

```

library(devtools)
devtools::load_all("../")

## Loading rmangal
## Loading required namespace: rjson
## Loading required namespace: plyr
## Loading required namespace: igraph
## Loading required package: rjson
## Loading required package: httr
## Loading required package: plyr
## Loading required package: igraph

devtools::document()

## Loading required package: roxygen2

## Error: No description at
## /home/tpoisot/Projects/Code/rmangal/vignettes/DESCRIPTION

# library(rmangal)

```

## rmangal - R access to hosted MANGAL API

The `mangal` project is a [data specification](#) and [API][api], designed to facilitate the retrieval, archival, and re-use of data on ecological interactions.

### An overview of the mangal format

%%TODO the replicated-web paradigm  
 %%TODO general statement about the philosophy

### Informations about interactions

### Informations about network nodes

### Getting to know the API

The only information needed to start working is the URL of the database you want to interact with. By default, `rmangal` will connect you to the main database (at the *Université du Québec à Rimouski*) - you can access the [website](#) to know more.

```
netdb <- mangalapi()
```

The `netdb` object is used by all other functions to know where to connect to do a particular operation. We can see the list of methods that are available to work with:

```
names(netdb)
```

```
## [1] "base"          "trail"          "dataset"        "interaction"    "network"
## [6] "population"    "taxa"
```

As an user, you won't have to use this information yourself, but it's important for the `rmangal` package to know which URL to use to retrieve information. The first thing one might want to do, is get a list of all datasets available, and print their name:

```
all_datasets <- listDataset(netdb)
```

```
## 1 object(s) found
```

```
lapply(all_datasets, function(x) x$name)
```

```
##                                     1
## "North-American terrestrial metawebs"
```

In other situations, you may know the `id` of the dataset you want to work with. You can use the `getDataset` function to access it directly, see its name, and how many networks are in it.

```
first_dataset <- getDataset(netdb, 1)
first_dataset$name
```

```
## [1] "North-American terrestrial metawebs"
```

```
length(first_dataset$networks)
```

```
## [1] 1
```

All functions to access information within `rmangal` follow the same naming convention: `get*` will retrieve a *single* object identified by its `id`, and `list*` will retrieve a list of *all* objects of this type. The type of object to retrieve is the *singular* of the object name with its first letter capitalized (*e.g.* networks are `*Network`, taxa are `*Taxa`, ...).

## My first network

In this section, we'll reconstruct a network and plot it using `igraph`.

```
plot(network_as_graph(netdb, 1))
```

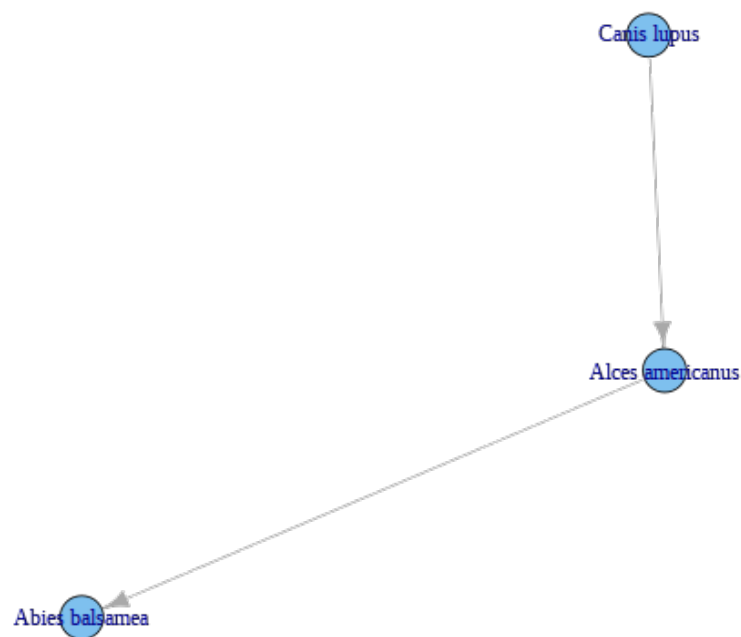


Figure 1: plot of chunk iPlot

Done!

The `network_as_graph` function