Analysis of Multiplex Social Networks with R

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Abstract

Multiplex social networks are characterized by a common set of actors connected through multiple types of relations. The multinet package provides a set of R functions to analyze multiplex social networks within the more general framework of multilayer networks, where each type of relation is represented as a layer in the network. The package contains functions to import/export, create and manipulate multilayer networks, implementations of several state-of-the-art multiplex network analysis algorithms, e.g., for centrality measures, layer comparison, community detection and visualization. Internally, the package is mainly written in native C++ and integrated with R using the Rcpp (Eddelbuettel and François 2011) library.

Keywords: networks, multiplex, multilayer, social network analysis, R.

1. Introduction and background

Multiplex social networks are characterized by a common set of actors connected through multiple types of relations. In this article we introduce multinet, an R package to analyze multiplex social networks represented within the more general framework of multilayer networks.

In the multilayer framework, each relation type is represented as a layer, so that for example a layer can be used to store friendship ties while another layer contains working ties among the same set of actors. Such a network can be used to study the relationships between these two types of social ties, for example counting how often colleagues are also friends, and also to study the relationships between actors and types of relations, for example whether a specific actor tends to befriend all her co-workers or to keep these two social contexts separated.

Several packages for network analysis are available in R. Notable examples are statnet (Handcock, Hunter, Butts, Goodreau, and Morris 2003), containing a collection of packages such as
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sna (Butts 2016), network (Butts 2015, 2008) and ergm (Hunter, Handcock, Butts, Goodreau, and Morris 2008), igraph (Csardi and Nepusz 2006) and RSiena (Ripley, Snijders, Bóda, Vörös, and Preciado 2018). Multinet complements this collection with several functions to analyze multiplex networks. In particular, the package provides functions focusing on the multilayer structure of the networks, for example to find how relevant some layers are for an actor or to discover communities spanning multiple layers. Individual layers of a multiplex network, each corresponding to a simple network, can instead be analyzed using the above-mentioned packages, and in particular multinet contains functions to translate the layers into igraph objects. The methods provided by multinet are distinct from the ones provided by multiplex (Ostoic 2018).

Throughout this work we will follow the terminology described in (Dickison, Magnani, and Rossi 2016). In particular, we will use the term “multilayer social network” to indicate a network where vertices ($V$) are organized into multiple layers ($L$) and each vertex corresponds to an actor ($A$), where the same actor can be mapped to vertices in different layers. More formally, a multilayer social network as implemented in this package is a graph $G = (V, E)$ where $V \subset A \times L$. This model, when used to describe multiplex networks, is a simplified version of (Magnani and Rossi 2011), where the same actor can correspond to multiple vertices in the same layer, and (Kivelä, Arenas, Barthelemy, Gleeson, Moreno, and Porter 2014), where layers can be identified by an array of features called aspects (for example, each layer may correspond to both a type of social relationship and a time).

Using multiple layers we can represent both edges among vertices in the same layer, called intra-layer edges, and edges among vertices in different layers, called inter-layer edges. To simplify the notation, both types of edges are defined in the package by a quadruple containing two actor names $i, j \in A$ and two layer names $l_i, l_j \in L$, where $(i, l_i)$ and $(j, l_j)$ represent the two ends of the edge. Intra-layer edges are characterized by having the same layer $l_i = l_j$ at the two ends, and in this article we mostly focus on multiplex networks, where only intra-layer edges exist.

2. The Rcpp_RMLNetwork class

The multinet package defines a class to represent multilayer networks (Rcpp_RMLNetwork). Objects of this type are used as input or returned as output by most functions provided by the package.

Internally, all the objects constituting the network are stored in sets with logarithmic lookup and random access time, implemented as skip lists. This solution is (linearly) less efficient than using a set in the C++ standard library, but supports quick random access to the objects in the set, which is important when synthetic networks are generated. For efficiency reasons, most of the functions in the package are written in native C++ and integrated with R using the Rcpp (Eddelbuettel and François 2011) library. Storage requirements for the network class are on the order of the number of vertices plus the total number of edges (inter-layer and intra-layer).

The ml_empty() function returns an empty multilayer network, not containing any actor, layer, vertex or edge\(^1\). The function accepts an optional character argument name, indicating

\(^1\)Other ways to create networks, explained later, are the function read_ml() to load networks from files and the grow_ml() function to produce synthetic networks.
the name of the network.

R> ml_empty()

Multilayer Network [0 actors, 0 layers, 0 vertices, 0 edges (0,0)]

For convenience, the call to any of the network’s constructors and readers returns an \texttt{S4} object compatible with the \texttt{R} \texttt{print} function. Otherwise, all the other functions’ return types are, by design, either (i) a named list of elements (if the data is not relational) or (ii) a data frame.

2.1. Adding, retrieving and deleting network objects

Objects in a \texttt{Rcpp_RMLNetwork} object can be queried using a set of utility functions. Built-in functions for retrieving and updating objects have the same signature name: \texttt{<op>_<objects>_ml}, where \texttt{<objects>} can be \texttt{actors}, \texttt{layers}, \texttt{vertices} or \texttt{edges}, and \texttt{<op>} is either blank, if we want to list the objects, or is the name of a specific operation: \texttt{num}, to compute the number of objects of the requested type, \texttt{add} or \texttt{delete}. If the number of actors is requested without specifying any layer, the total number of actors is returned, including those not present in any layer.

