

mangal – making complex ecological network analysis simpler

T. Poisot, D. Gravel

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1 The study of ecological networks is severely limited by (i) the difficulty to access
2 data, (ii) the lack of a standardized way to link meta-data with interactions, and (iii)
3 the disparity of formats in which ecological networks themselves are represented.
4 To overcome these limitations, we conceived a data specification for ecological net-
5 works. We implemented a database respecting this standard, and released a R
6 package (`rmangal`) allowing users to programmatically access, curate, and deposit
7 data on ecological interactions. In this article, we show how these tools, in conjunc-
8 tions with other frameworks for the programmatic manipulation of open ecological
9 data, will streamline the analysis process, and improve reproducibility in studies
10 of ecological networks.

11 `## Error: impossible de trouver la fonction "as"`

12 Introduction

13 Ecological networks enable ecologists to accommodate the complexity of natural communi-
14 ties, and to discover mechanisms contributing to their persistence, stability, resilience, and
15 functioning. Most of the “early” studies of ecological networks were focused on understand-
16 ing how the structure of interactions within one location affected the ecological properties

1 of this local community. This led to classical results, such as the buffering impact of mod-
2 ularity on species loss Stouffer & Bascompte (2011), the increase in robustness along with
3 increases in connectance Dunne et al. (2002), and {add_example}. More recently, new studies
4 introduced the idea that different networks can be meaningfully compared, either to under-
5 stand the importance of environmental gradients on the realisation of ecological interactions
6 [atylanakis_habitat_2007], or to understand the mechanisms behind variation in the structure
7 of ecological networks (Poisot *et al.* 2012). Yet, meta-analyses of a large number of ecologi-
8 cal networks are still extremely rare, and most of the studies comparing several networks do
9 so within the limit of particular systems (Schleuning *et al.* 2011; Dalsgaard *et al.* 2013). In
10 part, this can be attributed to the limited methods allowing to compare networks in which
11 no species are in common. However, the severe shortage of data in the field also restricts
12 the power of large-scale analyses. Indeed, most of the studies working on several types of
13 interactions focused on comparing emerging properties (Thebault & Fontaine 2008).

14 An increasing number of approaches are being put forth to *predict* the structure of ecological
15 networks, either relying on latent variables (Rohr *et al.* 2010) or actual traits (Gravel *et al.* 2013).
16 These approaches, so as to be adequately calibrated, require easily accessible data. Comparing
17 the efficiency of different methods will also be facilitated if there is an homogeneous way of
18 representing ecological interactions, and the associated metadata. In this paper, we (i) estab-
19 lish the need of a data specification serving as a *lingua franca* among network ecologists, (ii)
20 describe this data specification. Finally, we (iii) describe `rmanga1`, a R package and `compagnon`
21 database, relying on this data specification. We provide some use cases showing how this
22 new approach makes complex analyzes simpler, and allows for the integration of new tools to
23 manipulate biodiversity resources.

24 **Networks need a data specification**

25 Ecological networks are (often) stored as their *adjacency matrix* (or as the quantitative link
26 matrix), that is a series of 0 and 1 indicating, respectively, the absence and presence of an

1 interaction. This format is extremely convenient for *use* (as most network analysis packages,
2 *e.g.* *bipartite*, *betalink*, *foodweb*, require data to be presented this way), but is extremely
3 inefficient at *storing* meta-data. In most cases, an adjacency matrix will inform on the identity
4 of species (in cases where rows and columns headers are present), and the presence or absence
5 of interactions. If other data about the environment (*e.g.* where the network was sampled) or
6 the species (*e.g.* the population size, trait distribution, or other observations) are available,
7 they are most either given in other files, or as accompanying text. In both cases, making
8 a programmatic link between interaction data and relevant meta-data is difficult and error-
9 prone.

10 By contrast, a data specification provides a common language for network ecologists to inter-
11 act, and ensure that, regardless of their source, data can be used in a shared workflow. Most
12 importantly, a data specification describes how data are *exchanged*. Each group retains the abil-
13 ity to store the data in the format that is most convenient for in-house use, and only needs to
14 provide export options (*e.g.* through an API) respecting the data specification. This approach
15 ensures that *all* data can be used in meta-analyses, and will in time increase the impact of data.

