using any of these libraries is more powerful. Identifying datasets  
119 appropriate for a research question is helpful as you can get metadata for each dataset, and track down  
120 dataset specific problems, if any.

121 The `dataset_search()` function in `rgbif` is one way to search for datasets. Here, we search for the  
122 term “oregon”, which finds any datasets that have words matching that term.

```
res <- dataset_search(query = "oregon")
res$data$datasetTitle[1:10]
#> [1] "Oregon State Ichthyology Collection"
#> [2] "Oregon State University Herpetological Collection"
#> [3] "Mygalomorph spiders from southwestern Oregon, USA, with descriptions of four new species"
#> [4] "A new species of Helobdella (Hirudinida: Glossiphoniidae) from Oregon, USA"
#> [5] "Annotated Checklist of the large branchiopod crustaceans of Idaho, Oregon and Washington"
#> [6] "A new species of Chrysobothris Eschscholtz from Oregon and Washington, with notes on other species"
#> [7] "Three new species of Grylloblatta Walker (Insecta: Grylloblattodea: Grylloblattidae), from Oregon"
#> [8] "A new species of Cladotanytarsus (Lenziella) from Oregon supports the systematic concept of the genus"
#> [9] "A new monster from southwest Oregon forests: Cryptomasterbehemoth sp. n. (Opiliones, Laniatores)"
#> [10] "Two new species of Fluminicola (Caenogastropoda, Lithoglyphidae) from southwest Oregon, USA"
```

123 See also `datasets()` and `dataset_suggest()` in `rgbif` for searching for datasets.

124 In Python, we can similarly search for datasets. Here, search for datasets of type `OCCURRENCE`:

```
from pygbif import registry
registry.datasets(type="OCCURRENCE")
```

125 In Ruby, we can do the same. Here, search for datasets of type `OCCURRENCE`:

```
require 'gbifrb'
registry = Gbif::Registry
registry.datasets(type: "OCCURRENCE")
```

126 *Dataset metrics.* Dataset metrics are another useful way of figuring out what datasets you may want to  
127 use. One drawback is that these metrics data are only available for datasets of type *checklist*, but there  
128 are quite a lot of them (21502).

129 Here, in R we search for dataset metrics for a single dataset, with uuid `ec93a739-1681-4b04-b62f-3a687127a17f`,  
130 a checklist of the ants (Hymenoptera: Formicidae) of the World.

```
res <- dataset_metrics(uuid='ec93a739-1681-4b04-b62f-3a687127a17f')
data.frame(rank = names(res$countByRank),
           count = unname(unlist(res$countByRank)))
```

rank	count
SPECIES	13710
SUBSPECIES	3234
GENUS	726
TRIBE	53
SUBFAMILY	20
FAMILY	2
KINGDOM	1
PHYLUM	1
CLASS	1
ORDER	1

131 And in Python, get metrics for the same dataset as above:

```
from pygbif import registry
registry.dataset_metrics(uuid='ec93a739-1681-4b04-b62f-3a687127a17f')
```

132 The same in Ruby:

```
require 'gbifrb'
registry = Gbif::Registry
registry.dataset_metrics(uuid: 'ec93a739-1681-4b04-b62f-3a687127a17f')
```

133 *Networks, nodes, and installations*

134 Networks, nodes and installations are at a higher level of organization above datasets, but can be  
 135 useful if you want to explore data from given organizations. Here, in R we search for the first 10 GBIF  
 136 networks, returning just the title field.



```

networks(limit = 10)$data$title
#> [1] "GBIF Backbone Sources"
#> [2] "Canadensys"
#> [3] "Southwest Collections of Arthropods Network (SCAN)"
#> [4] "VertNet"
#> [5] "Dryad"
#> [6] "GBIF Network"
#> [7] "The Knowledge Network for Biocomplexity (KNB) "
#> [8] "Online Zoological Collections of Australian Museums (OZCAM)"
#> [9] "Catalogue of Life"
#> [10] "Ocean Biogeographic Information System (OBIS)"

```

137 And in Python:

```

from pygbif import registry
registry.networks(limit = 10)

```

138 And in Ruby:

```

require 'gbifrb'
registry = Gbif::Registry
registry.networks(limit: 10)

```

139 *Taxonomic names*

140 The GBIF taxonomic names API services are spread across five functions in `rgbif`:

- 141 • Search GBIF name backbone - `name_backbone()`
- 142 • Search across all checklists - `name_lookup()`
- 143 • Quick name lookup - `name_suggest()`
- 144 • Name usage of a name according to a checklist - `name_usage()`
- 145 • GBIF name parser - `parsenames()`

146 pygbif and gbifrb have all the same functions, except the name parser goes by `name_parser()` in  
147 pygbif and gbifrb.

148 The goal of these name functions is often to settle on a taxonomic name known to GBIF's database.  
149 This serves two purposes: 1) when referring to a taxonomic name, you can point to a URI on the  
150 Internet, and 2) you can search for metadata on a taxon, and occurrences of that taxon in GBIF.

151 Taxonomic names are particularly tricky. Many different organizations have their own unique codes for  
152 the same taxonomic names, and some taxonomic groups have preferred sources for the definitive names  
153 for that group. That's why it's best to determine what name GBIF uses, and its associated identifier,  
154 for the taxon of interest instead of simply searching for occurrences with a taxonomic name.