All the aforementioned functions require an \texttt{Rcpp_RMLNetwork} object as first argument. Listing functions operating on actors and vertices also require an array of layer names: only the actors/vertices in the input layers are returned. If the array is empty, all the actors/vertices in the network are returned. Listing functions operating on edges, instead, require two parameters: one indicating the layer(s) from where the edges to be extracted start, and a second one with the layer(s) where the edges to be extracted end. If an empty list of starting layers is passed (default), all the layers are considered, while if an empty list of ending layers is passed (default), the ending layers are set as equal to those in the first parameter.

Now we can show a small example of how these functions work together. We start by creating an empty network with two layers, named UL (upper layer) and BL (bottom layer), respectively.

R> net <- ml_empty()
R> add_layers_ml(net, c("UL", "BL"))
R> layers_ml(net)

[1] "BL" "UL"

New layers are by default undirected, that is, edges added to them are treated as undirected. Directed layers are created by setting the \texttt{directed} parameter to \texttt{TRUE}, or using the \texttt{set_directed_ml()} function, which is necessary if we want to set directed intralayer edges.

This function takes an \texttt{Rcpp_RMLNetwork} object and a \texttt{directionality} data frame as input. The next fragment of code changes the directionality of the inter-layer edges between the bottom and upper layers.

R> dir <- data.frame(layer1="UL", layer2="BL", dir=1)
R> set_directed_ml(net, dir)
R> is_directed_ml(net)
Then, we create three actors $A = \{A_1, A_2, A_3\}$.

\[
R> \text{add_actors_ml(net, "A")}
R> \text{add_actors_ml(net, c("B", "C"))}
\]

We can check that the actors have been added correctly:

\[
R> \text{num_actors_ml(net)}
\]

[1] 3

\[
R> \text{actors_ml(net)}
\]

[1] "C" "A" "B"

The next step to populate a network is to add actors to layers, where a pair actor-layer defines a vertex. Notice that if we try to create the vertices without having added the corresponding actors, the function will raise an error.

\[
R> \text{vertices <- data.frame(}
+ \quad \text{actors = c("A", "B", "C", "A", "B", "C"),}
+ \quad \text{layers = c("UL", "UL", "UL", "BL", "BL", "BL")})
R> \text{vertices}
\]

actors layers
1  A  UL
2  B  UL
3  C  UL
4  A  BL
5  B  BL
6  C  BL

\[
R> \text{add_vertices_ml(net, vertices)}
R> \text{vertices_ml(net)}
\]

actor layer
1  C  BL
2  A  BL
3  B  BL
4  C  UL
5  A  UL
6  B  UL
From the previous command you can see how the objects in a network are stored into (mathematical) sets, that is, they are unordered: we cannot assume that actor A will always be listed before actor B, and we have to sort the results if we want to keep a specific order.

We can now add some intra-layer edges, in this case between all the vertices in the upper layer and between vertices A and C in the bottom one. In addition, we create inter-layer edges between vertices ((A,UL),(B,BL)) and ((A,UL),(C,BL)). We begin by creating two data frames, one for each type of edges:

```r
R> intra_layer_edges <- data.frame(
+   actors_from = c("A", "A", "B", "A"),
+   layers_from = c("UL", "UL", "UL", "BL"),
+   actors_to = c("B", "C", "C", "C"),
+   layers_to = c("UL", "UL", "UL", "BL"))
```

```r
R> intra_layer_edges
actors_from layers_from actors_to layers_to
1     A       UL       B       UL
2     A       UL       C       UL
3     B       UL       C       UL
4     A       BL       C       BL
```

```r
R> inter_layer_edges <- data.frame(
+   actors_from = c("A", "A"),
+   layers_from = c("UL", "UL"),
+   actors_to = c("B", "C"),
+   layers_to = c("BL", "BL"))
```

```r
R> inter_layer_edges
actors_from layers_from actors_to layers_to
1     A       UL       B       BL
2     A       UL       C       BL
```

Now we can add these edges to the network, and observe the result.

```r
R> add_edges_ml(net, intra_layer_edges)
R> add_edges_ml(net, inter_layer_edges)
R> edges_ml(net)
```

```r
from_actor from_layer to_actor to_layer dir
1     A       BL       C       BL     0
2     A       BL       B       UL     1
3     A       BL       C       UL     1
4     A       UL       B       UL     0
5     B       UL       C       UL     0
6     A       UL       C       UL     0
```

```r
R> edges_ml(net, layers1 = "BL")
```
from_actor from_layer to_actor to_layer dir
1   A     BL   C     BL   0

Notice that as we have only passed one argument (layers1 = "BL"), edges_ml() returns only the intra-layer edges in the BL layer.

