ESSnet Big Data II

Grant Agreement Number: 847375-2018-NL-BIGDATA

https://webgate.ec.europa.eu/fpfis/mwikis/essnetbigdata
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Workpackage I

Mobile Network Data

Deliverable I.4 (Information Techonologies)

Some IT tools for the production of official statistics with mobile network data

Final version, 11 November, 2020

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Executive summary

This document addresses the software implementation of the methodological framework designed to incorporate mobile phone data into the current production chain of official statistics. It presents an overview of the architecture of the software stack, its components, the interfaces between them and shows how they can be used.
The modules of our software implementation are four `R` packages:

- `destim` - it estimates the spatial distribution of the mobile devices providing the location probability for each device, at each time instant for each tile of the grid.
- `deduplication` - it classifies the devices as being in 1:1 or 2:1 correspondence with its owner. This classification is probabilistic, thus, assigning each device a probability to belong to one of the two classes already mentioned.
- `aggregation` - it estimates the number of individuals detected by the network starting from the number of devices and the duplicity probabilities. It also estimates the number of individuals moving from one geographical region to another, i.e. the origin-destination matrix.
- `inference` - combines the number of individuals provided by the previous package with other information like the population count from an official register and the mobile operator penetration rates to provide an estimation of the target population count.

All `R` packages are freely available and they can be installed from *github* account of our project, `https://github.com/MobilePhoneESSnetBigData`.

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Introduction

This document contains a description of the software implementation of the methodological framework built within the Work Package I of the ESSnet Big Data II project with the purpose of incorporating mobile network data into the current production of official statistics. Thus, an interested reader should be familiarized with the content of this methodological approach which is given in Deliverable I.3 (Methodology) - A proposed production framework with mobile network data (Salgado et al., 2020).

The document is divided into the following chapters. In chapter 2 we present an overall view of the architecture of the software implementation, describing the rationale behind this architecture, its main components/modules, and the interfaces between them. In chapter 3 we deal with the first layer in the software stack, namely the *Data acquisition and preprocessing layer*. The next chapter is dedicated to the *geolocation* module which produces the posterior location probabilities at the level of each device and (discrete) location on the map. In chapter 5 we describe the implementation of the *deduplication* module which has the role of computing the duplicity probability for each device detected by the network, i.e. the probability for a mobile device to be in a 2-to-1 correspondence with its owner. In chapter 6 we show how the number of detected mobile devices, combined with the duplicity probability for each device and the location probabilities are transformed into the number of individuals detected by the network. Chapter 7 is dedicated to the inference module that takes as inputs the number of detected individuals and other auxiliary data sources (such as a population register) and produces the population counts for each time instants and geographical units under consideration. Finally, in chapter 8 we comment on future prospects and several open issues. The software tools that we developed to implement the above mentioned methodological framework consists in a set o R packages that are freely available on *github* at the following address: `https://github.com/MobilePhoneESSnetBigData`

2.1. The programming languages of the IT components

We start this introductory chapter by giving some reasons for selection the programming language for our software implementation. Firstly, we considered the recent trends in the development of the computing systems which shows a clear movement from the INTEL hardware platform to ARM (Morgan, 2020; Dipert, 2011; Blem et al., 2013). Moreover, the first supercomputer in Top500 supercomputers in 2020 (TOP500.org, 2020), Fugaku, is powered by Fujitsu's 48-core A64FX SoC which is an ARM processor. This trend is a clear indication for us that a software developed now with the intention to be used in the future should be portable at the

level of source code. In fact this is one of the main goals of software portability (Mooney, 2004a,b).

Secondly, our final goal is to produce a software for statisticians, not for computer scientists. Thus, the language of the implementation should be familiar for statisticians and easy to use by them. We decoupled in a certain degree the task of using the software from the task of developing the software. While using the software should be easy (as much as such a highly specialized software could be) the development could include techniques not very familiar to statisticians and computer scientists are still needed.

Thirdly, we planned to use only open source tools like libraries, IDEs, debuggers, profilers, etc. to maintain the software development process under a strict control regarding the associated costs. Moreover, the programming language together with these tools should have a large community of programmers and users which can be seen as a free technical support.

Fourthly, the programming language should have support for parallel and distributed computing. Since all the algorithms involved by our methodological approach are computational intensive, and the size of mobile phone data could be very large, this is a mandatory requirement.

Last but not least important, the criteria of programming efficiency and resources needed to run the software even on normal desktops/laptops were considered when we selected a programming language.

We've built a pool of possible languages that fulfill the above mentioned criteria and rejected some of them from the beginning because they were considered of being too low level to be enough user-friendly (plain `C` and `C++`) or not widely used among official statistics community (`Java`, `Scala` or `Julia`) Schissler et al. (2019). Eventually, we came to the following two software ecosystems: `R` (R Core Team, 2020) or `Python` (Van Rossum and Drake, 2009). Both systems meet our criteria and have a large community of users but while `Python` is generally considered to be more computationally efficient (see for example Schissler et al. (2019) or the results of the benchmarks here `https://modelingguru.nasa.gov/docs/DOC-2676`), `R` is better suited for statistical purposes and it seems to gain ground among the official statistics community (Templ and Todorov, 2016; Kowarik and van der Loo, 2018). Since our target audience is the official statistics community, we decided to develop our software modules mainly by using `R` and write few specific functions that are computationally demanding using C++ to fasten the execution. We list below some of the advantages of our choice:

- there are around 16,500 packages available in CRAN (`https://cran.r-project.org/` with a wide range of them developed specially for official statistics (they can be found at the following URL: `https://github.com/SNStatComp/awesome-official-statistics-software`);
- `R` has good support for parallel and distributed processing;
- `R` can be easily interfaced and work together with high performance languages like `C++` (Eddelbuettel and François, 2011; Eddelbuettel, 2013; Eddelbuettel and Balamuta, 2017) when the performance of plain `R` is not enough;
- `R` can be interfaced with computing ecosystems used in the big data area such as `Hadoop` (White, 2009) or `Spark` (Zaharia et al., 2016). There are several packages that allow a neat interface between `R` and these systems: RHadoop (which is in fact a collection of packages - rhdfs, plyrmr, rmr2, ravro), Hadoop Streaming, hive, SparkR, sparklyr (Oancea and

Dragoescu, 2014; Rosenberg, 2012; Feinerer and Theussl, 2020; Venkataraman et al., 2016; Luraschi et al., 2020) which means that, if needed, all modules of our software stack can be integrated with such systems for a production pipeline, with much or less programming effort.

We mention from the beginning that during the development of our software implementation we used only simulated data for testing and profiling purposes but using real mobile phone data requires no changes in the software but only a preprocessing step to bring the real data sets to the format required by the current software. Bilateral collaborations on testing the software on real data have been started, but data protection, data sharing restrictions, and access limitations make this a slow and difficult task.

If the size of real data is too big to be supported by the current implementation, all software modules developed within this project can be transformed to work with `Hadoop` or `Spark` as mentioned before and ported to a cloud computing environment.

2.2. The layered structure of the IT components

Functional modularity in the statistical process is a central element when working with new data sources that are technology dependent. In the area of mobile phone data there are already specific proposals to organize a methodological framework (Ricciato, 2018). Our methodological approach is in line with this proposal (which we will call *ESS Reference Methodological Framework*) and is organized based on the following principles:

- modularity - the division of the production process into separate parts/modules;
- abstraction - the design and division of these parts/modules so that their interaction takes place only through the interfaces making the internals of each module as much independent of the rest of modules;

In terms of methodology, the process steps are represented in Figure 2.1 and described in detail by Salgado et al. (2020).