155 When searching for occurrences (see below) you can search by taxonomic name (and other filters, e.g.,  
156 taxonomic rank), but you're probably better off figuring out the taxonomic key in the GBIF backbone  
157 taxonomy, and using that to search for occurrences. The `taxonkey` parameter in the GBIF occurrences  
158 API expects a GBIF backbone taxon key.

### 159 *GBIF Backbone*

160 The GBIF backbone taxonomy is used in GBIF to have a consistent way to refer to taxonomic  
161 names throughout their services. The backbone has 5869207 unique names and 2818534 species  
162 names. The backbone taxonomy is also a dataset with key `d7dddbf4-2cf0-4f39-9b2a-bb099caae36c`  
163 (<https://www.gbif.org/dataset/d7dddbf4-2cf0-4f39-9b2a-bb099caae36c>).

164 We can search the backbone taxonomy with the function `name_backbone()` in all three clients. Here,  
165 we're searching for the name *Poa*, restricting to genera, and the family *Poaceae*, in R

```
res <- name_backbone(name='Poa', rank='genus', family='Poaceae')
res[c('usageKey', 'kingdom')]
#> $usageKey
#> [1] 2704173
#>
#> $kingdom
#> [1] "Plantae"
```

166 And in Python

```

from pygbif import species
res = species.name_backbone(name='Poa', rank='genus', family='Poaceae')
[ res[x] for x in ['usageKey', 'kingdom'] ]

```

167 And in Ruby

```

require 'gbifrb'
species = Gbif::Species
res = species.name_backbone(name: 'Poa', rank: 'genus', family: 'Poaceae')
res.select { |k,v| k.match(/usageKey|kingdom/) }

```

168 *Name searching*

169 One of the quickest ways to search for names is using `name_suggest()`, which does a very quick search  
 170 and returns minimal data. Here, we're searching for the query term *Pum*, and we get back many names:

```

name_suggest(q='Pum', limit = 6)

```

key	canonicalName	rank
2142856	Althepus pum	SPECIES
8589398	Pumiliopimoidae	FAMILY
8783253	Pumililema	GENUS
4823360	Pumiliopareia	GENUS
4635949	Pumilina	GENUS
4648228	Pumilopaurus	GENUS

171 The same in Python

```

from pygbif import species
species.name_suggest(q='Pum', limit = 6)

```

172 And in Ruby

```
require 'gbifrb'
species = Gbif::Species
species.name_suggest(q: 'Pum', limit: 6)
```

With these results, you can then proceed to search for occurrences with the taxon key(s), or drill down further with other name searching functions to get the exact taxon of interest.

### *Occurrences*

GBIF provides two ways to get occurrence data: through the `/occurrence/search` route (see `occ_search` in `rgbif`, `occurrences.search` in `pygbif`, `Occurrences.search` in `gbifrb`), or via the `/occurrence/download` route (many functions, see below).

`occ_search()/occurrences.search/Occurrences.search` are the main functions for the search route, and are more appropriate when you want less data, while the download functions are more appropriate for larger data requests.

Small vs. large amounts of data of course is all relative. GBIF imposes for any given search a limit of 200,000 records in the search service, after which point you can't download any more records for that search. However, you can download more records for different searches.

We think the search service is still quite useful for many people even given the 200,000 limit. For those that need more data, we have created a similar interface in the download functions that should be easy to use with minimal work. Users should take note that using the download service has a few extra steps to get data into R, but is straight-forward.

The download service, like the occurrence search service, is rate-limited. That is, you can only have one to three downloads running simultaneously for your user credentials. However, simply check when a download job is complete, then you can start a new download request. See “Queueing Download Requests” below for help automating many download requests in R.

### *Download API*

The download API syntax is similar to the occurrence search API in that the same parameters are used, but the way in which the query is defined is different. For example, in the download API you can do greater than searches (i.e., `latitude > 50`), whereas you cannot do that in the occurrence search

197 API. Thus, unfortunately, we couldn't make the query interface exactly the same for both search and  
198 download functions.

199 Using the download service can consist of as few as three steps: 1) Request data via a search; 2)  
200 Download data; 3) Import data into R.

201 Request data download given a query. Here, we search for the taxon key 3119195, which is the key for  
202 *Helianthus annuus* (<http://www.gbif.org/species/3119195>).

```
occ_download('taxonKey = 3119195')  
#> <<gbif download>>  
#> Username: xxxx  
#> E-mail: xxxx  
#> Download key: 0000840-150615163101818
```

203 You can check on when the download is ready using the functions `occ_download_list()` and  
204 `occ_download_meta()`. When it's ready use `occ_download_get()` to download the dataset to your  
205 computer.

```
(res <- occ_download_get("0000840-150615163101818", overwrite = TRUE))  
#> <<gbif downloaded get>>  
#> Path: ./0000840-150615163101818.zip  
#> File size: 3.19 MB
```

206 What's printed out above is a very brief summary of what was downloaded, the path to the file, and its  
207 size (in human readable form).