2.2. Handling attributes

When we study a multilayer network, we can be interested in representing different types of actors, add some categorical attribute to vertices or use a numerical value to represent the strength of the ties. The multinet package provides a set of functions to create attributes and add and retrieve attribute values. attributes_ml() returns a data frame with two columns, the name of the attribute and its type. As most of the functions in the package, the function accepts a filtering parameter, target, to limit the query to specific types of objects: “actor” (attributes attached to actors), “vertex” (attributes attached to vertices) or “edge” (attributes attached to edges). All the functions handling attributes use target = "actor" by default.

R> attributes_ml(net)

[1] name type
<0 rows> (or 0-length row.names)

The list of attributes of a newly created network is empty. We can create attributes by calling the add_attributes_ml() function and passing an Rcpp_RMLNetwork object, names of the attributes, types of the attributes (“string” or “numeric”) and the target as parameters. For example, the following code creates two string attributes for actors (notice that "actors" is the default target, and "string" is the default attribute type):

R> add_attributes_ml(net, c("name", "surname"))
R> attributes_ml(net)

    name  type
1  name   string
2 surname string

Using the add_attributes_ml() function we can also specify different attributes for nodes and edges on individual layers, for which we must supply the layer parameter. If we want, instead, to manage inter-layer edges two parameters are needed, layer1 and layer2, so that the attribute only applies to inter-layer edges from the first layer to the second and vice-versa. The example below shows how to use these parameters in practice to create a string attribute for the vertices in the bottom layer.

R> add_attributes_ml(net, "username", type = "string", target = "vertex", + layer = "BL")
R> attributes_ml(net, target = "vertex")

    layer  name  type
1     BL username string
At this point the `get_values_ml()` and `set_values_ml()` functions can be used to set and retrieve attribute values.

```r
R> set_values_ml(net, "name", c("A", "B"), values = c("Alice", "Scrondo"))
R> get_values_ml(net, "name", c("A", "C"))

   value
1  Alice
2
```

3. Input, output and generation of RMLNetwork data

In the previous section we have introduced the `Rcpp_RMLNetwork` class and various methods to modify `Rcpp_RMLNetwork` objects. However, users would more often create `Rcpp_RMLNetwork` objects by reading them from a file, artificially generating them, or loading some of the datasets directly available in the package.

3.1. Importing and exporting data

The `multinet` package provides two input/output functions: `read_ml()` and `write_ml()`. Networks can be read from files using a package-specific text-based format, and written to file using the same format or the GraphML syntax\(^2\). The `multinet` format is not compatible with other packages, but it allows us to specify various details, such as the directionality of intra-layer edges and attributes, as in the following example:

```
#VERSION
2.0

#TYPE
multiplex

#LAYERS
research, UNDIRECTED
twitter, DIRECTED

#ACTOR ATTRIBUTES
affiliation,STRING

#VERTEX ATTRIBUTES
twitter, num_tweets, NUMERIC

#EDGE ATTRIBUTES
research, num_publications, NUMERIC
```

\(^2\)http://graphml.graphdrawing.org
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#ACTORS
Luca,ITU
Matteo,UU
Davide,UU

#VERTICES
Luca,twitter,53
Matteo,twitter,13

#EDGES
Luca,Matteo,research,9
Luca,Matteo,friendship

When we read this multiplex network we can also specify that we want all the actors to be present in all the layers, using the align parameter. The difference between the two obtained networks can be seen by checking the basic network statistics:

```R
R> net <- read_ml(file = "example_io.mpx")
R> net

Multilayer Network [3 actors, 2 layers, 4 vertices, 2 edges (2,0)]
```

```R
R> aligned_net <- read_ml("example_io.mpx", align = TRUE)
R> aligned_net

Multilayer Network [3 actors, 2 layers, 6 vertices, 2 edges (2,0)]
```

Both Rcpp_RMLNetwork objects, net and aligned_net, have two layers and three actors; but the align = TRUE parameter in the second call to the read_ml() adds a new vertex to each layer for every actor in the input file.

When no special information is needed, e.g., there are no attributes, no isolated nodes and all edges are undirected, the format becomes as simple as a list of layer-annotated edges:

Luca,Matteo,research
Davide,Matteo,research
Luca,Matteo,friendship

A multiplex network can also be created starting from igraph objects, where each graph represents a layer. For this to be possible, the vertices of the graphs must have a name attribute indicating the name of the corresponding actor.

For example, consider the following graphs:

```R
R> l1 <- read.graph("example_igraph1.dat", format = "ncol")
R> l1
```
igraph 838463a UN-- 3 3 --
+ attr: name (v/c)
+ edges from 838463a (vertex names):

R> l2 <- read.graph("example_igraph2.dat", format = "ncol")
R> l2
igraph ac5a772 UN-- 2 1 --
+ attr: name (v/c)
+ edge from ac5a772 (vertex names):
[1] A--C

They can be added as layers of a multiplex network as follows:

R> n <- ml_empty()
R> add_igraph_layer_ml(n, l1, "layer1")
R> add_igraph_layer_ml(n, l2, "layer2")
R> n
Multilayer Network [3 actors, 2 layers, 5 vertices, 4 edges (4,0)]

R> edges_ml(n)