16 Elements of the data specification

17 The data specification (Fig. XX) is built around the idea that (ecological) networks are col-
18 lections of relationships between ecological objects, each element having particular meta-data
19 associated. In this section, we detail highlight the way networks are represented in the *mangal*
20 specification. An interactive webpage with the elements of the data specification can be found
21 online at <http://mangal.uqar.ca./doc/spec/>. The data specification is available either at the
22 API root (*e.g.* <http://mangal.uqar.ca/api/v1/?format=json>), or can be viewed using the
23 *whatIs* function from the R package (see *Supp. Mat. 1*). Rather than giving an exhaustive list
24 of the data specification (which is available online at the aforementioned URL), this section
25 will propose an overview of each element, and of how they interact.

26 We propose JSON as the most efficient data format for the following reasons. First, it has

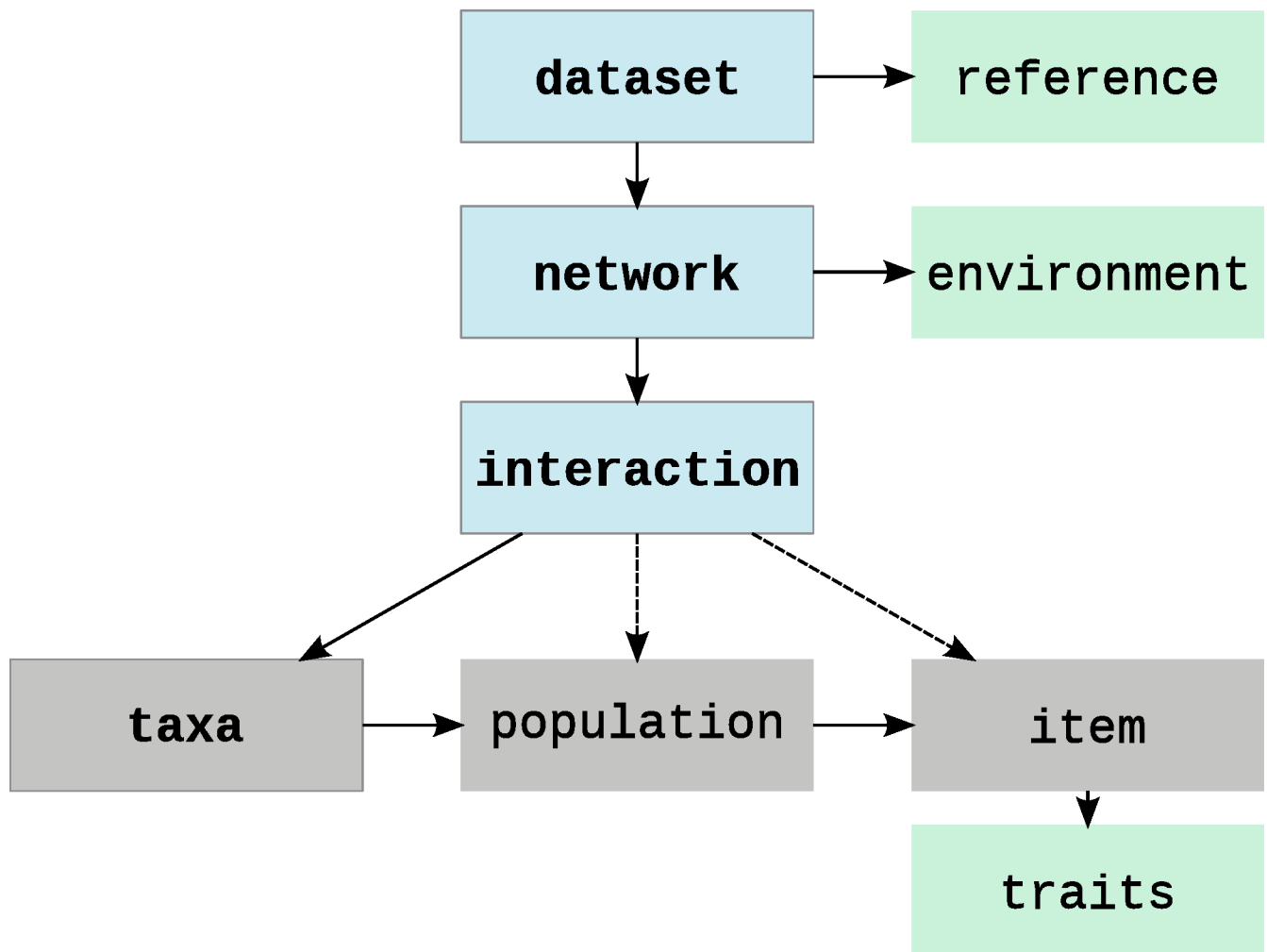


Figure 1: An overview of the data specification, and the hierarchy between objects. Each box correspond to a level of the data specification. Grey boxes are nodes, blue boxes are interactions and networks, and green boxes are metadata. The **bold** boxes (dataset, network, interaction, taxa) are the minimal elements needed to represent a network.