208 Next, read the data in to R using the function `occ_download_import()`.

```
library("dplyr")  
dat <- occ_download_import(res)  
dat %>%  
  select(gbifID, decimalLatitude, decimalLongitude)  
#>      gbifID abstract accessRights accrualMethod accrualPeriodicity accrualPolicy alternative  
#> 1  725767384      NA              NA              NA              NA              NA
```

```
#> 2 725767447 NA NA NA NA NA
#> 3 725767450 NA NA NA NA NA
#> 4 725767513 NA NA NA NA NA
#> 5 725767546 NA NA NA NA NA
#> 6 725767579 NA NA NA NA NA
#> 7 725767609 NA NA NA NA NA
#> 8 725767645 NA NA NA NA NA
#> 9 725767678 NA NA NA NA NA
#> 10 725767681 NA NA NA NA NA
#> .. ... .. ... .. ... .. ...
#> Variables not shown: available (lgl), bibliographicCitation (chr), conformsTo (lgl), contribu
#> coverage (lgl), created (chr), creator (lgl), date (lgl), dateAccepted (lgl), dateCopyri
#> (lgl), dateSubmitted (lgl), description (lgl), educationLevel (lgl), extent (lgl), forma
#> hasFormat (lgl), hasPart (lgl), hasVersion (lgl), identifier (chr), instructionalMethod
```

209 In Python

```
from pygbif import occurrences as occ
occ.download('taxonKey = 3119195')
(res = occ.download_get("0000840-150615163101818", overwrite = True))
```

210 We don't have `pygbif` functionality at the moment for importing data, but it's coming soon.

211 The Ruby library `gbifrb` does not yet have occurrence download functionality.

212 *Downloaded data format.* The downloaded dataset from GBIF is a Darwin Core Archive (DwC-A), an  
 213 internationally recognized biodiversity informatics standard (<http://rs.tdwg.org/dwc/>). The DwC-A  
 214 downloaded is a compressed folder with a number of files, including metadata, citations for each of the  
 215 datasets included in the download, and the data itself, in separate files for each dataset as well as one  
 216 single `.txt` file. In `rgbif::occ_download_import()`, we simply fetch data from the `.txt` file. If you  
 217 want to dig into the metadata, citations, etc., it is easily accessible from the folder on your computer.

218 *Queueing Download Requests.* FILL IN TEXT HERE ...

## 219 *Search API*

220 The search API follows the GBIF API and is broken down into the following functions:

- 221 • Get a single numeric count of occurrences - `rgbif: occ_count()` / `pygbif: occurrences.count`  
222 / `gbifrb: Occurrences.count`
- 223 • Search for occurrences - `rgbif: occ_search()` / `pygbif: occurrences.search` / `gbifrb:`  
224 `Occurrences.search`
- 225 • A simplified and optimized version of `rgbif: occ_search()` or `occ_data()` / `none` / `none`
- 226 • Get occurrences by occurrence identifier - `rgbif: occ_get()` / `pygbif: occurrences.get` /  
227 `gbifrb: Occurrences.get`
- 228 • Get occurrence metadata - `rgbif: occ_metadata()` / `pygbif: various` / `gbifrb: various`

229 *Search for occurrences.* The main search work-horse is `occ_search()`. This function allows very flexible  
230 search definitions. In addition, this function does paging internally, making it such that the user does  
231 not have worry about the 300 records per request limit - but of course we can't go over the 200,000  
232 maximum limit.

233 The output of `occ_search()` presents a compact `data.frame` so that no matter how large the  
234 `data.frame`, the output is easily assessed because only a few of the records (rows) are shown, only a few  
235 columns are shown (with others shown in name only), and metadata is shown on top of the `data.frame`  
236 to indicate data found and returned, media records found, unique taxonomic hierarchies returned, and  
237 the query executed.

238 The output of these examples, except one, aren't shown.

239 Search by species name, using `name_backbone()` first to get key

240 **R**

```
library(rgbif)

(key <- name_suggest(q = 'Helianthus annuus', rank = 'species'))$key[1])
#> [1] 9206251

occ_search(taxonKey = key, limit = 2)
```

```

#> Records found [17858]
#> Records returned [2]
#> No. unique hierarchies [1]
#> No. media records [1]
#> No. facets [0]
#> Args [limit=2, offset=0, taxonKey=9206251, fields=all]
#> # A tibble: 2 x 75
#>           name          key decimalLatitude decimalLongitude
#>           <chr>        <int>          <dbl>          <dbl>
#> 1 Helianthus annuus 1433793045      59.66859      16.54257
#> 2 Helianthus annuus 1434024463      63.71622      20.31247
#> # ... with 71 more variables: issues <chr>, datasetKey <chr>,
#> #   publishingOrgKey <chr>, publishingCountry <chr>, protocol <chr>,
#> #   lastCrawled <chr>, lastParsed <chr>, crawlId <int>, extensions <chr>,
#> #   basisOfRecord <chr>, ...

```

## 241 Python

```

from pygbif import species
from pygbif import occurrences as occ

key = species.name_suggest(q = 'Helianthus annuus', rank = 'species')['data'][0]['key']
occ.search(taxonKey = key, limit = 2)

```

## 242 Ruby

```

require 'gbifrb'

species = Gbif::Species
occ = Gbif::Occurrences

key = species.name_suggest(q: 'Helianthus annuus', rank: 'species')['data'][0]['key']
occ.search(taxonKey: key, limit: 2)

```

243 Instead of getting a taxon key first, you can search for a name directly

## 244 R



```
occ_search(scientificName = 'Ursus americanus')
```

## 245 Python

```
occ.search(scientificName = 'Ursus americanus')
```

## 246 Ruby

```
occ.search(scientificName: 'Ursus americanus')
```

## 247 Search for many species

## 248 R

```
splist <- c('Cyanocitta stelleri', 'Junco hyemalis', 'Aix sponsa')
keys <- sapply(splist, function(x) name_suggest(x)$key[1], USE.NAMES = FALSE)
occ_search(taxonKey = keys, limit = 5, return = 'data')
```