Organizing the modules that made up our software implementation in such a way to minimize their interaction is achieved by layering/stacking them in a hierarchy. Following this idea, the software implementation uses a layered design which is one of the most common architecture patterns in software design (Richards, 2015). Besides following closely the architecture of the methodological framework, the layered design that we used for the software implementation has other advantages too:

- easy to develop and maintain;
- easy to test;
- changing the implementation of one layer (component) does not affect the rest of the components;

We organized our stack of software modules as follows:

Data acquisition and preprocessing layer. This layer deals with capturing the network events and applying o series of preprocessing operations to bring them into a form that can be statistically exploited. It is a component that is strongly dependent on the mobile network technology which can vary among different MNOs and geographical regions. This component is not implemented in our software stack because we lacked access to a

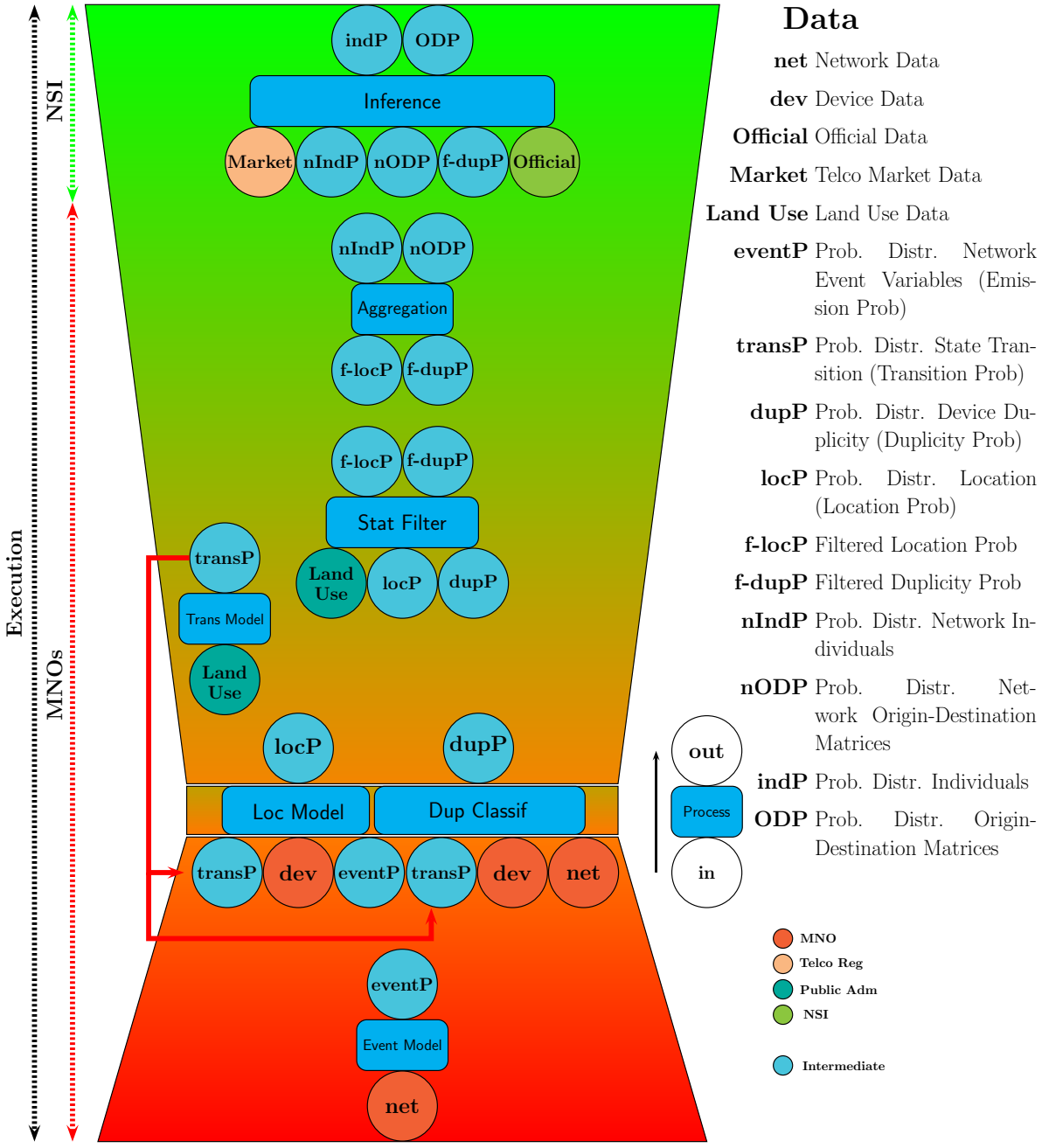


Figure 2.1: Representation of the Process Steps framed in the ESS Reference Methodological Framework. See also Ricciato (2018).

real mobile network during the process of writing the code. Instead, we used a mobile network data simulator that was described in detail by Oancea et al. (2019).

Geolocation layer. Its main purpose is to exploit the network events data and to derive the probability of localization for each device at the level of geographical units. This is done using a Hidden Markov Model and is implemented in the `R` package `destim` available from the following URL: `https://github.com/MobilePhoneESSnetBigData/destim`. It provides the location probability for each individual device as well as the joint location

probabilities.

Deduplication layer. The purpose of this component is to classify each device d as corresponding to an individual with only one device (1:1 correspondence between devices and individuals) or as corresponding to an individual with two devices (2:1 correspondence between devices and individuals). This classification is a probabilistic one, thus assigning a probability $p_d^{(n)}$ of duplicity to each device d carrying $n = 1, 2$ devices. The layer is implemented in the `R` package `deduplication` available here: `https://github.com/MobilePhoneESSnetBigData/deduplication`.

Aggregation layer. The purpose of this layer is to estimate the number of detected individuals starting from the number of detected mobile devices and making use of the duplicity probability for each device provided by the previous layer. It is implemented in the `R` package `aggregation` available here: `https://github.com/MobilePhoneESSnetBigData/aggregation`.

Inference layer. The role of this layer is to compute the probability distribution for the number of individuals in the target population conditioned on the number of individuals detected by the network and some auxiliary information coming from telco penetration rates and population registers. It is also implemented in an `R` package `inference` available here: `https://github.com/MobilePhoneESSnetBigData/inference`.

One can easily note that a module is missing comparing with the methodological framework. This is the statistical filtering layer. We choose not to implement it because we lack data to test such a module and it is also domain-specific. Instead, we pass the entire set of data from the aggregation layer to the inference layer, thus counting the entire population present in a geographical territory.

All the layers in this hierarchy communicate with theirs (direct and distance) neighbors, receiving data from the layer/layers below and passing the results to the layer/layers above. Some layers not only provide their output only to the immediate upper layer but also to others layers on top of them. For example, the `aggregation` layer receives its input from the layer immediately below, the `deduplication` layer, and also from the `geolocation` layer and the `inference` layer takes its input from the `aggregation`, `deduplication` and `geolocation` layers. The data that flows to an indirect upper layer practically "tunnels" the direct upper layer. Besides, some auxiliary data such as the sequence of time instants, the division of the geographical area in tiles and regions, some parameters of the mobile network, etc. are available for all layers. Instead of passing the data as memory data objects (as it is happening in an enterprise application for example), each layer uses a secondary storage where it puts the results and makes them available for the next layer in the hierarchy. We opted for this approach taking into consideration the volume of mobile phone data sets. All intermediate results are stored as using one of the widespread file formats: `csv` files. Thus, even if the implementation of a layer is changed in the future and the new one is using another programming language/system, these intermediate results can be easily accessed, any programming language having libraries/-facilities to read/write such files. In figure 2.2 we depict this layered structure of the software implementation, showing the components (layers) and the data flow between them.

From a user perspective all our software modules provide two types of functions:

High-level functions Provide an easy way to access the main functionality of each package, hiding the complexity of implementation from the normal user.