1 emerged as a *de facto* standard for web platform serving data, and accepting data from users.
2 Second, it allows *validation* of the data: a JSON file can be matched against a scheme, and one
3 can verify that it is correctly formatted. Finally, JSON objects are easily and cheaply (memory-
4 wise) parsed in the most common programming languages, notably R (equivalent to `list`)
5 and python (equivalent to `dict`). For most users, the format in which data are transmitted will
6 be entirely transparent, as the interaction will happen within R – as such, knowing how JSON
7 objects are organised is only useful for those who want to interact with the API directly.

8 **Node informations**

9 **Taxa**

10 Taxa are a taxonomic entity of any level, identified by their name, vernacular name, and
11 their identifiers in a variety of taxonomic services. Associating the identifiers of each taxa is
12 important to leverage the power of the new generation of open data tools, such as `taxize`
13 [`@chamberlain_taxize:2013`]. The data specification currently accomodates `ncbi`, `gbif`, `itis`,
14 `eol` and `bold` identifiers.

15 **Population**

16 A population is one observed instance of a taxa object. If your experimental design is repli-
17 cated through space, then each taxa will have a population object corresponding to each
18 locality. Populations do not have associated meta-data, but serve as “containers” for item
19 objects.

20 **Item**

21 An item is an instance of a population. Items have a `level` argument, which can be either
22 `individual` or `population`; this allows to represent both individual-level networks (*i.e.* there
23 are as many items attached to a population than there were individuals of this population

1 sampled), and population-level networks. When `item` represents a population, it is possible
2 to give a measure of the size of this population. The notion of `item` is particularly useful
3 for time-replicated designs: each observation of a population at a time-point is an `item` with
4 associated `trait` values, and possibly population size.

5 **Network informations**

6 **Interaction**

7 An interaction links, *a minima*, two `taxa` objects (but can also link pairs of populations or
8 `items`). The most important attributes of interactions are the type of interaction (of which
9 we provide a list of possible values, see *Supp. Mat. 1*), and its nature, *i.e.* how it was observed.
10 This field will help differentiate from direct observations, text mining, and inference. Note
11 that the nature field can also take absence as a value; this will be useful for, *e.g.*, “cafeteria”
12 experiments in which there is high confidence that the interaction did not happen.

13 **Network**

14 A network is a series of interaction object, along with (i) informations on its spatial posi-
15 tion (provided at the latitude and longitude), (ii) the date of sampling, and (iii) references to
16 measures of environmental conditions.

17 **Dataset**

18 A dataset is a collection of one or several `network`(s). Datasets also have a field for data
19 and papers, both of which are references to bibliographic or web resources describing, respec-
20 tively, the source of the data, and the papers in which these data have been significantly used.
21 Datasets are the preferred entry point in the resources.

1 **Meta-data**

2 **Trait value**

3 Objects of type `item` can have associated `trait` values. These consist in the description of the
4 trait being measured, the value, and the units in which the measure was taken.

5 **Environmental condition**

6 Environmental conditions are associated to `network`. These are defined by the environmental
7 property measured, its value, and the units.

8 **References**

9 References are associated to datasets. They accomodate the DOI, JSON or PubMed identifiers,
10 or a URL. When possible, the DOI should be preferred as it offers more potential to interact
11 with other on-line tools, such as the *CrossRef* API.

12 **Use cases**

13 In this section, we present use cases using the `rmangal` package for R, to interact with a
14 database implementing this data specification, and serving data through a RESTful API (<http://mangal.uqar.ca>).
15 It is possible for users to deposit data into this database, through the R package. Data are made
16 available under a *CC-0 Waiver*. Detailed informations about how to upload data are given in
17 the vignettes and manual of the `rmangal` package. So as to save room in the manuscript,
18 we source each example. The complete `r` files to reproduce the examples of this section are
19 attached as *Suppl. Mat.*.

