

APPENDIX C. INSTALLATION OF THE DEVELOPMENT VERSION OF TAXIZE AND API KEYS

Installing and using the development version of taxize

Stable versions of taxize are available on the Comprehensive R Archive Network (CRAN) by the following process

```
install.packages("taxize")
library(taxize)
```

Development versions of taxize are available at Github at this link https://github.com/ropensci/taxize_, where the codebase is actively developed. This is also a good place to report bugs, submit feature requests, etc. on the Issues page https://github.com/ropensci/taxize_/issues?state=open.

The process of installing is a little bit more involved than from CRAN, but still quite easy using the package devtools <http://cran.r-project.org/web/packages/devtools/index.html>. You need to install development tools if you haven't already:

- On Windows, download and install Rtools: <http://cran.r-project.org/bin/windows/Rtools/>. This is not an R package.
- On Mac, make sure you have either XCode (free, available in the app store) or the "Command Line Tools for Xcode" (needs a free apple id, available from <http://developer.apple.com/downloads>)
- On Linux, make sure you've installed not only R, but the R development devtools. This a linux package called something like r-base-dev.

You can check you have everything installed and working by running this code:

```
library(devtools)
has_devel()
```

Once that is taken care of, install taxize from Github.

```
install_github("taxize_", "ropensci")
```

Then load taxize into R.

```
library(taxize)
```

See an introduction to devtools here <http://adv-r.had.co.nz/Philosophy.html>.

API keys

Some of the data sources we provide access to in taxize require authentication through API (Application Programming Interface) keys. Navigate to your *.Rprofile* file, which should be

```
open .Rprofile
```

Then write in your API key to that file and save. Let's say we are writing a key for uBio. Put an entry in your *.Rprofile* file with a key of *uBioApi* and a value of your API key in quotes. You'll also need to restart R after you save your *.Rprofile* file.

```
# uBio API key
options(uBioApi = "youralphanumerickey")
```

When you use the taxize package, the function *ubio_namebank()* will look for that key and use it in the API call. If the key is not found in your *.Rprofile* file the function will fail and tell you the key could not be found.

Alternatively, you can pass in the key in the function call like *ubio_namebank(searchName = 'elephant', sci = 1, vern = 0, keyCode=yourapikey)*

Functions in taxize that require API keys look for key values like *uBioApi* in your *.Rprofile* file. Therefore, unless you are passing your API key in the function call, save your keys in your *.Rprofile* file with the following key names (and their associated function names):

- *uBio*: ubio_namebank
- *EOLApi*: eol_dataobjects, eol_hierarchy, eol_pages, eol_ping, eol_search
- *tropicoskey*: tp_acceptednames, tp_namedistributions, tp_namereferences, tp_summary, tp_synonyms
- *pmkey*: plantminer