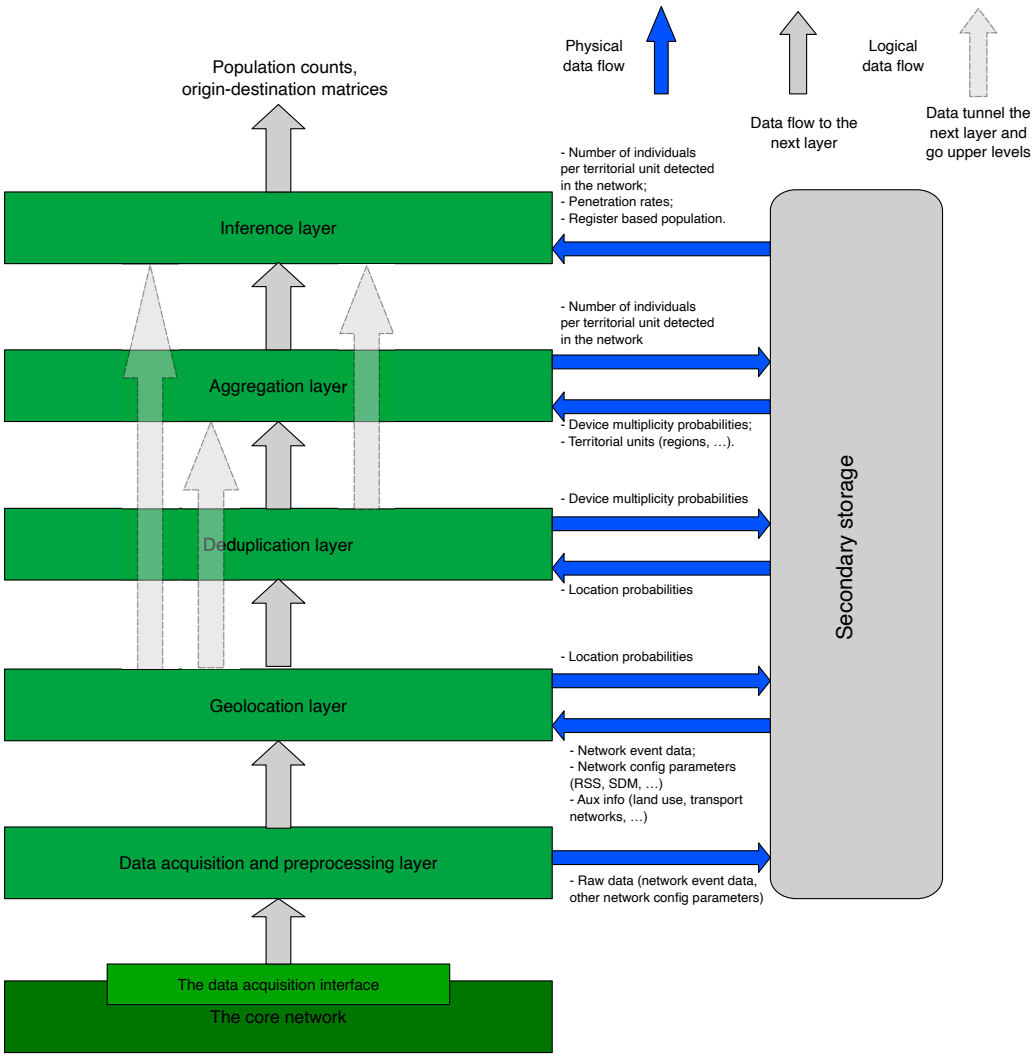


Figure 2.2: The layered structure of the software implementation.

Low-level functions They are fundamental functions to execute the core methods and usually they are not exposed to users, but we decided to make them public and accessible for external users having in mind that this is only a first tentative to implement such a complex process and letting users access the intricacies of each computation step facilitates further developments and improvements.

All packages have a reference manual (included in this document as annexes) and vignettes. They are intended to show the continuously evolving status of the packages. At some initial point this deliverable and the vignettes had a high degree of overlapping, but as we progress in our work (beyond the ESSnet Big Data II project towards the new ESS Task Force on MNO data and national and international projects) the packages and the vignettes will evolve.

2.3. The interfaces between layers

The modules composing the software stack are entirely decoupled. One layer receives some data as input from the layer(s) below it and provides data to the upper layer(s) as output. Setting a clear format for these data sets that flow from one layer to another make the layers independent and easy to change their implementation. The single request is to adhere to the format of the

data sets passed as input and to the ones provided as the output of the layer. We define the interface between consecutive layers as the format of the data sets flowing from one layer to another. In the following we describe the structure of these data sets that are passed between consecutive layers. For these initial versions of our R packages the name of the columns in the `csv` files are fixed but there is an ongoing work to standardize the formats (column names, data types, accepted values, etc.) and define these standards using `xsd` and `xml` files. Then, all R packages from our software stack will first read the files describing the structure of the data and after that read the files themselves.

We mention that besides these data that flow vertically, from the bottom layer to the upper one, there are other general parameters available to all layers from the secondary storage. We don't deal here with the input data for the first layer *Data acquisition and preprocessing* since it is technology dependent and out of the control of statisticians. We only present how the output of this layer should look like to be accepted as input for the *geolocation* layer.

Data aquisition and preprocessing layer

The outputs of this layer are a combination of data sets coming from the network after a preprocessing stage. This preprocessing stage is necessary to eliminate all the parameters that are dependent on a specific mobile network technology and transform the acquired data in a simple form, suitable for statistical processing.

There are three main data sets produced by this layer: the *network events* registered by the MNO during a period of time, a measure of the *radio signal* computed by the MNO in the center of each tile of the grid and a file that define the *coverage area* (antenna cell) for each antenna inside the geographical territory under consideration. Our methodological approach can use one of two types of radio signal value: the signal strength or the signal quality (also known as signal dominance). Both models of radio wave propagation are described in detail by Salgado et al. (2020) and Oancea et al. (2019).

Below we give the structure of the `csv` files for the network events.

```
t, Antenna ID, Event Code, Device ID
...
```

There are four columns in this file:

- **t** - the time instant when the event was generated and recorded by an antenna;
- **Antenna ID** - a unique ID of the antenna that recorded this event;
- **Event Code** - an integer that represents the code of the network event. Currently, our methodology uses only the connection events, i.e. the events generated by a mobile device when it connects to an antenna. We encoded this event with the value 0;
- **Device ID** - a unique ID of the device that generated the event interacting with the antenna under consideration. This ID uniquely identifies each mobile device in the whole data set;

The signal strength or the signal quality/dominance is a key information used to compute the location likelihood and it must be computed in the center of each tile of the grid. The values in this file depend on the technical parameters of the network as well as on the characteristics of the geographical region (open field, cities etc.) It has the following columns:

```
Antenna ID, Tile0, Tile1, Tile2,..., TileN-1
...
```

The **Antenna ID** is the unique ID of the antenna and the rest of the columns represents the IDs of the tiles of the grid: **Tile0** means the tile with index 0, and so on. The tile indexing mechanism follows the same schema described in Oancea et al. (2019): Tile0 is the tile from the bottom left corner while **TileN-1** is the tile from the upper right corner. Here N represents the total number of tiles in the grid. We decided to use this (flat) file format because it avoids redundancy and results in the smallest possible file size.

The coverage area of an antenna is defined as the geographical area where the signal strength or the signal quality is greater than a predefined minimum value. The type of the physical measure used to compute this area (strength or quality) is determined by the handover mechanism used by the network. For omnidirectional antennas this area is a circle while for directional antennas it has a shape similar to an ellipse.