20 The data we use for this example come from Ricciardi et al. (2010). These were previously
21 available on the *InteractionWeb DataBase* as a single `xls` file. We uploaded them in the `mangal`
22 database at <http://mangal.uqar.ca/api/v1/dataset/{todo}>.

1 **Link-species relationships**

2 In the first example, we visualize the relationship between the number of species and the
3 number of interactions, which Martinez (1992) propose to be linear (in food webs).

```
source("usecases/1_ls.r")
```

4 Producing this figure requires less than 10 lines of code. The only information needed is the
5 identifier of the network or dataset, which we suggest should be reported in publications as:
6 “These data were deposited in the mangal format at <URL>/api/v1/dataset/<ID>”. This will
7 encourage re-use of the data.

8 **Network beta-diversity**

9 In the second example, we use the framework of network β -diversity (Poisot *et al.* 2012) to
10 measure the extent to which networks that are far apart in space have different interactions.
11 Each network in the dataset has a latitude and longitude, meaning that it is possible to measure
12 the geographic distance between two networks.

13 For each pair of network, we measure the geographic distance (in km.), the species dissimilar-
14 ity (β_S), the network dissimilarity when all species are present (β_{WN}), and finally, the network
15 dissimilarity when only shared species are considered (β_{OS}).

```
source("usecases/2_beta.r")
```

16 As shown in Fig. XX, while species dissimilarity and overall network dissimilarity increase
17 when two networks are far apart, this is not the case for the way common species interact.
18 This suggests that in this system, network dissimilarity over space is primarily driven by
19 species turnover. The ease to gather both raw interaction data and associated meta-data make
20 producing this analysis extremely straightforward.