<table>
<thead>
<tr>
<th>from_actor</th>
<th>from_layer</th>
<th>to_actor</th>
<th>to_layer</th>
<th>dir</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>layer1</td>
<td>B</td>
<td>layer1</td>
<td>0</td>
</tr>
<tr>
<td>A</td>
<td>layer1</td>
<td>C</td>
<td>layer1</td>
<td>0</td>
</tr>
<tr>
<td>B</td>
<td>layer1</td>
<td>C</td>
<td>layer1</td>
<td>0</td>
</tr>
<tr>
<td>A</td>
<td>layer2</td>
<td>C</td>
<td>layer2</td>
<td>0</td>
</tr>
</tbody>
</table>

3.2. Generation

The package provides basic functionality to generate synthetic multiplex networks, following the approach proposed by Magnani and Rossi (2013a). This problem is approached by allowing layers to evolve at different rates, based on internal or external dynamics. Internal dynamics can be modelled using existing network models (for example, preferential attachment), assuming that how the layer grows can be explained only looking at the layer itself. External dynamics involve importing edges from other layers. Within this perspective the intuition is that relations existing on a layer might naturally expand over time into other layers (e.g., co-workers starting to add each other as friends on Facebook). The package also allows different growing rates for different layers.

In the following example we create a multiplex network with 3 layers based on the Preferential Attachment (Barabási and Albert 1999) and the Erdos-Renyi models (Erdos and Rényi 1960). The first and last layers will only evolve according to their internal models (\texttt{pr.external} = 0), while the second will have a probability of .8 of evolving according to external dynamics, that is, importing edges from other layers (\texttt{pr.external} = .8). Note that all the probability...
vectors must have the same number of fields, one for each layer. By defining `pr.internal` and `pr.external`, we are also implicitly defining `pr.no.action` (1 minus the other probabilities, for each field/layer). In the example, the third layer grows at a lower speed than the others, having an (implicitly defined) `pr.no.action = .1`.

```r
R> models_mix <- c(evolution_pa_ml(3, 1), evolution_er_ml(100), + evolution_er_ml(100))
R> pr.internal <- c(1, .2, .9)
R> pr.external <- c(0, .8, 0)
```

The probability to import edges from the other layers in case external events happen is specified using a dependency matrix. The following matrix specifies that the second layer should import edges from the first layer with probability 1 if an external evolutionary event is triggered. It is expected that the values on each row of the matrix add to 1.

```r
R> dependency <- matrix(c(1, 1, 0, 0, 0, 0, 0, 0, 1), 3, 3)
R> dependency

     [,1] [,2] [,3]
[1,]  1  0  0
[2,]  1  0  0
[3,]  0  0  1
```

We can now generate the network, with 100 actors and 100 growing steps.

```r
R> ml_generated_mix <- grow_ml(100, 100, models_mix, pr.internal, pr.external, + dependency)
R> num_edges_ml(ml_generated_mix, layers1 = "l0")

[1] 84
R> num_edges_ml(ml_generated_mix, layers1 = "l1")

[1] 100
R> num_edges_ml(ml_generated_mix, layers1 = "l2")

[1] 56
```

### 3.3. Predefined data

Another way to obtain network data without having to manually construct it is to load some well-known networks already available inside the package. These are loaded using functions beginning with “ml”, followed by the name of the network, e.g., `ml_florentine()`.

In the remainder of the article we will use the AUCS network, included in the current version of the `multinet` package as an example dataset and often used in the literature to test new methods. The data, described by Dickison et al. (2016), were collected at a university research department and include five types of online and offline relations. The population consists of 61 employees, including professors, postdocs, PhD students and administrative staff.
R> net <- ml_aucs()
R> net

Multilayer Network [61 actors, 5 layers, 224 vertices, 620 edges (620,0)]

R> layers_ml(net)

[1] "facebook" "leisure" "coauthor" "lunch" "work"

4. Data exploration

Multinet provides a basic visualisation function. We can produce a default visualization just by executing \texttt{plot(net)}, but to make the plot more readable we shall add a few details. In particular: (1) we explicitly compute a layout that draws each layer independently of the others, as declared by setting interlayer weights (w\_inter) to 0, (2) we plot the layers on two rows, to better use the space on the page (grid), (3) we remove the labels from the vertices, to increase readability (vertex.labels = ""), and (4) we add a legend with the names of the layers. The multiforce layout, used for all graph visualizations in this article, is described in (Fatemi, Magnani, and Salehi 2018). The result of the following command is shown in Fig. 1.

R> l <- layout_multiforce_ml(net, w_inter = 0, gravity = 1)
R> bk <- par("mar")
R> par(mar=c(0,0,0,0))
R> plot(net, layout = l, grid = c(2, 3), vertex.labels = "",
+     legend.x = "bottomright", legend.inset = c(.05, .05))
R> par(mar=bk)

We can also use the attributes to inspect the relationship between the role of the actors and the topology of the network. We start by retrieving the role of each vertex (vertex\_roles), and a list of all the distinct roles.