The coverage areas for all antennas are stored in a file with the following structure:

```
AntennaId,Cell Coordinates
```

The cell coordinates of the coverage area are saved using the *WKT* format. The geometric object used to represent this area is a polygon which covers both cases: omnidirectional and directional antennas. Below is an excerpt from such a file. For convenience, we erased some points from the polygon defining this area. Each row of the file contains the unique antenna ID and a *WKT* string that specifies the coverage area.

```
AntennaId,Cell Coordinates
2,POLYGON ((2400.5 7500.0, 2395.5 7650.5, 2381.5 7801.0, 2358.0 7950.0,
2325.0 8097.0, 2283.0 8242.0,  2232.0 8383.5, 2172.0 8522.0, 2103.5 8656.5,
2026.5 8786.0, 1942.0 8911.0, 1849.5 9030.0, 1750.0 9143.0, 1643.0 9250.0,
1530.0 9349.5, 1411.0 9442.0, 1286.0 9526.5, 1156.5 9603.5, 1022.0 9672.0,
...

2395.5 7349.5, 2400.5 7500.0))

3,POLYGON ((3400.5 2500.0, 3395.5 2650.5, 3381.5 2801.0, 3358.0 2950.0,
3325.0 3097.0, 3283.0 3242.0, 3232.0 3383.5, 3172.0 3522.0, 3103.5 3656.5,
3026.5 3786.0, 2942.0 3911.0, 2849.5 4030.0, 2750.0 4143.0, 2643.0 4250.0,
2530.0 4349.5, 2411.0 4442.0, 2286.0 4526.5, 2156.5 4603.5, 2022.0 4672.0,
...

3358.0 2050.0, 3381.5 2199.0, 3395.5 2349.5, 3400.5 2500.0))
```

The geolocation layer The inputs of this layer are provided by the previous layer and they are network events file and signal file. Besides these files some general parameters like the parameters of the grid overlapping the geographical area of concern are also needed.

There are two main types of outputs for this layer: the location probabilities for each device and each tile and the joint location probabilities.

The first output is mainly a matrix with N rows and $nTimes$ columns where N is the total number of tiles in the grid and $nTimes$ is the total number of time instants when the network events were recorded. A value $p(i, j)$ in this matrix is the location probability for tile i and time instant j for the device under consideration. Here j is the index of the time instant in the sequence of time instants, not the true (or real) time instant. Since:

- we have a grid of such an extension that in a given time increment a device cannot reach most of its cells, and
- we have such a time and spatial resolution in the grid and the event information that a device cannot reach most of the cells in a time increment

the matrices with location probabilities are sparse and the natural choice for storing these matrices is to use one of the special file formats for sparse matrices. We used a format similar to the Coordinate Text File (see for example Boisvert et al. (1997) for a full description of this file format) to store these matrices where a row in the file contains a tuple $(i, j, a[i, j])$ giving the number of row, column, and a nonzero entry in the matrix. The single between our file format compared to Coordinate Text File format is that the first row specifying the total number of rows, columns and nonzeros in the matrix is missing because we already have these numbers from other sources (for example, in case of using simulated data from the simulation configuration fil). Below we give the structure for the location probability file for a device.

```
tile, time, probL
...
```

It has three columns:

- **tile** - is the tile index (see the tile indexing system mentioned above) and it corresponds to the row number in the matrix;
- **time** - is the time instant for which the location probability is computed. Its index in the time instants sequence corresponds to the column number in the matrix;
- **probL** - is the value of the location probability. Only non-zero values are stored in this file

We mention that there is a separate file for each mobile device.

The joint location probabilities files stores the probability of being in tile i at time instant $t-1$ and tile j at time instant t for all combinations of time consecutive time instants and tiles. We store again only the non-zero probabilities. The structure of this file is given below:

```
time_from, time_to, tile_from, tile_to , probL
....
```

The columns in this file has the following meanings:

- **time_from** - is the initial time instant;
- **time_to** - is the final time instant;
- **tile_from** - is the initial tile;
- **tile_to** - is the destination tile;
- **probL** - is the value of the location probability, i.e. the probability of a device to move from tile **tile_from** to **tile_to** during the time interval (**time_from** , **time_to**). Only non-zero values are stored.

We mention again that there is a separate file for each mobile device.

The deduplication layer The inputs of this layer are the outputs of the previous layer, i.e. the two sets of files with the location probabilities and joint location probabilities for each device. Besides these two data sets, the deduplication layer also needs some files that come directly from the data acquisition and preprocessing layer: the network events file and the antennas cell file. Both files were already described in the beginning of this section. An additional input of this layer is an information from an external source that gives the apriori probability of a person to hold two mobile devices.

The output for the deduplication layer is a single `csv` file that contains the duplicity probability for each device. It has two columns:

```
deviceID, dupP
```

Here **deviceID** is the unique Id of a device and **dupP** is the probability of the device to be in a 2-1 correspondence with its owner. There is one row for each device registered by the network.

The aggregation layer The inputs of this layer are:

- the `csv` file with duplicity probabilities produced by the previous layer;
- a `csv` file defining the geographical regions for which we want to compute the number of individuals detected by the network. We provide below an excerpt from such a file;
- the general parameters defining the grid (number of rows and columns, the tile dimensions on OX and OY axes);
- the sequence of time instants when the network events were recorded.

The file defining the geographical regions is a simple `csv` file where each region is defined as a collection of tiles. An example of such a file is given below:

```
tile,region
1560,3
1561,3
1562,3
1563,3
1564,3
1565,3
1566,3
1567,3
1568,3
....
```

We are aware that there is a certain degree of redundancy in this file, but the dimension of such a file is relatively small and poses no difficulties in the process of processing it.

There are two outputs of this layer: the number of individuals in each region at each time instant and the number of individuals moving from one region to another. Both numbers are computed from a Poisson-multinomial distribution and since there is no analytical form of the PMF we generate a sequence of random numbers from this distribution which can be used to compute a point estimation (mean, mode, median), as well as accuracy measures (credible intervals, posterior variance).

The number of individuals for each time instant and region is saved in a `csv` file like in the example below:

```
time, region,  N, iter
  0,      1,  10,    1
  0,      1,  10,    2
  0,      1,  10,    3
  0,      1,  12,    4
  0,      1,  13,    5
  0,      1,  12,    6
  ...
```

time represents the time instant, **region** is the region number and **N** is the number of individuals. For each combination of time instant and region there are several random values generated for **N** and their index is given in **iter** column.

The number of individuals moving from a region to another is saved in a `csv` file with the structure given in the following example:

```
time_from, time_to, region_from, region_to, Nnet, iter
     0,      10,          1,         1,        10,   1
     0,      10,          2,         1,         0,   1
     0,      10,          3,         1,         0,   1
     0,      10,          4,         1,         1,   1
     0,      10,          5,         1,         0,   1
     0,      10,          6,         1,         0,   1
     ...
```

The name of the columns are self-explanatory. For each distinct combination (**time_from, time_to, region_from, region_to**) there are several random values generated for the number of individuals and their index is given in **iter** column.

The inference layer
The inputs of this layer are:

- the posterior location probabilities, one file per device (we already described the structure of these files);
- a `csv` file with the duplicity probabilities for each device, which is the output of the **(**deduplication) layer (already described);
- a `csv` file defining the geographical regions (already described);
- a `csv` with file the general parameters defining the grid (already described);
- a `csv` with information from a population register, giving the population count for all geographical regions under consideration;
- a `csv` with the penetration rate of the mobile network operator for all geographical regions under consideration;
- a `csv` with the number of individuals for each time instant and region which is an output from the `aggregation` package (already described);
- a `csv` with the number of individuals moving from a region to another which is also an output from the `aggregation` package (already described).

The information from the population register is organized on two columns as showed below:

```
region, N0
   1,   38
   2,   55
   3,   65
   4,   39
   ...
```

Here, **region** is the region number and **N0** is the population count in the corresponding region.

The penetration rate file has a similar structure:

```
region, pntRate
   1,  0.3684211
   2,  0.4
   3,  0.4153846
   4,  0.4615385
   ...
```

The second column, **pntRate**, is the penetration rate obtained from the mobile network operator.

There are three main results of this package: the population count for each region computed at the initial time instant, the population count for each region and all time instants $t > t_0$, and the origin-destination matrices for all pairs of time instants. All these results are computed in three versions: using the Beta Negative Binomial distribution, using the Negative Binomial distribution and using the state process Negative Binomial distribution. Details about how these distributions are used to infer the target population are given by Oancea et al. (2019).

