Biodiversity & Taxonomy Software Tools in R

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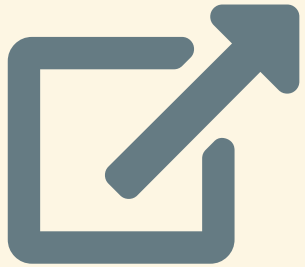

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pdf slides 960x720
pdf slides 1280x720

Keyboard shortcuts: press ?

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ropensci.org

rOpenSci Does

Community Software Review

Why?

Questions addressed using our software

Comparative genomics in the Asteraceae reveals little evidence for parallel evolutionary change in invasive taxa

A BOTANICAL INVENTORY OF FOREST ON KARSTIC LIMESTONE AND METAMORPHIC SUBSTRATE IN THE CHIQUIBUL FOREST, BELIZE, WITH FOCUS ON WOODY TAXA

Retrieving taxa names from large biodiversity data collections using a flexible matching workflow

The changing patterns of plant naturalization in Australia

A quantitative synthesis of the importance of variables used in MaxEnt species distribution models

Australian acacias as invasive species: lessons to be learnt from regions with long planting histories§

Aligning marine species range data to better serve science and conservation

Refining area of occupancy to address the modifiable areal unit problem in ecology and conservation

Evolutionarily Stable Strategies for Fecundity and Swimming Speed of Fish

Citations of rOpenSci Biodiv Software

Taxonomy

package	citations
taxize	71
rentrez	13
ritis	1
taxa	1
worrms	1

Occurrences

package	citations
rgbif	51
rfishbase	24
spocc	8
rfisheries	2
rredlist	2
rvertnet	2
AntWeb	1
pangaear	1
rotl	8

use case 1

Hodgins, K. A., Turner, et al. (2015). Comparative genomics in the Asteraceae reveals little evidence for parallel evolutionary change in invasive taxa. Mol Ecol, 24(9), 2226–2240. 10.1111/mec.13026

in the methods section:

... using the Encyclopedia of Life invasive species comprehensive list, which was accessed programmatically on August 12, 2014 using the `taxize` *package in R .*

use case 2

Hodgins, K. A., Turner, et al. (2015). Comparative genomics in the Asteraceae reveals little evidence for parallel evolutionary change in invasive taxa. Mol Ecol, 24(9), 2226–2240. 10.1111/mec.13026

in the methods section:

... we used rOpenSci's `worrms` package in R to standardize spellings of species names and synonyms ...

Taxonomy

- taxa - Taxonomic classes and taxonomically aware data manipulation
- taxize - Taxonomic "toolbelt" - work w/ taxonomy web APIs
- taxizedb - taxize, but with local SQL databases
- rentrez - NCBI's Entrez, including taxonomy
- worrms - WORMS web service
- ritis - USGS's ITIS web service
- ... many others

Taxonomic data from >20 sources - taxize

always try to move from:

- taxonomic name -- to
- taxonomic ID -- to
- whatever other data
  (e.g., synonyms, classifications, etc.)

Taxonomic data from >20 sources - taxize

Taxonomic hierarchies from NCBI/ITIS/COL/etc

```
library('taxize')
id <- get_gbifid("Chironomus riparius")
classification(id)
```

```
#> $`Chironomus riparius`
#>                  name    rank      id
#> 1           Animalia kingdom       1
#> 2          Arthropoda  phylum      54
#> 3             Insecta   class     216
#> 4             Diptera   order     811
#> 5        Chironomidae  family    3343
#> 6          Chironomus   genus 1448033
#> 7 Chironomus riparius species 1448237
```