R> attr_values <- get_values_ml(net, actors = vertices_ml(net)[[1]],
+   attribute = "role")
R> vertex\_roles <- as.factor(attr_values[[1]])
R> num\_distinct\_roles <- length(levels(vertex\_roles))
R> levels(vertex\_roles)

[1] "Admin" "Assistant" "Associate"
[4] "Emeritus" "NA" "PhD"
[7] "Phd (visiting)" "Postdoc" "Professor"

Now we can map each vertex role into a color, representing the role of the corresponding actor. To do this, we use the \texttt{RColorBrewer} package, allowing us to produce an appropriate combination of colors.
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Figure 1: A basic visualization of the AUCS network

```r
R> color_map = brewer.pal(num_distinct_roles, "Paired")
R> vertex_colors <- color_map[vertex_roles]

Plotting works as usual, with an additional parameter to set the vertex colors (vertex.color) and two legends for the edge types and for the roles.

```r
R> bk <- par("mar")
R> par(mar=c(0,0,0,0))
R> plot(net, layout = l, grid = c(2, 3), vertex.labels = ",",
+ vertex.color = vertex_colors)
R> par(mar=bk)
R> legend("bottomright", legend=levels(vertex_roles), col = color_map,bty = "n",
+ pch = 20, pt.cex = 1, cex = .5, inset = c(0.05, 0.05))
R> legend("bottomright", legend=selected_ml(net), bty = "n", pch = 20, pt.cex = 1,
+ cex = .5, inset = c(0.2, 0.05))
```
5. Measuring a network

A traditional way of measuring a multiplex network is to focus on each layer at a time, considering it as an independent graph. For example, the `summary()` function computes a selection of measures on all the layers, and also on the flattened network.

```r
R> summary(net)
```

<table>
<thead>
<tr>
<th></th>
<th>n</th>
<th>m</th>
<th>dir</th>
<th>nc</th>
<th>dens</th>
<th>cc</th>
<th>apl</th>
<th>dia</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>flat</em></td>
<td>61</td>
<td>620</td>
<td>0</td>
<td>1</td>
<td>0.33879781</td>
<td>0.4761508</td>
<td>2.062842</td>
<td>4</td>
</tr>
<tr>
<td>coauthor</td>
<td>25</td>
<td>21</td>
<td>0</td>
<td>8</td>
<td>0.07000000</td>
<td>0.4285714</td>
<td>1.500000</td>
<td>3</td>
</tr>
<tr>
<td>facebook</td>
<td>32</td>
<td>124</td>
<td>0</td>
<td>1</td>
<td>0.25000000</td>
<td>0.4805687</td>
<td>1.955645</td>
<td>4</td>
</tr>
<tr>
<td>leisure</td>
<td>47</td>
<td>88</td>
<td>0</td>
<td>2</td>
<td>0.08140611</td>
<td>0.3430657</td>
<td>3.115911</td>
<td>8</td>
</tr>
<tr>
<td>lunch</td>
<td>60</td>
<td>193</td>
<td>0</td>
<td>1</td>
<td>0.10903955</td>
<td>0.5689261</td>
<td>3.188701</td>
<td>7</td>
</tr>
<tr>
<td>work</td>
<td>60</td>
<td>194</td>
<td>0</td>
<td>1</td>
<td>0.10960452</td>
<td>0.3387863</td>
<td>2.390395</td>
<td>4</td>
</tr>
</tbody>
</table>

The columns indicate:
1. \textbf{n} order (number of vertices)
2. \textbf{m} size (number of edges)
3. \textbf{dir} directionality
4. \textbf{nc} number of connected components (strong components for directed networks)
5. \textbf{dens} density
6. \textbf{cc} clustering coefficient (directed networks are treated as undirected)
7. \textbf{apl} average path length
8. \textbf{dia} diameter

To compute other functions or perform another type of layer-by-layer analysis we can convert the layers into \texttt{igraph} objects, using the \texttt{as.igraph()} function, for a single (group of) layer(s), or the \texttt{as.list()} function to obtain a list with all the layers as \texttt{igraph} objects in addition to the flattened network. Once the \texttt{igraph} objects have been generated, all the network measures available in \texttt{igraph} can be computed. The following code, for example, uses \texttt{igraph} to compute the degree centralization of the \texttt{facebook} layer:

\begin{verbatim}
R> layers <- as.list(net)
R> names(layers)
[1] "_flat_" "coauthor" "facebook" "leisure" "lunch" "work"
R> centralization.degree(layers[[3]])$centralization
[1] 0.233871
\end{verbatim}

As another example of layer-by-layer analysis, Fig. 3 shows the degree distribution of each layer, and also the degree distribution of the flattened network.

### 5.1. Layer comparison

In addition to a layer-by-layer analysis, we can compare layers using several different approaches. All the methods mentioned in this section are explained and evaluated in (Brodka, Chmiel, Magnani, and Ragozini 2018).

For example, to quantify the difference between the degree distributions in different layers we can use the \texttt{layer_comparison_ml()} function to produce a table with pair-wise comparisons. The following code computes the dissimilarity between degree distributions, computed using the Jeffrey dissimilarity function (the higher the values, the most dissimilar the two layers).

\begin{verbatim}
R> layer_comparison_ml(net, method = "jeffrey.degree")
\end{verbatim}
Figure 3: Frequency distribution for vertices degree on each layer.