For the population at the initial time instant t_0 the `inference` package generates two tables: one with a some descriptive statistics about the distribution another one with the random values generated for each region. The descriptive statistics of the population count distribution are showed below:

```
 region Mean Mode Median Min Max Q1 Q3 IQR  SD    CV   CI_LOW CI_HIGH
      1   43   33     39  11 133 30 51  21 17.90 41.96  21.00   73.00
      2   59   51     56  21 126 47 68  21 15.85 27.09  37.00   88.00
      3   82   68     78  38 185 68 94  26 20.84 25.38  54.97  121.00
      4   39   32     37  14  92 30 45  15 11.58 30.07  23.47   59.50
      5   77   75     74  31 185 62 90  28 23.07 29.84  47.50  120.00
      6   47   42     44  15 152 36 56  20 17.32 36.59  25.00   78.06
      7   72   62     69  28 174 57 84  26 21.36 29.56  43.50  109.00
      8   25   24     24  11 107 20 29   9  8.22 32.48  15.97   39.50
      9   67   66     66  36 132 57 75  18 14.40 21.53  46.50   91.50
     10   48   50     46  20 110 39 55  16 13.01 27.16  31.50   70.00
```

The random values generated according to the corresponding distribution are organized in a table with the following structure:

```
   region   N   NPop
     1     11.0 53.0
     1      9.0 35.0
     1     13.0 56.0
     1     12.0 46.0
     1     12.0 33.0
     1     12.5 65.5
...
```

where **region** is the region number, **N** is the number of individuals detected by the network and **NPop** is the target population count.

The output for the population count distribution at time instants $t > t_0$ is organized as a list with one element for each time instant t. An element for a time instant t is also a list with one or two items, depending on a parameter passed to the function that perform the computations (see chapter 7 for details). The first item is a table with descriptive statistics and the second one contains the random values generated according to the corresponding distribution. the structure of these tables are identical with the previous ones.

The third output, the origin-destination matrices for all pairs of time instants **time_from-time_to** is also a list with one element for each pair of time instants. An element for a pair **time_from-time_to** is a list with one or two elements, as in the previous case. The first element is a table with descriptive statistics for the origin-destination matrix with the structure as in the example shown below:

region_from	region_to	Mean	Mode	Median	Min	Max	Q1	Q3	IQR	SD	CV	CI_LOW	CI_HIGH
1	1	34	29	33	9	93	26	41	15	11.62	33.81	19.00	54.00
1	2	0	0	0	0	6	0	0	0	0.84	391.64	0.00	2.21
1	3	0	0	0	0	0	0	0	0	0.00	NaN	0.00	0.00
1	4	0	0	0	0	7	0	0	0	0.69	485.36	0.00	0.00
1	5	0	0	0	0	0	0	0	0	0.00	NaN	0.00	0.00
1	6	0	0	0	0	0	0	0	0	0.00	NaN	0.00	0.00
1	7	0	0	0	0	0	0	0	0	0.00	NaN	0.00	0.00
1	8	0	0	0	0	0	0	0	0	0.00	NaN	0.00	0.00
1	9	0	0	0	0	0	0	0	0	0.00	NaN	0.00	0.00
1	10	0	0	0	0	0	0	0	0	0.00	NaN	0.00	0.00
2	1	1	0	0	0	11	0	0	0	1.44	211.19	0.00	3.55
2	2	68	73	67	28	133	58	77	19	14.67	21.47	47.60	93.00
2	3	1	0	0	0	12	0	3	3	2.06	150.07	0.00	5.46
2	4	0	0	0	0	2	0	0	0	0.15	1020.93	0.00	0.00
2	5	0	0	0	0	7	0	0	0	0.99	279.62	0.00	2.91

...

The second element of the list gives the random values generated for the population moving from one region to another and it looks like in the example below:

region_from	region_to	iter	NPop
1	1	1	40
1	2	1	0
1	3	1	0
1	4	1	0
1	5	1	0
1	6	1	0

...

NPop is the random value while **iter** represents the index of the corresponding random value in the whole set.

We summarize in the following tables all the files produced by different layers in the stack and those provided from external sources. It is important to note that although the last 5 files mentioned in table 2.2 are provided by our simulation software (the particle "MNO1" was the generic name given to our hypothetical MNO), the information contained in these files can be provided by a real MNO.

Table 2.1: Files produced by the R packages

File name	Output of:	Input for:	Short description
postLocDevice_ID.dt.csv	destim	deduplication, inference	posterior location probabilities for a device, for each tile and time instant
postLocJointProbDevice_ID.dt.csv	destim	aggregation	posterior joint location probabilities for a device, for each tile and time instant
duplicity.csv	deduplication	aggregation, inference, aggregation	duplicity probability for each device
nnet.csv	aggregation	inference	random values for number of individuals for each geographical region
nnetod.csv (.zip)	aggregation	inference	random values for number of individuals moving from one geographical region to another

Table 2.2: Files provided from external sources (simulation software, MNOs, NSOs)

File name	Source	Description
grid.csv	NSO	Defines the parameters of the grid overlapping the geographical area considered
regions.csv	NSO	Defines the geographical regions as sets of tiles of the grid
pnt_rate.csv	MNOs, other national telecommunication authorities	Defines the penetration rate of an MNO for each geographical region
pop_reg.csv	NSO	Gives the population count for each region, from a population register
AntennaCells_MNO1.csv	MNO	Defines the mobile network cells
AntenaInfo_MNO_MNO1.csv	MNO	Gives the network events registered inside a geographical area, during a time period
SignalMeasure_MNO1.csv	MNO	Gives the signal strength/quality emitted by each antenna in the center of each tile of the grid
antennas.xml	MNO	Contains technical parameters of each antenna
simulation.xml	NSO, MNO	Gives some general parameters such as start time, end time, time increment, etc.

3

The data acquisition and preprocessing layer

3.1. MNO data

Network events data ensure the operation of the network but as far as we know they are either not currently stored in by any MNO or need some investment to be used for statistical purposes. So, the first step in implementing our methodological approach would be to design an acquisition system for the network events. Such a system is technology dependent (GSM, UMTS, LTE, ...) and can only be designed and put in place by the MNO itself. The network events are usually captured at the interfaces of the core network by means of installing network probes (Ostermayer et al., 2016). At least the following variables should be saved:

- timestamp - the exact time instant when the event was captured;
- deviceID - a unique identifier of the mobile device that generated the event (could be for example IMEI);
- antenna/cell ID - uniquely identifies the antenna (cell) the mobile device is currently connected to;
- event - a code for the captured event.

The network events data sets tend to be very large therefore it is likely that specific big data technologies such as a NoSQL database or the Hadoop Distributed File System should be used to store these data (Lyko et al., 2016). There are technical solutions to interface such systems with R to allow data processing: see for example the `nodbi R` package Chamberlain et al. (2019) that allows R to interact with `MongoDB`, `Redis`, `CouchDB`, `Elasticsearch`, `SQLite` or more specialized packages such as `mongolite` Ooms (2014) package allowing an `R-mongodb` interface, `R4CouchDB` Bock (2017) allowing R to access `CouchDB`, `RCassandra` provinding an interfce between R and Apache Cassandra or `rhdfs` package that allows R to access files on a HDFS. An overview of the data acquisition process for network events can be found by Wang et al. (2017).

Once acquired, the network events should be depersonalised and preprocessed to be brought in a usable form for our statistical needs. The term mobile network data for statistical purposes makes reference to an abstraction which should be given a concrete substantiation within the extraordinarily complex data ecosystem associated to cellular telecommunication networks. All MNOs tend to underline the resources needed to preprocess and prepare data for statistical purposes, therefore a clear win-win partnership should be put in place between NSIs and MNOs.