Wrangling data paired with taxonomy - taxa

```
library('taxa')
ex_taxmap
```

```
<Taxmap>
  17 taxa: b. Mammalia, c. Plantae, d. Felidae ... p. sapiens, q. lycopersicum, r. tuberosum
  17 edges: NA->b, NA->c, b->d, b->e, b->f, c->g, d->h, d->i ... g->l, h->m, i->n, j->o, k->p, l->q, l->r
  4 data sets:
    info:
      # A tibble: 6 x 4
        taxon_id name  n_legs dangerous
        <chr>    <chr>  <dbl> <lgl>
      1 m        tiger      4 TRUE
      2 n        cat        4 FALSE
      3 o        mole       4 FALSE
      # ... with 3 more rows
    phylopic_ids: a named vector of 'character' with 6 items
       m. e148eabb-f138-43c6-b1e4-5cda2180485a ... r. 63604565-0406-460b-8cb8-1abe954b3f3a
    foods: a list of 6 items named by taxa:
       m, n, o, p, q, r
    abund:
      # A tibble: 8 x 5
        taxon_id code  sample_id count taxon_index
        <chr>    <fct> <fct>     <dbl>       <int>
      1 m        T     A             1           1
      2 n        C     A             2           2
      3 o        M     B             5           3
```

Wrangling data paired with taxonomy - taxa

```
filter_taxa(ex_taxmap, startsWith(taxon_names, "t")) # filter
```

```
<Taxmap>
  3 taxa: m. tigris, o. typhlops, r. tuberosum
  3 edges: NA->m, NA->o, NA->r
  4 data sets:
    info:
      # A tibble: 3 x 4
        taxon_id name   n_legs dangerous
        <chr>    <chr>   <dbl> <lgl>
      1 m        tiger       4 TRUE
      2 o        mole        4 FALSE
      3 r        potato      0 FALSE
    phylopic_ids: a named vector of 'character' with 3 items
       m. e148eabb-f138-43c6-b1e4-5cda2180485a, o. 11b783d5-af1c-4f4e-8ab5-a51470652b47, r. 63604565-(
be954b3f3a
    foods: a list of 3 items named by taxa:
       m, o, r
    abund:
      # A tibble: 4 x 5
        taxon_id code  sample_id count taxon_index
        <chr>    <fct> <fct>     <dbl>       <int>
      1 m        T     A             1           1
      2 o        M     B             5           3
      3 m        T     A             6           1
      # ... with 1 more row
  1 functions:
    reaction
```

ENTREZ in R - rentrez

Retrieve downstream taxonomy from a given taxon

```
library(rentrez)
x <- entrez_search(db = "taxonomy", term = "Satyrium[Next Level]", retmax = 10)
z <- entrez_summary(db = "taxonomy", id = x$ids)

data.frame(t(
  extract_from_esummary(z, c("uid", "scientificname", "rank"))
))

#> uid             scientificname    rank
#> 2023262     Satyrium liltvedianum species
#> 1888668          Satyrium calanus species
#> 1847691 Satyrium sp. BOLD:ABX6433 species
#> 1825277     Satyrium sp. XQX-2016 species
#> 1824831          Satyrium grandis species
#> 1430660         Satyrium favonius species
#> 1423409         Satyrium sylvinus species
#> 1405335             Satyrium mera species
#> 1405334           Satyrium iyonis species
#>  985828    Satyrium situsanguinum species
```