```
facebook leisure coauthor lunch work
facebook 0.0000000 1.0177980 2.0214010 0.4207678 0.7106788
leisure 1.0177980 0.0000000 0.4521076 1.3288250 0.2118452
coauthor 2.0214010 0.4521076 0.0000000 2.8966530 0.5917494
lunch 0.4207678 1.3288250 2.8966530 0.0000000 0.8372414
work 0.7106788 0.2118452 0.5917494 0.8372414 0.0000000
```

The `layer_comparison_ml()` function can also be used to compute multiplex-specific comparisons considering the fact that the same actors may be present on the different layers. In fact, one important comparison can be made to check to what extent this is true:

```
R> layer_comparison_ml(net, method = "jaccard.actors")
```

```
facebook leisure coauthor lunch work
facebook 1.0000000 0.5192308 0.2954545 0.5333333 0.5333333
leisure 0.5192308 1.0000000 0.4117647 0.7833333 0.7833333
coauthor 0.2954545 0.4117647 1.0000000 0.4166667 0.4166667
lunch 0.5333333 0.7833333 0.4166667 1.0000000 0.9672131
work 0.5333333 0.7833333 0.4166667 0.9672131 1.0000000
```

The function returns 0 if there are no common actors between the pair of layers, and 1 if the same actors are present in the two layers. If there is a strong overlapping between the actors, then we can ask whether actors having a high (or low) degree on one layer behave similarly in other layers. To do this we can compute the correlation between the degrees:
The Pearson (or linear) correlation between the degree of actors in the two layers is in the interval \([-1, 1]\). The smallest value (-1) indicates that high-degree actors in one layer are low-degree in the other and vice versa, while the largest value (1) is returned if high-degree (resp., low-degree) actors in one layer are high-degree (resp., low-degree) actors in the other. It is important to note that the correlation only depends on the number of incident edges for each pair (actor, layer), and not on which actors are adjacent: they can be the same or different actors.

We can also check to what extent actors are adjacent to the same other actors in different layers, by checking the amount of overlapping between edges in the two layers, which will be 0 if no actors that are adjacent in one layer are also adjacent in the other and 1 if all pairs of actors are either adjacent in both layers or in none.

The package provides additional similarity functions, listed in Table 1.

5.2. Degree and degree deviation

Various functions can be used to measure individual actors. As a starting point, the following is the list of highest-degree actors on the whole multiplex network:

\[ R > \text{deg} \leftarrow \text{head(sort(degree_ml(net), decreasing = T))} \]

\[ R > \text{deg} \]

\begin{verbatim}
U4 U67 U91 U79 U123 U110 49 47 46 44 44 41
\end{verbatim}

However, in a multiplex context degree becomes a layer-specific measure. We can no longer just ask “who is the most central actor” but we should ask “who is the most central actor on this layer?” Let us see how the most central actors look like when we “unpack” their centrality on the different layers:
Table 1: Similarity functions provided in the package.

<table>
<thead>
<tr>
<th></th>
<th>Overlapping</th>
<th>Distribution dissimilarity</th>
<th>Correlation</th>
</tr>
</thead>
<tbody>
<tr>
<td>jaccard.actors</td>
<td>dissimilarity.degree</td>
<td>pearson.degree</td>
<td></td>
</tr>
<tr>
<td>jaccard.edges</td>
<td>KL.degree</td>
<td>rho.degree</td>
<td></td>
</tr>
<tr>
<td>jaccard.triangles</td>
<td>jeffrey.degree</td>
<td></td>
<td></td>
</tr>
<tr>
<td>coverage.actors</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>coverage.edges</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>coverage.triangles</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>sm.actors</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>sm.edges</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>sm.triangles</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>rr.actors</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>rr.edges</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>rr.triangles</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>kulczynski2.actors</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>kulczynski2.edges</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>kulczynski2.triangles</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>hamann.actors</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>hamann.edges</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>hamann.triangles</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

\[
R> data.frame(
+   facebook = degree_ml(net, actors = names(deg), layers = "facebook"),
+   leisure = degree_ml(net, actors = names(deg), layers = "leisure"),
+   lunch = degree_ml(net, actors = names(deg), layers = "lunch"),
+   coauthor = degree_ml(net, actors = names(deg), layers = "coauthor"),
+   work = degree_ml(net, actors = names(deg), layers = "work"),
+   flat = deg)
\]

From the above result we can see how neighbors may not be equally distributed across the layers. Actor \(U4\), for example, has the largest degree within the 6 actors analyzed in both the facebook layer and the flattened network. However, it has no presence in the coauthor layer and a very small degree in the leisure layer. If we want to quantify to what extent actors have similar or different degrees on the different (combinations of) layers, we can compute the standard deviation of the degree:

\[
R> sort(degree_deviation_ml(net, actors = names(deg)))
\]
5.3. Neighborhood and exclusive neighborhood

The neighbors of an actor \( a \) are those distinct actors that are adjacent to \( a \) on a specific input layer, or on a set of input layers. While on a single layer degree and neighborhood have the same value, they can be different when multiple layers are taken into account, because the same actors can be adjacent on multiple layers leading to a higher degree but not a higher neighborhood.

\[
\text{R> degree_ml(net, actors = "U4", layers = c("work", "lunch"))}
\]

\[U4
36\]

\[
\text{R> neighborhood_ml(net, actors = "U4", layers = c("work", "lunch"))}
\]

\[U4
21\]

The \text{neighborhood_ml()} function (exclusive neighborhood) counts the neighbors that are adjacent to a specific actor only on the input layer(s) \cite{Berlingerio:2012}. A high exclusive neighborhood on a layer (or set of layers) means that the layer is important to preserve the connectivity of the actor: if the layer disappears, those neighbors would also disappear.

\[
\text{R> neighborhood_ml(net, actors = "U91", layers = c("facebook", "leisure"))}
\]

\[U91
22\]

\[
\text{R> xneighborhood_ml(net, actors = "U91", layers = c("facebook", "leisure"))}
\]

\[U91
13\]

5.4. Relevance

Based on the concept of neighborhood, we can define a measure of layer relavance for actors \cite{Berlingerio:2013}. \text{relevance_ml()} computes the ratio between the neighbors of an actor on a specific layer (or set of) and the total number of her neighbors. Every actor could be described as having a specific “signature” represented by her presence on the different layers.
R> data.frame(
+ facebook = relevance_ml(net, actors = "U123", layers = "facebook"),
+ leisure = relevance_ml(net, actors = "U123", layers = "leisure"),
+ lunch = relevance_ml(net, actors = "U123", layers = "lunch"),
+ coauthor = relevance_ml(net, actors = "U123", layers = "coauthor"),
+ work = relevance_ml(net, actors = "U123", layers = "work"))

   facebook leisure lunch coauthor work
U123 0.3793103 NA 0.2068966 NA 0.9310345

Similarly to neighborhood also relevance can be defined using the concept of exclusive neighbor. The xrelevance_ml() function measures how much the connectivity of an actor (in terms of neighbors) would be affected by the removal of a specific layer (or set of layers):

R> data.frame(
+ facebook = xrelevance_ml(net, actors = "U123", layers = "facebook"),
+ leisure = xrelevance_ml(net, actors = "U123", layers = "leisure"),
+ lunch = xrelevance_ml(net, actors = "U123", layers = "lunch"),
+ coauthor = xrelevance_ml(net, actors = "U123", layers = "coauthor"),
+ work = xrelevance_ml(net, actors = "U123", layers = "work"))

   facebook leisure lunch coauthor work
U123 0.0689652 NA 0 NA 0.5172414

5.5. Distances

In addition to single-actor measures, the package can also be used to compute multilayer distances between pairs of actors. Distances are defined by Magnani and Rossi (2013b) as sets of lengths of Pareto-optimal multidimensional paths. As an example, if two actors are adjacent on two layers, both edges would qualify as Pareto-optimal paths from one actor to the other, as edges on different layers are considered incomparable (that is, it is assumed that it makes no sense in general to claim that two adjacent vertices on Facebook are closer or further than two adjacent vertices on the co-author layer). Pareto-optimal paths can also span multiple layers.

R> distance_ml(net, "U91", "U4")

   from to facebook leisure coauthor lunch work
1  U91 U4 1 0 0 0 0 0
2  U91 U4 0 3 0 0 0 0
3  U91 U4 0 0 2 1 0 0
4  U91 U4 0 0 0 0 0 0
5  U91 U4 0 1 0 0 1 0
6  U91 U4 0 0 2 0 0 1
7  U91 U4 0 0 0 1 1 0
8  U91 U4 0 0 0 0 0 2
9  U91 U4 0 1 0 0 1 0
10 U91 U4 0 2 1 0 0 0
6. Community detection

A common network mining task is the identification of communities. An imprecise but generally accepted definition of community is as a subgroup of actors who are more densely connected among themselves than with the rest of the network.

The function `glouvain_ml()` uses the algorithm described by Mucha, Richardson, Macon, Porter, and Onnela (2010) to find community structures across layers, where vertices in different layers can belong to the same or a different community despite corresponding to the same actor. This method belongs to the class of community detection methods based on modularity optimization, that is, it tries to find an assignment of the vertices to communities so that the corresponding value of modularity is as high as possible. Multilayer modularity is a quality function that is high if most of the edges are between vertices in the same community and if vertices corresponding to the same actors are also often in the same community. The function `glouvain_ml()` accepts three parameters to modify the resolution of the modularity (\(\gamma\)), the inter-layer weight connectivity (\(\omega\)) and the number of nodes after which the algorithm will make the computation on the fly without keeping the full data in memory (\(\text{limit}\)).