Although there are technologies borrowed from the Privacy-Preserving Computation Techniques area like the Secure Multi Party Computation technique that could allow NSIs to process the network events data remotely in a secure environment currently, we envisage that execution of almost all modules should be conducted by MNOs in their own premises.

3.2. Synthetic data

The use of synthetic data to develop the implementation of the processes and the validation of the methodology is not only a matter of the lack of real data. Synthetic data are essential to check that every step of the process is executed as expected and to have the possibility to compare the possible methods againts the reality. With the aim to build synthetic dataset it has been crucial the usage of a simulator.

3.2.1. The simulation software

A simulator for network event data has already been developed as it is described in Oancea et al. (2019). This tool has given the opportunity to deal with synthetic data that come from scenarios with real characteristics. Figure 3.1 shows a schematic view of the data flow in the process of generating synthetic network events data.

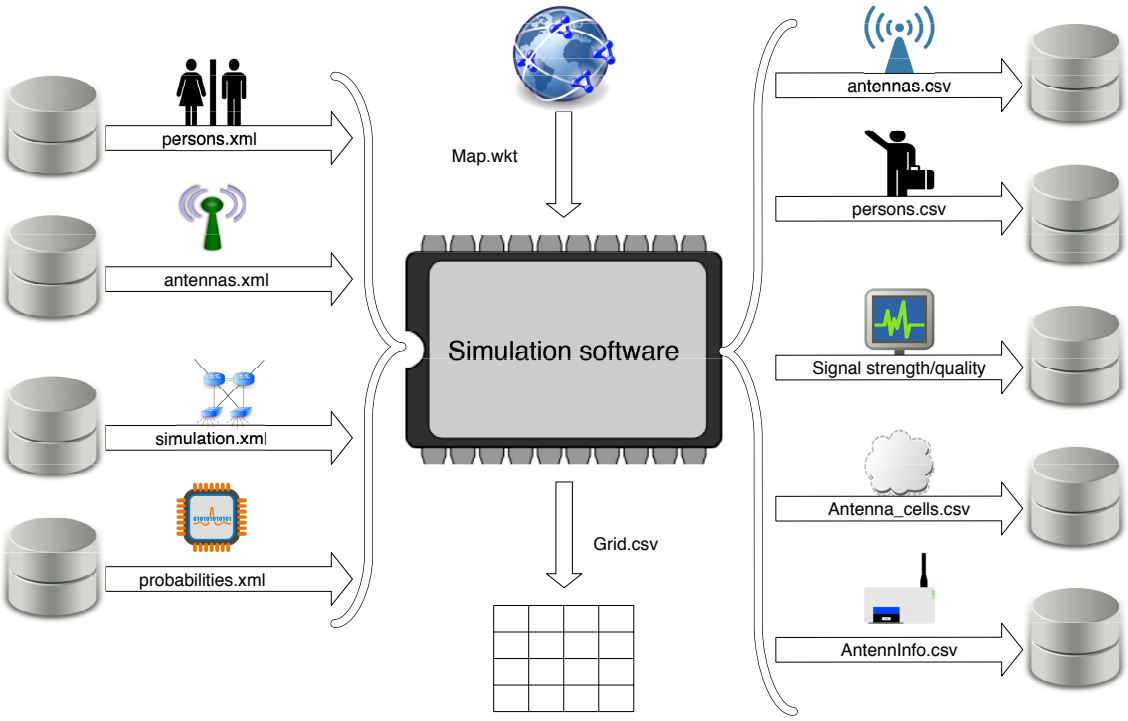


Figure 3.1: Data flow diagram

The simulation software takes as input a series of configuration files:

- a Map file - it is the map where the simulation take place. It is given as a *WKT* file that contains only the external boundary of the geographical area of concern;
- a file with the general parameters of the synthetic population - named `persons.xml` in Figure 3.1 which contains information like the number of persons in the synthetic population, the age distribution, the share of males/females, the speed of the displacement, the share of the population starting from the same initial position in each simulation;
- a file with the location and the technical parameters of the antennas needed to compute the signal strength or signal quality/dominance;
- a file with parameters for the simulation process. This file define the general parameters of the simulation: the initial and the final time instant of the simulation as well as the time increment, information about the mobile network operators, the type of the displacement of persons, the type of the handover mechanism, the dimensions of a tile in the grid and the name of some of the output files;
- an optional file that provides information necessary to compute the location probabilities of the mobile devices. These probabilities were used only in the initial process of development, now the `destim` package provides a more accurate estimation of them.

The software outputs the synthetic information generated during the simulation in `csv` files:

- a grid file that contains the full description of the rectangular grid overlapped on the map, named `grid.csv` in Figure 3.1;
- a file that stores the antennas location on the map at the initial time instant, named `antennas.csv` in Figure 3.1;
- a file that contains the exact position on the map and grid of each person, at each time instant of the simulation, named `persons.csv` in the same figure. The role of this file was essential in the process of developing the methodological framework because it provides "the ground truth" allowing us to estimate the accuracy of our methods. Such information is not available for real MNO data, therefore we emphasize again the importance of the simulation software;
- a file where the signal strength / quality is saved, depending on the handover mechanism used. The signal strength / quality is computed in the center of each tile of the grid named `SignalMeasure.csv`;
- a file that contains the coverage areas for each antenna, named `AntennaCells_[MNOname].csv` in Figure 3.1;
- a file that contains the events generated by the interaction between mobile devices and antennas, together with the exact location of the mobile devices that generated the events, named `AntennaInfo_MNO_[name].csv` in Figure 3.1.

Some of these configuration and output files (`simulation.xml`, `antennas.xml`, `AntennaInfo_[MNOname].csv`, `AntennaCells_[MNOname].csv`, `SignalMeasure.csv`) are used by the R packages (see also table 2.2).

A full description of the simulation software was already provided by Oancea et al. (2019). The software is freely available in the form of the source code together with the makefile necessary to build the executable at the following address: `https://github.com/MobilePhoneESSnetBigData/simulator`. To facilitate the process of installing and running the program we also provide a docker image.

3.2.2. Simulation scenarios

Name of the scenarios: scenario_1_2_3_4_5_6

1. *number of antennas*: total number of antennas in the net.
2. *type connection*: *strength* or *quality*.
3. *tile size*: in meters.
4. *movement type*: *drift* in case of random_walk_closed_map_drift or *nodrift* in case of random_walk_closed_map.
5. *number of persons*: total number of persons in the population (with and without device).
6. *speed car*: in meter per second. Remember this is in mean speed, not the maximum speed.

At the time to build a good scenario there are some points to avoid:

Lack of signal: It can appear in two ways.

- *Useless Antennas.* Many antennas are like deactivated because their signal is too low then there is no tile from which a device can be connected to them.
- *Tiles without coverage.* There are some tiles inside the map where no signal is received from any antenna.

Excessive domination of one antenna. If some antenna is dominating a large part of the territory, it causes problems in several steps. In the case of geolocation, in the area of coverage of this antenna the accuracy is much worse. In the case of duplicity detection, it causes an increase in the rate of false positive. Since all devices connected to this antenna seems to be mistakenly from the same individual.

Several scenarios have been built with the aim to study the behaviour of the developed methodology. However, there is one scenario that has been used more deeply, scenario 1, explained below. After this scenario just a mention to other possibilities but without results shown in this document.

3.2.2.1. Scenario 1: scenario_70_strength_250_drift_500_16

This scenario has been built with the aim of correct the problems detected in scenario 0. In this case there are two types of zones but not so different. In the left upper corner there is a semi-urban area while in the right bottom corner there is a urban area.