## 249 Python

```
from pygbif import species
from pygbif import occurrences as occ
splist = ['Cyanocitta stelleri', 'Junco hyemalis', 'Aix sponsa']
keys = [ species.name_suggest(x)['data'][0]['key'] for x in splist ]
occ.search(taxonKey = keys, limit = 5)
```

## 250 Ruby

```
species = Gbif::Species
occ = Gbif::Occurrences
splist = ['Cyanocitta stelleri', 'Junco hyemalis', 'Aix sponsa']
keys = [ species.name_suggest(x)['data'][0]['key'] for x in splist ]
occ.search(taxonKey: keys, limit: 5)
```

251 Spatial search, based on well known text format (Herring, 2011), or a bounding box set of four co-  
252 ordinates. The well known text string and the bounding box in the below example specify the same

253 rectangular area in California, centering approximately on Sacramento. Whereas the bounding box for-  
254 mat requires longitude SW corner, latitude SW corner, longitude NE corner, latitude NE  
255 corner, the well known text string requires an extra long/lat pair to close the polygon.

256 **R**

```
# well known text
wkt <- 'POLYGON((-122.6 39.9,-120.0 39.9,-120.0 37.9,-122.6 37.9,-122.6 39.9))'
occ_search(geometry = wkt, limit = 20)

# bounding box
occ_search(geometry = c(-122.6,37.9,-120.0,39.9), limit = 20)
```

257 **Python**

```
from pygbif import occurrences as occ

# well known text
occ.search(geometry = 'POLYGON((30.1 10.1, 10 20, 20 40, 40 40, 30.1 10.1))', limit = 20)

# bounding box
occ.search(geometry = '-125.0,38.4,-121.8,40.9', limit = 20)
```

258 **Ruby**

```
occ = Gbif::Occurrences

# well known text
occ.search(geometry: 'POLYGON((30.1 10.1, 10 20, 20 40, 40 40, 30.1 10.1))', limit: 20)

# bounding box
occ.search(geometry: '-125.0,38.4,-121.8,40.9', limit: 20)
```

259 Get only occurrences with lat/long data using the `hasCoordinate` parameter

260 **R**

```
occ_search(hasCoordinate = TRUE, limit = 5)
```

261 **Python**

```
from pygbif import occurrences as occ
occ.search(hasCoordinate = True, limit = 5)
```

## 262 Ruby

```
occ = Gbif::Occurrences
occ.search(hasCoordinate: true, limit: 5)
```

263 Get only those occurrences with spatial issues. Spatial issues are a set of issues that are returned in  
 264 the `issues` field. They each indicate something different about that record. For example, the issue  
 265 `COUNTRY_COORDINATE_MISMATCH` indicates that the interpreted occurrence coordinates fall outside of  
 266 the indicated country. You can see how that might be useful when it comes to cleaning your data prior  
 267 to analysis/visualization.

## 268 R

```
occ_search(hasGeospatialIssue = TRUE, limit = 5)
```

## 269 Python

```
from pygbif import occurrences as occ
occ.search(hasGeospatialIssue = True, limit = 5)
```

## 270 Ruby

```
occ = Gbif::Occurrences
occ.search(hasGeospatialIssue: true, limit: 5)
```

271 *Data cleaning.* GBIF provides optional data issues with each occurrence record. These issues fall into  
 272 many different pre-defined classes, covering issues with taxonomic names, geographic data, and more  
 273 (see `rgbif::occ_issues_lookup()` to find out more information on GBIF issues; and the same data  
 274 on [GBIF's development site](#)).

275 `rgbif::occ_issues()` provides a way to easily filter data downloaded via `rgbif::occ_search()` based  
 276 on GBIF issues.

```

out <- occ_search(issue = 'DEPTH_UNLIKELY', limit = 500)
NROW(out)
#> [1] 5
out %>% occ_issues(-cudc) %>% .$data %>% NROW
#> [1] 0