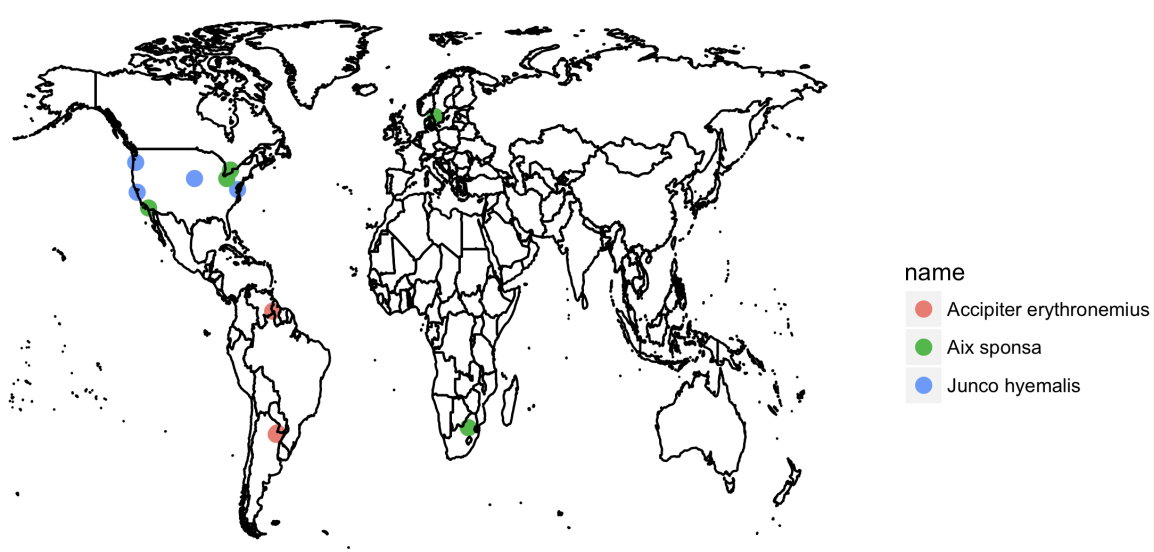
Occurrence data

- rgbif - GBIF
- rbison - USGS's BISON
- rvertnet - VertNet
- rebird - eBird (see also auk)
- spocc - one stop shop (of all above)
- finch - parse GBIF bulk data
  - EML - read and create EML
- ridigbio ALA4R robis *

GBIF data - rgbif

```
library(rgbif)
spp <- c('Accipiter erythronemius', 'Junco hyemalis', 'Aix sponsa')
keys <- unname(vapply(spp, function(x) name_backbone(name=x)$speciesKey, 1))
dat <- occ_search(taxonKey=keys, limit=5, hasCoordinate=TRUE)


library(mapr)
map_ggplot(dat)
```



GBIF p.s.

we also maintain GBIF clients in Python and Ruby

one stop shop for occurrence data - spocc

```
library('spocc')
gbifopts <- list(country = 'US')
idigbioopts <- list(fields = "scientificname")

out <- occ(query = 'Setophaga caerulescens',
    from = c('gbif','bison','inat','idigbio'), limit = 50,
    gbifopts = gbifopts, idigbioopts = idigbioopts)
dat <- occ2df(out)
head(dat); tail(dat)
#>  name                    longitude  latitude  prov  date       key
#> 1 Setophaga caerulescens -80.347459 25.743763 gbif  2018-01-20 1806338790
#> 2 Setophaga caerulescens -80.342233 25.77536  gbif  2018-01-19 1805421161
#> 3 Setophaga caerulescens -81.355815 28.569623 gbif  2018-03-14 1837766480
```

Standard interface to varied user inputs to the same things

- Pagination: `limit`, `start`, `page`
- Spatial search: `geometry`
- Records w/ coordinates: `has_coords`

future work / hard problems

taxonomy tools: in the works

- taxonomic name parsing: *fast & platform independent for other R tool builders* & tools for R users (see `pegax` poster)
- package taxa: needs more user testing - feedback plz!
- package taxadc: serialize R taxonomic data to Darwin Core- in early development
- package taxizedb - hard to a) make similar interface to SQL DB's as web services & 2) simplify varied database installs
- package taxview - summarise and visualize data sets from with respect to taxonomy

Summarise/visualize data sets by taxonomy - taxview

```
library('taxview')
x <- system.file("examples/plant_spp.csv", package = "taxview")
```

prepare data: clean, etc.

```
(dat <- tibble::as_tibble(
     data.table::fread(x, stringsAsFactors = FALSE,
       data.table = FALSE)))
       are> dat
#>  # A tibble: 130 x 2
#>    name                      id
#>    <chr>                  <int>
#>  1 Dianthus engleri       1531994
#>  2 Anacolosa frutescens   1618138
#>  3 Hymenophyllum plicatum  638568

(dat_clean <- tv_clean_ids(x, ids = dat$id, db = "ncbi"))
#>    name               rank         id     query
#>    <chr>              <chr>        <chr>  <chr>
#>  1 cellular organisms no rank      131567 1531994
#>  2 Eukaryota          superkingdom 2759   1531994
#>  3 Viridiplantae      kingdom      33090  1531994
```