Table 3.1: Main characteristics of the scenario 1

No. Antennas with signal	70
No. Directional antennas	3
Tile size (m)	250
No. Tiles	1600
No. Tiles without signal	0
Tiles without signal inside the map	no

The Figure 3.2 shows the signal strength (RSS) of each antenna in green with different intensity of the colour depending on the strength. Over that the coverage area of each antenna is

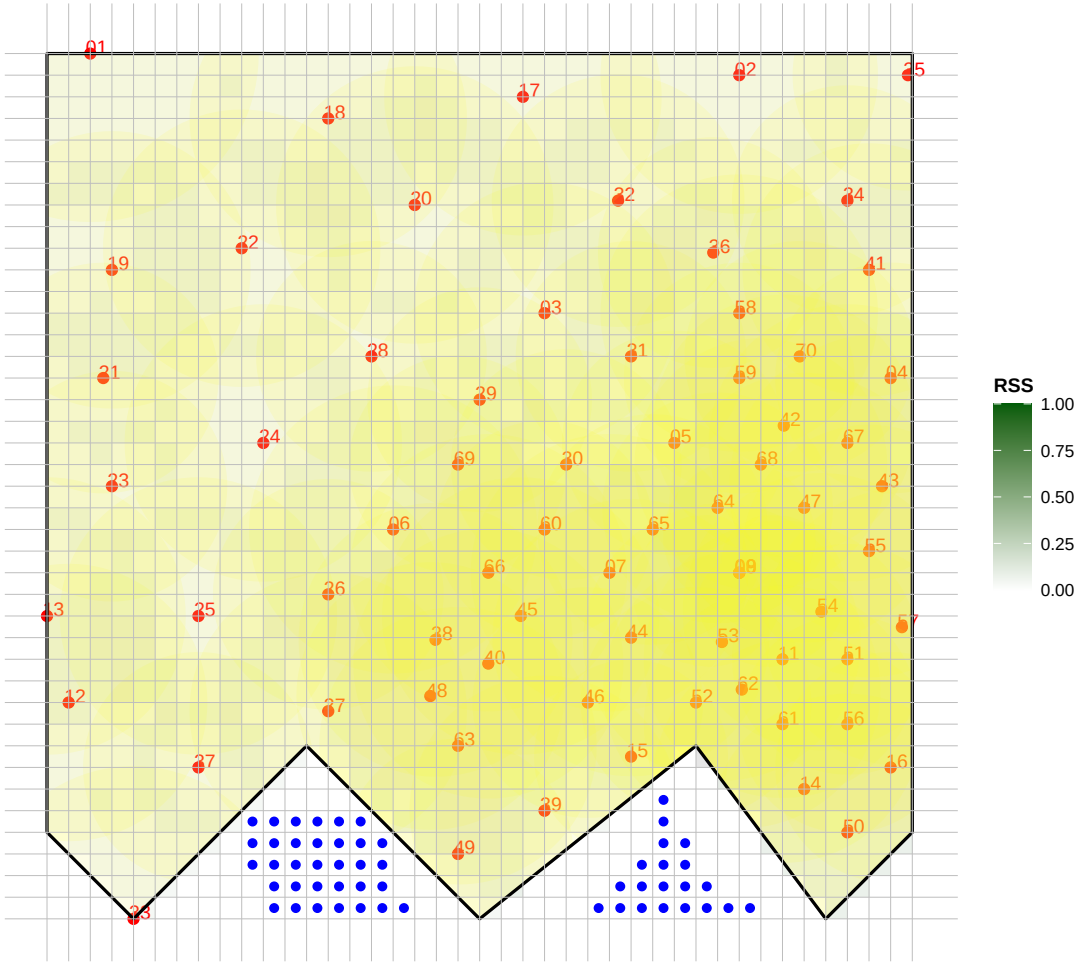


Figure 3.2: Antennas with signal and Tiles without signal

represented in yellow. All the antennas that give some signal to some tile are drawn in red with their corresponding label. The antennas without signal would be represented just with a dot point in black. Moreover, all the tiles without any signal from any antenna are marked with a blue dot point.

One can observe that there is no antennas deactivated and there is no tiles without coverage inside the map.

3.2.2.2. Scenario 2: scenario_20_strength_250_drift_500_16

This scenario will be built with the aim of analyse a territory with low density of antennas. Some different areas will be represented but paying attention to avoid the possible domination of any antenna.

Table 3.2: Main characteristics of the scenario 2

No. Antennas with signal	20
No. Directional antennas	3
Tile size (m)	250
No. Tiles	1600
No. Tiles without signal	0

3.2.2.3. Scenario 3: scenario_150_strength_250_drift_500_16

This scenario will be built with the aim of analyse a territory with high density of antennas. Some different areas will be represented but paying attention to avoid that some antennas are useless due to lack of giving signal to any tile or to have the whole domination of another neighbour antenna.

Table 3.3: Main characteristics of the scenario 3

No. Antennas with signal	150
No. Directional antennas	9
Tile size (m)	250
No. Tiles	1600
No. Tiles without signal	0

4

The geolocation layer

4.1. Introduction

In this chapter, the estimation of the spatial distribution of the devices is shown by following the methodology explained by Salgado et al. (2020) and by using the implementation done in the `R` package `destim` (Sanguiao et al., 2020). We illustrate the construction and adaptation of a hidden Markov model (HMM) to estimate the geolocation of a mobile device d in a reference grid. In sections 4.2 and 4.3 we give some insights on each computational step, showing how to use `destim` functions step by step for each stage of the location probabilities computation and in section 4.4 we provide an end-to-end `R` script that starts from input data and produces the location probabilities.

First, some remarks about the notation of the basic elements in our model. $T_d(t)$ is a random variable that represents the reference grid tiles where the device d is located at time t. They are the state (latent) variables in the HMM. The observed variables are the events in the network denoted as $E_d(t)$ which are the identification of the antenna connecting to the mobile device d at time t. The target quantities will be the probability mass functions associated to each random variable $T_d(t)$ and the joint probability functions for two consecutive time instants t and t'. Any auxiliary information will be denoted by $\mathbf{I}^{\text{aux}}$.

Thus, in mathematical terms, we shall focus on:

$$\gamma_{dti} \equiv \mathbb{P}\left(T_{di}(t)|\mathbf{E}_d, \mathbf{I}^{\text{aux}}\right) = \mathbb{P}\left(T_d(t) = i|\mathbf{E}_d, \mathbf{I}^{\text{aux}}\right) \tag{4.1a}$$

$$\gamma_{dtij} \equiv \mathbb{P}\left(T_{di}(t), T_{dj}(t')|\mathbf{E}_d, \mathbf{I}^{\text{aux}}\right) = \mathbb{P}\left(T_d(t) = i, T_d(t') = j|\mathbf{E}_d, \mathbf{I}^{\text{aux}}\right). \tag{4.1b}$$

We convene in calling (4.1a) **location probability** for mobile device d to be in tile i at time t and calling (4.1b) **joint location probability** for mobile device d to be in tiles i and j in consecutive time instants t and t'.

The estimation of the target variables is done with the procedure explained in the following stepwise procedure:

1. Model construction.
    - HMM initialization
    - Time discretization and reduction of parameters
    - Construction of the emission model

- Construction of the transition model

2. Model fitting.
   - Computation of the likelihood
   - Parameter estimation (likelihood maximization)
   - Posterior location probabilities estimation
   - The initial probability distribution

4.2. Model construction

In this section, we show how to use the functions in the R package **destim** for the geolocation of mobile devices. We will use the simulation with 70 antennas, see the simulation scenarios description in chapter 3.

4.2.1. HMM initialization

The representation of the territory is done in the model by using a grid. Then, the first step is to create a basic grid model. In our simulation scenario, we read the grid parameters from the simulation specification file:

```
gridParam <- fread('grid.csv', sep = ',', header = TRUE, stringAsFactors=FALSE)
ncol_grid <- gridParam[['No Tiles Y']]
nrow_grid <- gridParam[['No Tiles X']]
xDim_grid <- gridParam[['X Tile Dim']]
yDim_grid <- gridParam[['Y Tile Dim']]
```

Then, we use the function `HMMrectangle` of the package destim to create a rectangle model. This model represents a rectangular grid with square tiles, where you can only stay in the same tile or go to a contiguous tile. This means that there are nine non zero transition probabilities by tile. Moreover, horizontal and vertical transitions have the same probability, and diagonal transitions also have the same probability (but different to vertical and horizontal).

