

# taxize: taxonomic search and retrieval in R

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## Summary

**Taxize** is a R package that provides an interface to various taxonomic data sources around the web. Data cleaning steps, like fixing taxonomic names, aggregating data to a specific taxonomic level or matching tables with different taxonomic resolution are crucial steps before a statistical analysis. The functionality of taxize simplifies these steps and eases handling of taxonomic data in R.

## Data Sources

Taxize currently provides simple and programmatic access to taxonomic data from 14 data sources around the web.

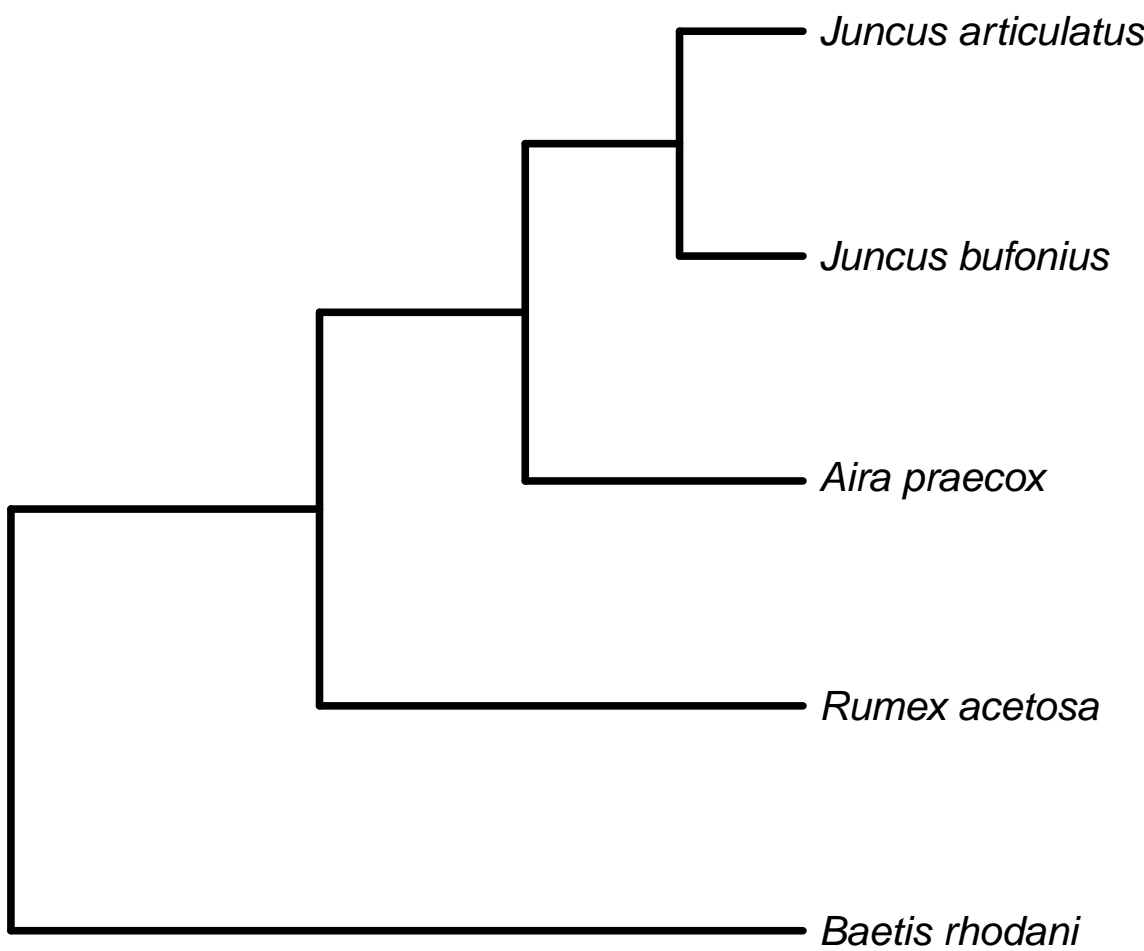


## Features (cont.)

### Building taxonomic trees

Using this taxonomic information we can build taxonomic trees. The can be used a surrogates when phylogenetic data is scarce.

```
species <- c("Juncus bufonius", "Juncus articulatus",
             "Aira praecox", "Rumex acetosa", "Baetis rhodani")
hier <- classification(species, db = 'ncbi')
plot(class2tree(hier))
```



### Aggregate data to a specific taxonomic rank

Using the taxonomic information taxa can be easily aggregated to different levels, e.g. to study effects on different taxonomic levels. This is provided via the `tax_agg()` function:

```
tax_agg(dune, rank = 'family', db = 'ncbi')
```

### Match tables with different taxonomic resolution

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```
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```

## Features

### Resolve taxonomic names

We often have a list of species names and we want to know  
a) if we have the most up-to-date names,  
b) if our names are spelled correctly,  
c) and the scientific name for a common name.  
Taxize provides an interface to the EOL Global Names Resolver and Taxonomic Name Resolution Service, e.g.

```
gnr_resolve('Baetis roodani')
##      submitted_name  matched_name
## 1 Baetis roodani Baetis rhodani
```

### Retrieve higher taxonomic names

Another common task is to retrieve the complete taxonomic hierarchy for a taxon:

```
classification('Baetis rhodani', db = 'col')
##      name      rank
## 1 Animalia Kingdom
## 2 Arthropoda Phylum
## 3 Insecta Class
## 4 Ephemeroptera Order
## 5 Baetoidea Superfamily
## 6 Baetidae Family
## 7 Baetis Genus
## 8 Baetis rhodani Species
```

### Retrieve children taxa

One can also search in the opposite direction, i.e. search species within a genus:

```
downstream('Baetis', db = 'col', downto = 'Species')
##      childtaxa_name childtaxa_rank
## 1 Baetis acceptus Species
## 2 Baetis aculeatus Species
## 3 Baetis acuminatus Species
## 4 Baetis adonis Species
## 5 Baetis aeneus Species
```

## Under the hood

taxize grabs data from the internet, formats and returns it to the user. This would not have been possible without the work of others:

### Calling Servers

httr and RCurl

### Parsing

XML and RJSONIO

### Data manipulation

stringr, plyr, reshape2 and vegan

And, of course, base-R ;)

## Get involved!

taxize is currently developed collaboratively on GitHub. Feature requests, bug reports and contributions are strongly encouraged!



<https://github.com/ropensci/taxize>