```r
R> ml_clust <- glouvain_ml(net)
R> head(ml_clust)

 actor layer cid
 1 U126 leisure 0
 2 U126 lunch 0
 3 U126 work 0
 4 U138 leisure 0
 5 U138 coauthor 0
 6 U138 lunch 0
```

The result of the function is a data frame with two columns identifying a vertex, as a pair (actor,layer), and a third column with a numeric value (\(\text{cid}\)) identifying the community to which the vertex belongs.

The package provides other community detection algorithms: multilayer clique percolation (ML-CPM) (Afsarmanesh and Magnani 2018), ABACUS (Berlingerio et al. 2013) (for overlapping and partial community detection) and Infomap (De Domenico, Lancichinetti, Arenas, and Rosvall 2015) (for partitioning/overlapping community detection on undirected or directed networks):

```r
R> c1 <- abacus_ml(net, 4, 2)
R> c2 <- clique_percolation_ml(net, 4, 2)
R> c3 <- glouvain_ml(net)
R> c4 <- infomap_ml(net)
```

We can now compare these community detection methods by computing some statistics about (1) the number of communities generated, (2) the average community size, (3) the percentage of vertices included in at least one cluster (which is 1 for complete community detection methods), (4) the percentage of actors included in at least one cluster (which is 1 for complete...
Figure 4: Multilayer representation of communities in the AUCS network detected using the generalized Louvain (glouvain) method.

Community detection methods) and (5) the ratio between the number of actor-community pairs and the number of clustered actors, indicating the level of overlapping (which is 1 for partitioning community detection methods and higher for overlapping methods). The corresponding statistics for the AUCS network are the following (code to build the dataframe not shown):

```
R> com_stats

         num avg_s clust_vertices clust_actors actor_overl
abacus 18 10.88889     0.5625     0.7704918   1.978723
clique p. 11 11.27273    0.3750     0.5081967   1.838710
louvain 5 44.80000     1.0000     1.0000000   1.000000
infomap 6 37.33333     1.0000     1.0000000   1.000000
```

The same comparison can be performed on some of the other datasets included in the library, for example the bank wiring network:
R> com_stats

<table>
<thead>
<tr>
<th></th>
<th>num</th>
<th>avg_s</th>
<th>clust_vertices</th>
<th>clust_actors</th>
<th>actor_overl</th>
</tr>
</thead>
<tbody>
<tr>
<td>abacus</td>
<td>10</td>
<td>8.8</td>
<td>0.6451613</td>
<td>0.7142857</td>
<td>3.8</td>
</tr>
<tr>
<td>clique p.</td>
<td>2</td>
<td>8.0</td>
<td>0.2580645</td>
<td>0.5714286</td>
<td>1.0</td>
</tr>
<tr>
<td>louvain</td>
<td>2</td>
<td>31.0</td>
<td>1.0000000</td>
<td>1.0000000</td>
<td>1.0</td>
</tr>
<tr>
<td>infomap</td>
<td>1</td>
<td>62.0</td>
<td>1.0000000</td>
<td>1.0000000</td>
<td>1.0</td>
</tr>
</tbody>
</table>

and the monastery network:

R> com_stats

<table>
<thead>
<tr>
<th></th>
<th>num</th>
<th>avg_s</th>
<th>clust_vertices</th>
<th>clust_actors</th>
<th>actor_overl</th>
</tr>
</thead>
<tbody>
<tr>
<td>abacus</td>
<td>51</td>
<td>16.19</td>
<td>0.7600000</td>
<td>1.0000000</td>
<td>15.55556</td>
</tr>
<tr>
<td>clique p.</td>
<td>4</td>
<td>9.50</td>
<td>0.1714286</td>
<td>0.5555556</td>
<td>1.70000</td>
</tr>
<tr>
<td>louvain</td>
<td>3</td>
<td>58.33</td>
<td>1.0000000</td>
<td>1.0000000</td>
<td>1.00000</td>
</tr>
<tr>
<td>infomap</td>
<td>1</td>
<td>175.00</td>
<td>1.0000000</td>
<td>1.0000000</td>
<td>1.00000</td>
</tr>
</tbody>
</table>

7. Conclusion

In this article we have presented the multinet package and some of its functions to create and analyze multiplex networks. The package provides a wide range of network analysis methods to analyze individual actors, identify groups (communities) and compare layers, in addition to functions to explore and generate network data. multinet is also integrated with igraph, so that single layers or flattened sets of layers can also be analyzed using more traditional methods.

Acknowledgments

We thank Mikael Dubik for the implementation of the generalized Louvain method, and several people who participated in our training workshops or contacted us to suggest features and report bugs. The multinet package includes the following external code: eclat\(^3\) (for association rule mining), Eigen\(^4\) and spectra\(^5\) (for matrix manipulation), Infomap\(^6\) (for the Infomap community detection method) and Howard Hinnant’s date and time library\(^7\).

This work was partially supported by the European Community through the project “Values and ethics in Innovation for Responsible Technology in Europe” (Virt-EU) funded under Horizon 2020 ICT-35-RIA call Enabling Responsible ICT-related Research and Innovation.

References

\(^3\)http://www.borgelt.net/eclat.html
\(^4\)http://eigen.tuxfamily.org
\(^5\)https://spectralib.org
\(^6\)http://www.mapequation.org
\(^7\)https://github.com/HowardHinnant/date


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