```

277 There's no equivalent interface in pygbif or gbifrb yet.

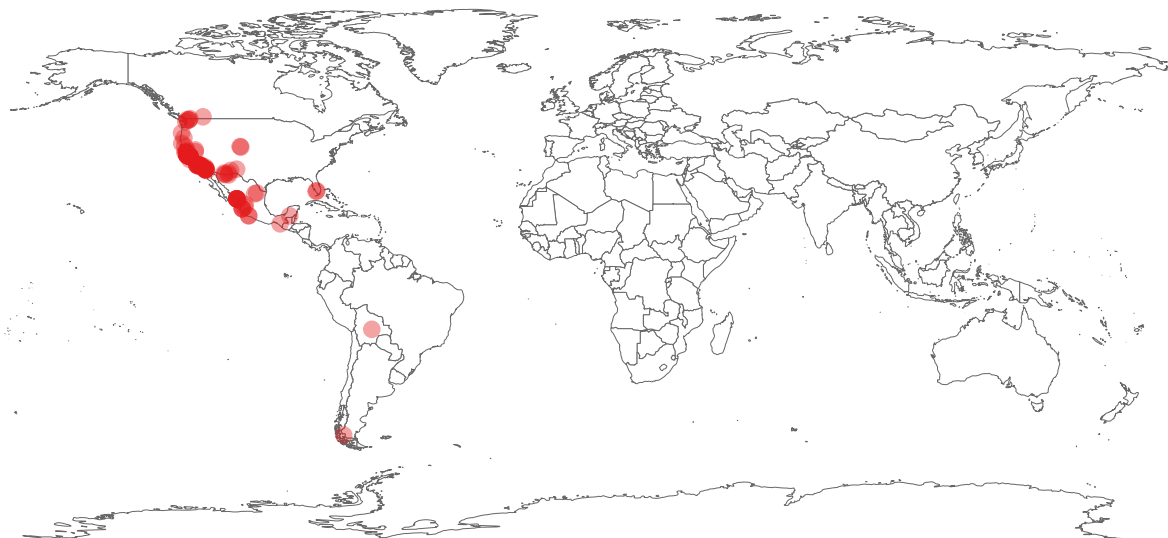
## 278 Mapping

279 An obvious downstream use case for species occurrence data is to map the data. `rgbif` per se is largely  
 280 not concerned with making this easier, although we do have a simple wrapper around `ggplot2` to make  
 281 it easy to get a quick plot of occurrence data. For example, here we plot 100 occurrences for *Puma*  
 282 *concolor*.

```

key <- name_backbone(name='Puma concolor')$speciesKey
dat <- occ_search(taxonKey = key, limit = 100, hasCoordinate = TRUE)
gbifmap(dat$data)

```



283

284 Another package, `mapr`, is the perfect mapping companion to `rgbif`. It has convenient functions for  
 285 handling input data from `rgbif`, `spocc`, or arbitrary `data.frame`'s, and output plots for base plots,

286 `ggplot2`, `ggmap` (`ggplot2` with map layers underneath), and interactive maps on GitHub gists or with  
287 `Leaflet.js`.

288 There's no equivalent interface in `pygbif` or `gbifrb`.

### 289 *GBIF data in other R packages*

290 We discuss usage of GBIF data in other R packages throughout the manuscript, but provide a synopsis  
291 here for clarity.

#### 292 *taxize*

293 Some of the GBIF taxonomic services are also available in `taxize`, an R package that focuses on getting  
294 data from taxonomic data sources on the web. For example, with `get_gbifid()` one can get GBIF IDs  
295 used for a set of taxonomic names - then use those IDs in other functions in `taxize` to get additional  
296 information, like taxonomically downstream children.

#### 297 *spocc*

298 GBIF occurrence data is available in the R package `spocc` via `rgbif`. `spocc` is a unified interface  
299 for fetching species occurrence data from many sources on the web. For example, a user can collect  
300 occurrence data from GBIF, iDigBio, and iNaturalist, and easily combine them, then use other packages  
301 to clean and visualize the data.

### 302 **R vs. Python vs. Ruby**

303 Both R and Python are commonly used in science, and can be used for similar tasks. Python, however,  
304 is a more general programming language, and can be used in more contexts than R can be used in.

305 The `rgbif` and `pygbif` clients can do a lot of the same tasks. We envision `rgbif` as being more common  
306 in workflows of academics asking research questions, whereas `pygbif` can do that as well, but may be  
307 more easily used in a website.

308 The R client `rgbif` has much more development time than `pygbif`, but through time `pygbif` will  
309 become equally mature.

## 310 Use cases

311 The following are three use cases for the R library `rgbif`: niche modeling, spatial change in biodiversity,  
312 and distribution mapping.

### 313 *Ecological niche modeling*

314 In this example, we plot actual occurrence data for *Bradypus* species against a single predictor variable,  
315 BIO1 (annual mean temperature). This is only one step in a species distribution modelling workflow.

316 This example can be done using BISON data as well with our `rbison` package.

### 317 *Load libraries*

```
library("rgbif")
library("dismo")
library("maptools")
library("dplyr")
```

### 318 *Raster files*

319 Make a list of files that are installed with the `dismo` package, then create a `rasterStack` from these

```
files <- list.files(paste(system.file(package = "dismo"), "/ex", sep = ""),
                   "grd", full.names = TRUE)
predictors <- stack(files)
```