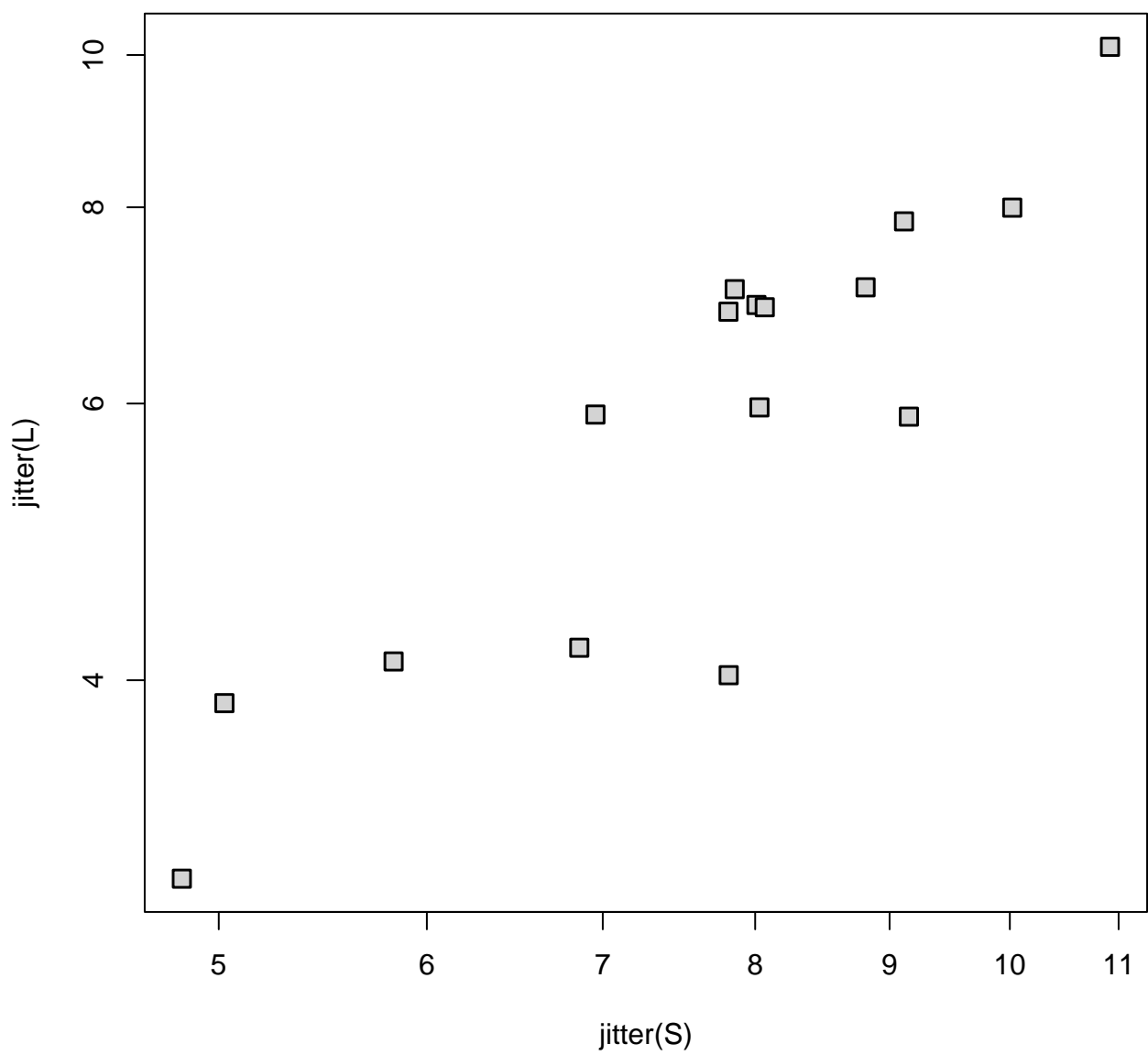


Figure 2: Relationship between the number of species and number of interactions in the anemonefish-fish dataset.

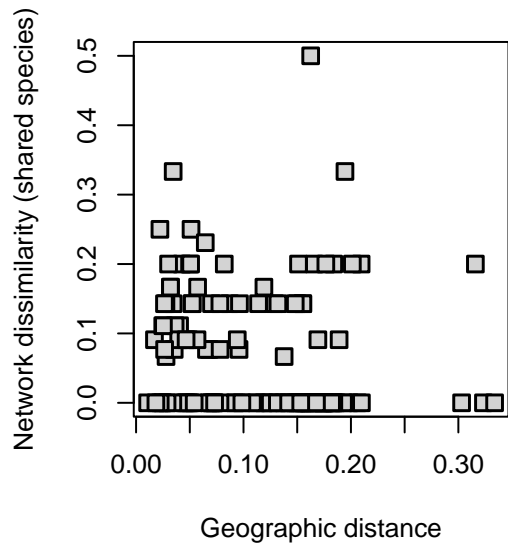
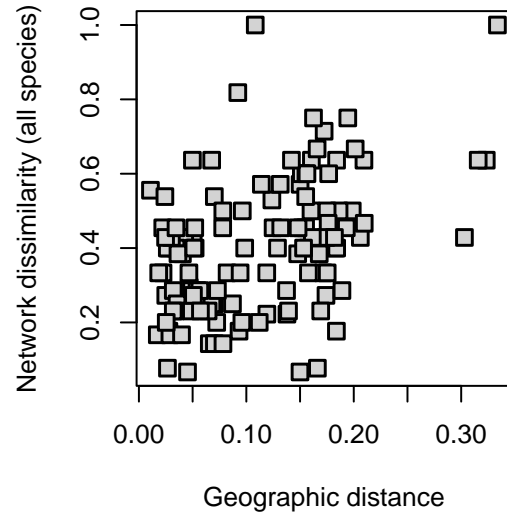
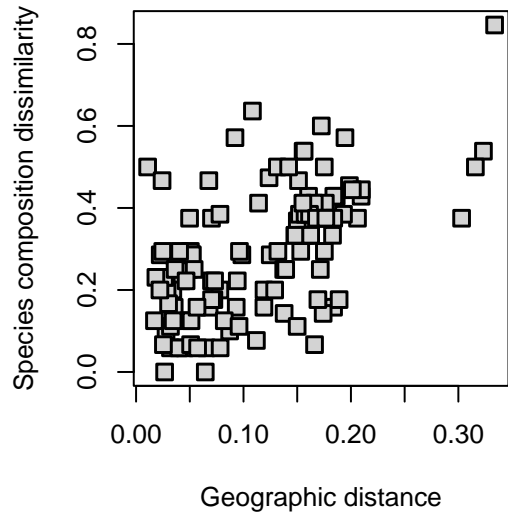


Figure 3: Relationships between the geographic distance between two sites, and the species dissimilarity, network dissimilarity with all, and only shared, species.