Summarise/visualize data sets by taxonomy - taxview

```
(sumdat <- tv_summarise(dat_clean))
```

```
#> <tv_summary>
#>  no. taxa: 129
#>  by rank: N (21)

#>  by rank name: N (594)
#>  within ranks: N (20)
```

```
sumdat$by_within_rank
#> $superkingdom
#> name      count percent
#> 1 Eukaryota   127      98
#> 2 Bacteria      2       2
sumdat$by_within_rank$subphylum
#>    name           count percent
#> 1 Streptophytina   119      96
#> 2 Craniata           2       2
#> 3 Hexapoda           2       2
#> 4 Chelicerata        1       1
```

Summarise/visualize data sets by taxonomy

coming ...

occurrence tools: in the works

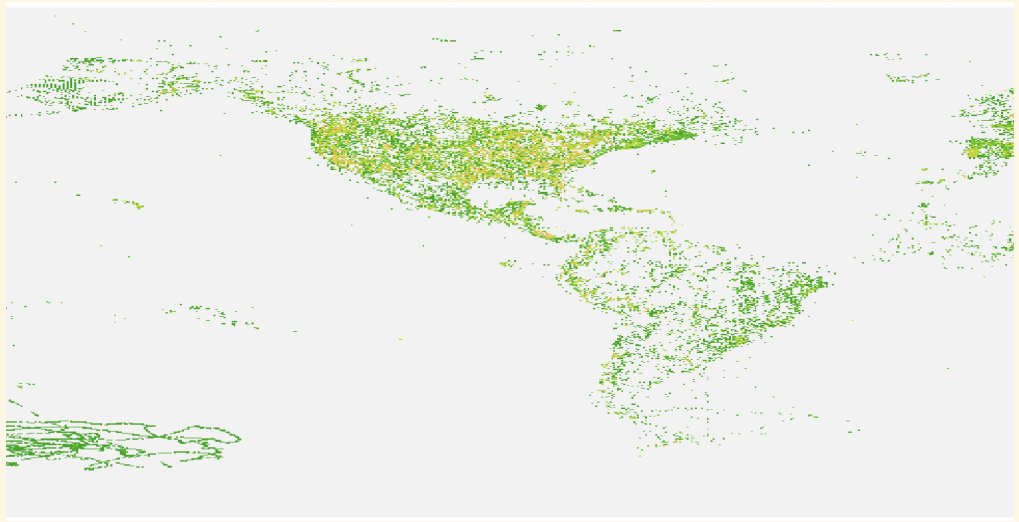
- taking the pain out of GBIF downloads: ropensci/rgbif#266: queuing tool for GBIF downloads - *hard problem*
- occurrence cleaning in R: *hard problem!* A few efforts:
  - package scrubr
  - package CoordinateCleaner
  - deduplication badly needed: aggregation up the data provider ladder

occurrence tools: questions

- DOIs for GBIF search service (and other services)?
- related to above: Sharing dataset associated with paper
- Visualzing huge occurrence datasets? (GBIF map API now in dev ver of `rgbif`)

GBIF map service (rasters) ~ static

```
library(rgbif) # development version remotes::install_github("ropensci/rgbif")
library(raster)
x <- map_fetch(search = "taxonKey", id = 3118771, year = 2010)
plot(x)
```



Perhaps scientists can use these rasters for analysis?

GBIF map service (rasters) ~ interactive

```
library(leaflet)
pal <- colorNumeric(c("#0C2C84", "#41B6C4", "#FFFFCC"), values(x), na.color = "tr
leaflet() %>%
    addTiles() %>%
    addRasterImage(x, colors = pal, opacity = 0.8) %>%
    addLegend(pal = pal, values = values(x),
        title = "Occurrences")
```

Hopefully use GBIF's Map Vector Tile (MVT) soon

talk to us 📣

what would you like to see?

discussion forum: discuss.ropensci.org

submit a package/review a package:
github.com/ropensci/onboarding

scotttalks.info/bocc

Made w/: reveal.js v3.2.0

Some Styling: Bootstrap v3.3.5

Icons by: FontAwesome v5.0.13