### 320 *Get world boundaries*

```
data(wrld_simpl)
```

### 321 *Get GBIF data using the `rOpenSci` package `rgbif`*

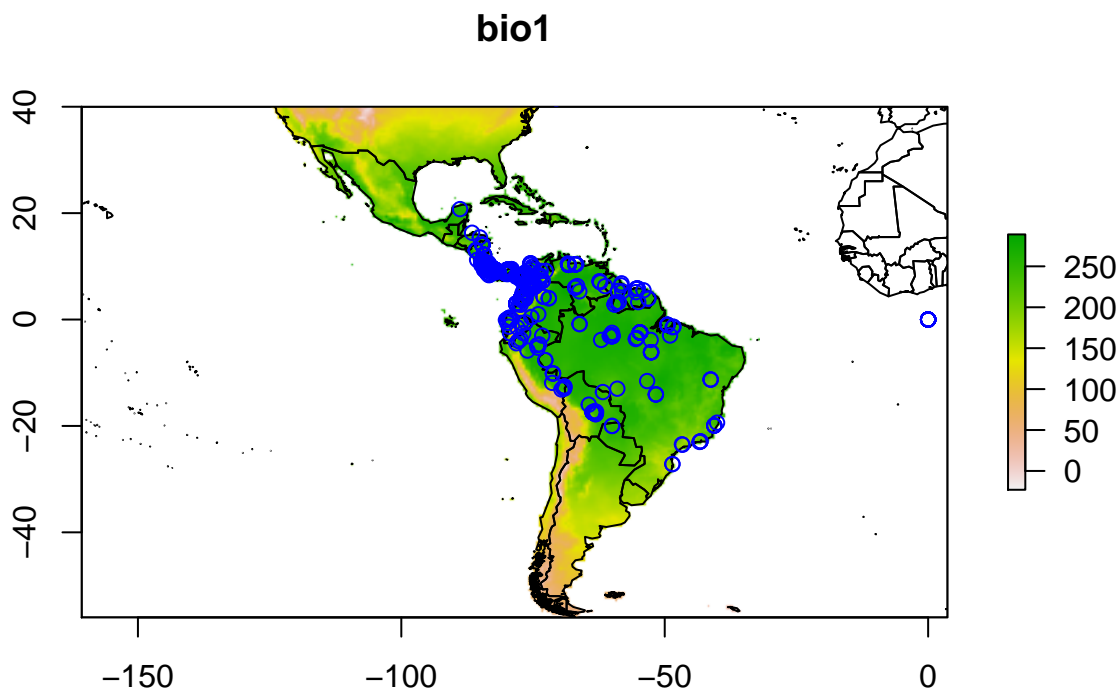
```
nn <- name_lookup("bradypus*", rank = "species")
nn <- na.omit(unique(nn$data$subKey))
df <- occ_search(taxonKey = nn, hasCoordinate = TRUE, limit = 500)
df_data <- df[ apply(df, function(x) any(class(x$data) %in% "tbl_df")) ]
```

```
df_data <- dplyr::bind_rows(lapply(df_data, "[", "data"))
df2 <- df_data %>% dplyr::select(decimalLongitude, decimalLatitude)
```

322 *Plot*

323 (1) Add raster data, (2) Add political boundaries, (3) Add the points (occurrences)

```
plot(predictors, 1)
plot(wrld_simpl, add = TRUE)
points(df2, col = "blue")
```



324

325 *Biodiversity in big cities*

326 In this example, we collect specimen records across different cities using GBIF data from the `rgbif`  
 327 package.

328 *Load libraries*

```
library("rgbif")
library("ggplot2")
library("plyr")
library("httr")
library("RColorBrewer")
library("wicket")
```

329 *Get bounding boxes for some cites*

330 Bounding lat/long data is from [https://raw.githubusercontent.com/amyxzhang/boundingbox-cities/master/](https://raw.githubusercontent.com/amyxzhang/boundingbox-cities/master/boundbox.txt)  
 331 [boundbox.txt](https://raw.githubusercontent.com/amyxzhang/boundingbox-cities/master/boundbox.txt).

```
url <- 'https://raw.githubusercontent.com/amyxzhang/
boundingbox-cities/master/boundbox.txt'
rawdat <- content(GET(sub("\n", "", url)), as = "text")
dat <- read.table(
  text = rawdat, header = FALSE,
  sep = "\t", col.names = c("city", "minlat", "maxlon", "maxlat", "minlon"),
  stringsAsFactors = FALSE)
dat <- data.frame(
  city = dat$city, minlon = dat$minlon,
  minlat = dat$minlat, maxlon = dat$maxlon,
  maxlat = dat$maxlat,
  stringsAsFactors = FALSE
)
```

332 A helper function to get count data. GBIF has a count API, but we can't use that with a geometry search  
 333 as that API doesn't support geospatial search. We can however use the search API via `occ_search()`  
 334 and set `limit = 1` so that we

```
getdata <- function(x){
  coords <- as.numeric(x[c('minlon', 'minlat', 'maxlon', 'maxlat')])
  wkt <- wicket::wkt_correct(wicket::bounding_wkt(values = coords))
```



```

num <- occ_search(geometry = wkt, limit = 1)$meta$count
data.frame(
  city = x['city'],
  richness = num,
  stringsAsFactors = FALSE
)
}

```

```

out <- apply(dat, 1, getdata)

```

335 *Merge to original table*

```

out <- merge(dat, ldply(out), by = "city")