1 Spatial visualisation of networks

2 Bascompte (2009) proposes an interesting visualisation for spatialized networks, in which each
3 species is laid out on a map at the center of mass of its area of occurrence; interactions are then
4 drawn between species, to show how species distribution determines biotic interactions. In
5 this final use case, we propose to reproduce a similar figure, using the RgoogleMaps package.

```
source("usecases/3_spatial.r")
```

6 Conclusions

7 In this contribution, we presented mangal, a data format for the exchange of ecological net-
8 works and associated meta-data. We deployed an online database with an associated API,
9 relying on this data specification. Finally, we introduced rmangal, a R package designed to
10 interact with APIs using the mangal format.

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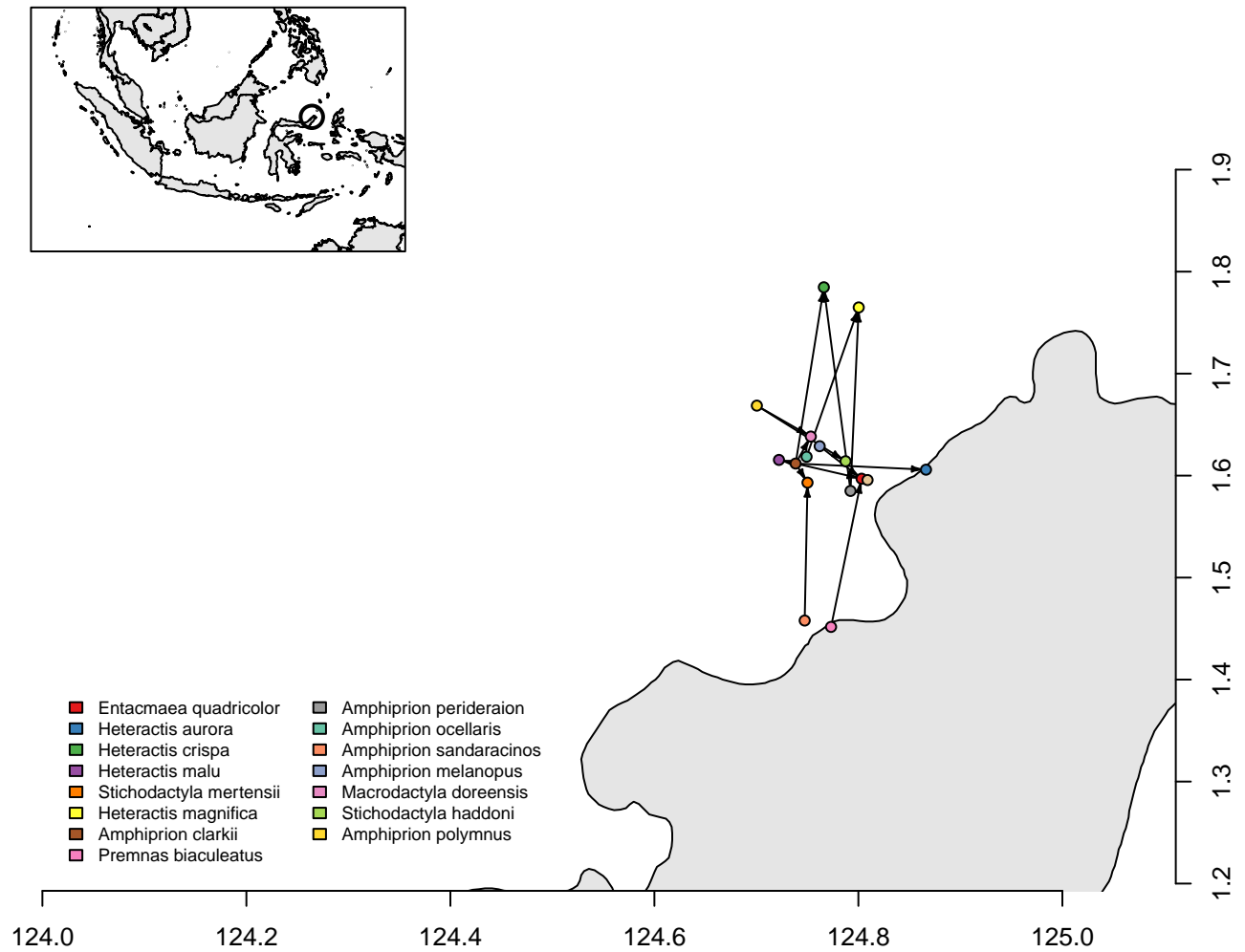


Figure 4: Spatial plot of a network, using the RgoogleMaps and rmangal packages.

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