```

336 *Add centroids from bounding boxes*

```

out <- transform(out, lat = (minlat + maxlat)/2, lon = (minlon + maxlon)/2)

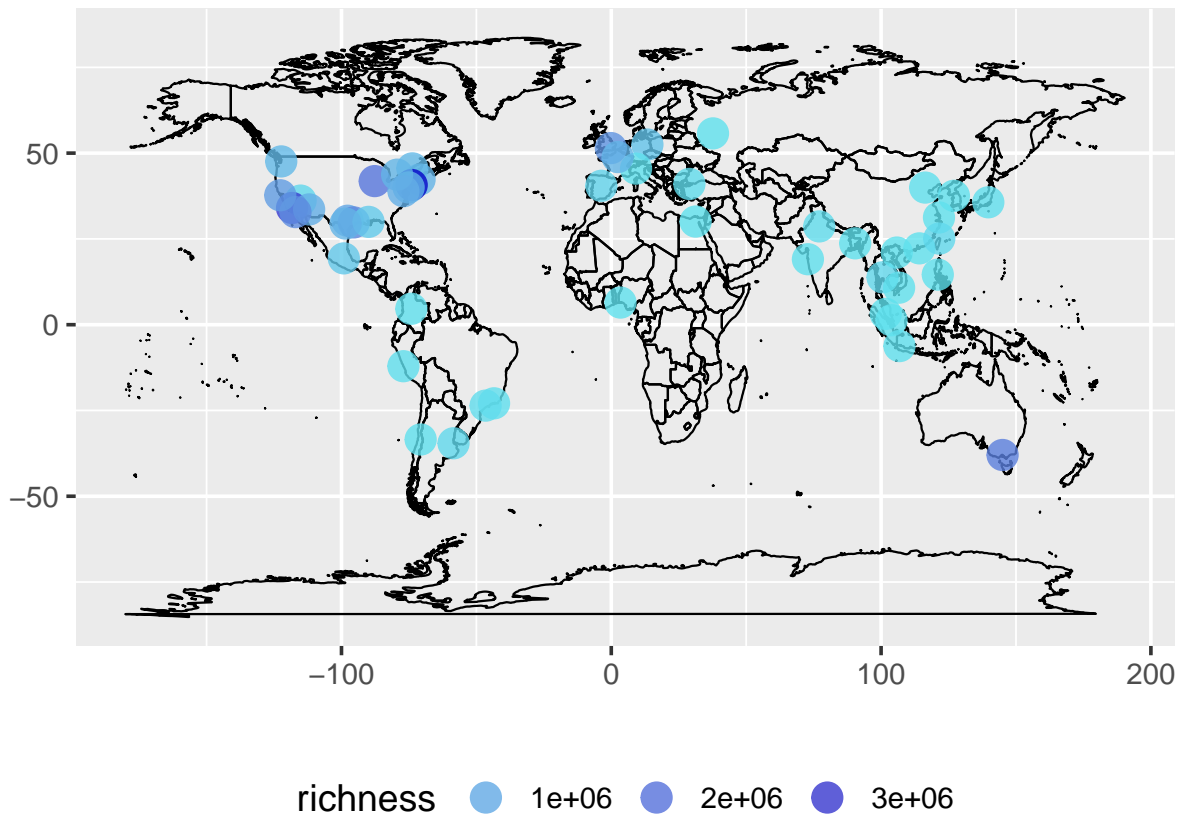
```

337 *Plot data*

```

mapp <- map_data('world')
ggplot(mapp, aes(long, lat)) +
  geom_polygon(aes(group=group), fill="white", alpha=0, color="black", size=0.4) +
  geom_point(data=out, aes(lon, lat, color=richness), size=5, alpha=0.8) +
  scale_color_continuous(low = "#60E1EE", high = "#0404C8") +
  labs(x="", y="") +
  theme_grey(base_size=14) +
  theme(legend.position = "bottom", legend.key = element_blank()) +
  guides(color = guide_legend(keywidth = 2))

```



338

339 *Valley oak occurrence data comparison*

340 This example comes from [Antonio J. Perez-Luque](#) who [shared his plot on Twitter](#). Antonio compared  
 341 the occurrences of Valley Oak (*Quercus lobata*) from [GBIF](#) to the distribution of the same species from  
 342 the [Atlas of US Trees](#).

343 *Load libraries*

```
library('rgbif')
library('raster')
library('sp')
library('sf')
library('rgeos')
library('scales')
```

344 *Get GBIF Data for Quercus lobata*

```
keyQ1 <- name_backbone(name='Quercus lobata', kingdom='plants')$speciesKey
dat.Q1 <- occ_search(taxonKey=keyQ1, return='data', limit=50000)
```

345 *Get Distribution map of Q. lobata Atlas of US Trees (Little, E.)*

346 From <http://esp.cr.usgs.gov/data/little>. And save shapefile in same directory

```
url <- 'https://github.com/sckott/gbifms/blob/gh-pages/querloba.zip?raw=true'
tmp <- tempdir()
download.file(url, destfile = "querloba.zip")
unzip("querloba.zip", exdir = tmp)
ql <- sf::read_sf(file.path(tmp, "querloba/querloba.shp"))
```

347 *Get Elevation data of US*

```
alt.USA <- getData('alt', country = 'USA')
```

348 *Create Hillshade of US*

```
alt.USA <- alt.USA[[1]]
slope.USA <- terrain(alt.USA, opt = 'slope')
aspect.USA <- terrain(alt.USA, opt = 'aspect')
hill.USA <- hillShade(slope.USA, aspect.USA, angle = 45, direction = 315)
```

349 *Plot map*

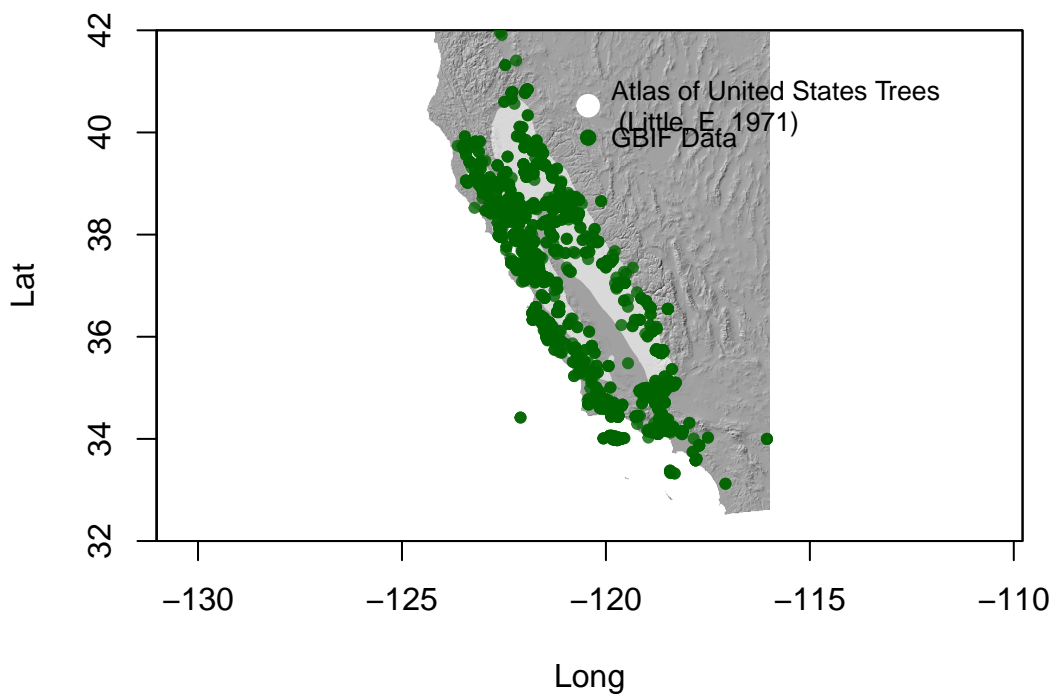
```
plot(hill.USA, col = grey(0:100/100), legend = FALSE,
     xlim = c(-125, -116), ylim = c(32, 42),
     main = 'Distribution of Quercus lobata',
     xlab = "Long", ylab = 'Lat')
# add shape from Atlas of US Trees
plot(ql, add = TRUE, col = alpha("white", 0.6),
     border = FALSE)
# add Gbif presence points
```

```

points(dat.Q1$decimalLongitude, dat.Q1$decimalLatitude,
       cex = .7, pch = 19, col = alpha("darkgreen", 0.8))
legend(x = -121, y = 40.5, "GBIF Data", pch = 19,
       col = 'darkgreen', bty = 'n', pt.cex = 1, cex = .8)
legend(x = -121, y = 41.5,
       legend = "Atlas of United States Trees \n (Little, E. 1971)",
       pt.cex = 1.5, cex = .8, pch = 19, col = 'white', bty = 'n')

```

## Distribution of *Quercus lobata*



350

## 351 Conclusions and future directions

352 The `rgbif`, `pygbif`, and `gbifrb` libraries provide programmatic interfaces to GBIF's application  
 353 programming interface (API) - a powerful tool for working with species occurrence data, and facilitating  
 354 reproducible research. In fact, the `rgbif` package has already been used in more than 20 scholarly  
 355 publications (as of 2016-08-10), including (Amano, Lamming & Sutherland, 2016, Bartomeus et al.  
 356 (2013), Barve (2014), Bone et al. (2015), Collins et al. (2015), Drozd & Šipoš (2013), Kong, Huang &

357 Duan (2015), Richardson, Roux & Wilson (2015), Turner, Fréville & Rieseberg (2015), Verheijen et al.  
358 (2015), Zizka & Antonelli (2015), Butterfield et al. (2016), Dellinger et al. (2015), Feitosa et al. (2015),  
359 Malhado et al. (2015), Werner et al. (2015), Robertson, Visser & Hui (2016), Davison et al. (2015),  
360 Janssens et al. (2016)).

361 The **rgbif** package is relatively stable, and should not have many breaking changes unless necessitated  
362 due to changes in the GBIF API. However, it will gain function(s) to work with the maps API in the  
363 near future.

364 The **pygbif** and **gbifrb** libraries are in early development, and will greatly benefit from any feedback  
365 and use cases.

366 One area of focus in the future is to attempt to solve many use cases that have been brought up with  
367 respect to GBIF data. For example, some specimens are included in GBIF that are located in botanical  
368 gardens. For many research questions, researchers are interested in “wild” type occurrences, not those  
369 in human curated scenarios. Making removal of these occurrences easy would be very useful, but is  
370 actually quite a hard problem. There are many other problems like this, for which these three libraries  
371 will help in making more efficient and reproducible.

## 372 **Acknowledgments**

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## 375 **Data Accessibility**

376 All scripts and data used in this paper can be found in the permanent data archive Zenodo under  
377 the digital object identifier (DOI). This DOI corresponds to a snapshot of the GitHub repository  
378 at <https://github.com/sckott/gbifms>. Software can be found at <https://github.com/ropensci/rgbif>,  
379 <https://github.com/sckott/pygbif>, and <https://github.com/sckott/gibfrb>, all under MIT licenses. We  
380 thank all the users that have used **rgbif**, **pygbif**, and **gbifrb** and have given feedback and reported  
381 bugs. In addition, we greatly appreciate all the contributors to the three libraries, found at [https://](https://github.com/ropensci/rgbif/graphs/contributors)  
382 [github.com/ropensci/rgbif/graphs/contributors](https://github.com/ropensci/rgbif/graphs/contributors), <https://github.com/sckott/pygbif/graphs/contributors>,  
383 and <https://github.com/sckott/gbifrb/graphs/contributors>.

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