The number of transitions can be very high even for small rectangles. Let us suppose a small rectangle of 10x10 tiles, it would have 784 transitions. Fortunatelly, we only need to fit two free parameters as it is explained in the following. Note that the number of constraints plus the number of free parameters agrees with the number of transitions.

In the present example, with the simulation of 70 antennas, a rectangular grid model of 40x40 tiles is created over the territory as follows:

```
c(nrow_grid, ncol_grid)
#> [1] 40 40
model <- HMMrectangle(nrow_grid, ncol_grid)
```

4.2.2. Time discretization and reduction of parameters

In practice, the package allows any linear constraint between the transition probabilities. There is also some support for non linear constraints.

Thus, we can use constraints to reduce the number of parameters as much as wanted. It is a good idea to keep small the number of (free) parameters: on one hand the likelihood optimization becomes less computationally expensive and on the other hand we get a more parsimonious model.

Let us see how to use the time discretization to have a reduction of parameters. The idea is based on the relation of the following three parameters, (i) the tile dimension l (we assume a square grid for simplicity), (ii) the time increment Δt between two consecutive instances, and (iii) an upper bound $v_{\max}$ for the velocity of the individuals in the population.

If we denote by N_T the number of tiles, we are going to have not less than N_T states, and for more complex models possibly more, so let us say we have $O(N_T)$ states. In a hidden Markov model, this means that we have $O(N_T^2)$ transition probabilities to estimate. Of course, this is not viable, so we are going to fix all transition probabilities to non-contiguous tiles to 0. With this aim, we impose that in the time interval Δt, the device d at most can displace from one tile to a contiguous tile. Under this condition, we can trivially set $\Delta t \lesssim \frac{l}{v_{\max}}$. For example, if $v_{\max} = 150\text{km/h} \approx 42\text{ms}^{-1}$, then $\Delta t \lesssim \frac{100}{42} \approx 2\text{s}$.

In real data, this restriction may not be fulfilled, for example in case that in the dataset the device d is detected at longer time periods, e.g. once in a minute. Then we carry out *time padding*, i.e. the artificial introduction of some missing values between every two observed values.

```
vMax_kmh <- 150
vMax_ms <- vMax_kmh * 1000 / 3600
timeIncrem <- 10
distMax <- vMax_ms * timeIncrem
pad_coef <- as.integer(ceiling(distMax / max(xDim_grid, yDim_grid))) + 1

events.dt <- fread('AntennaInfo_MNO_MNO1.csv',sep = ',',stringAsFactors = FALSE,
colClasses=c('integer', 'character', 'character','character',
'numeric', 'numeric', 'character'))
antennas_deviceID <- unlist(events.dt[deviceID == "103", c("antennaID")])

antennas_deviceID_pad <- rep(NA, pad_coef * length(antennas_deviceID))
antennas_deviceID_pad[seq(1,
length(antennas_deviceID_pad), by = pad_coef)] <- antennas_deviceID
antennas_deviceID[1:5]
#> antennaID1 antennaID2 antennaID3 antennaID4 antennaID5
#>       "33"       "33"       "33"       "33"       "33"
antennas_deviceID_pad[1:15]
#>  [1] "33" NA   NA   "33" NA   NA   "33" NA   NA   "33" NA   NA   "33" NA
#> [15] NA
```

4.2.3. Construction of the emission model

Up to this point we have as input data the sequence of observed and missing values $a_{t_n} \in \{0, 1, \ldots, N_A\}$ for $t_n = 0, 1, \ldots, T$ where N_A denotes the number of antennas in the geographical territory under analysis (0 stands for the missing value). The emission model is specified by the HMM emission probabilities $b_{ia} = \mathbb{P}\left(E_{t_n} = a \middle| T_{t_n} = i\right)$, where a stands for the antenna ID and i denotes the tile index. They constitute the entries of the emission matrix B. At most we need to compute $N_T \times N_A$ emission probabilities to conform the matrix $B = [b_{ia}]$,

$i = 1, \ldots, N_T$, $a = 1, \ldots, N_A$. This is done once and for all t (since we assume time homogeneity). Then, the computational cost of the emission probabilities is fixed in time.

Now, to compute b_{ia} we borrow the use of the simplified radio propagation model from the static analysis (see Tennekes et al., 2020) so that we can compute numerically these probabilities. Again, this is a modelling choice and several options could be possibly considered (see Appendix A of Salgado et al., 2020).

If missing values are to be used according to the preceding section, *for numerical convenience later on* the corresponding emission probabilities can be conveniently set to 1, i.e. $b_{i0} = \mathbb{P}\left(E_{t_n} = 0 \middle| T_{t_n} = i\right) = 1$. This will greatly facilitate the expression of the HMM likelihood and its further optimization. Remind that this probability is not real and is completely meaningless.

Notice that having the numerical values of the emission probabilities will allow us to simplify the computation of the likelihood for the HMMs reducing its parameter dependency only to the transition model.

Returning to the code, the emission probabilities are also stored in a matrix. Of course, the number of actually observed events is expected to be much smaller than the number of possible events (all antennas in the network). It could happen, though, that the number of columns of the emissions matrix matches the number of actually observed events. This way we do not save memory with the matrix, but it allows us to do the estimations. Note that, in particular, if any possible event corresponds to a column of the matrix of emissions, each row sums to 1. This does not happen in general, as the columns do not need to be exhaustive.

As we have not specified the emission probabilities in the HMM object created, they are set to NULL by default.

```
emissions(model)
#> NULL
```

Emission probabilities are expected to be computed separately, so the model is ready to directly insert the emissions matrix. We build the emission matrix based on the radio propagation model of our choice. Let us see an example of how to build the matrix from a data.table containing information about the radio propagation model.

```
RSS.dt <- fread('SignalMeasure.csv',sep = ',',
header = TRUE, stringAsFactors = FALSE)
RSS.dt
#>          antennaID tile     RSS       SDM  RSS_ori      SDM_ori nAntCover
#>       1:        01 1560 -75.198 0.5989279  -75.198 5.989279e-01         1
#>       2:        02 1560      NA        NA -112.091 7.867742e-12         1
#>       3:        03 1560      NA        NA -109.399 3.228188e-12         1
#>       4:        04 1560      NA        NA -120.112 2.097113e-16         1
#>       5:        05 1560      NA        NA -117.471 2.504505e-14         1
#>      ---
#> 111996:        66   39      NA        NA -107.986 1.151466e-11         1
#> 111997:        67   39      NA        NA -105.883 7.642586e-11         1
#> 111998:        68   39      NA        NA -107.646 1.563671e-11         1
#> 111999:        69   39      NA        NA -115.541 1.283116e-14         1
#> 112000:        70   39      NA        NA -112.674 1.693854e-13         1
```

```
#>          rasterCell
#>       1:          1
#>       2:          1
#>       3:          1
#>       4:          1
#>       5:          1
#>      ---
#>  111996:       1600
#>  111997:       1600
#>  111998:       1600
#>  111999:       1600
#>  112000:       1600
```

This data.table named `RSS.dt` provides the following variables:

- column `antennaID`: identification of the antenna for which we provide the radio propagation model information.
- column `tile`: identification of the tile for which we provide the radio propagation model information.
- column `RSS_ori`: signal strength (in dBm) from the corresponding antenna at the center of the corresponding tile according to the RSS model.
- column `RSS`: same value as `RSS_ori` when the strength is above the chosen threshold in the specification files; `NA` otherwise.
- column `SDM_ori`: signal dominance measure from the corresponding antenna at the center of the corresponding tile according to the SDM model.
- column `SDM`: same value as `SDM_ori` when the signal dominance measure is above the chosen threshold in the specification files; `NA` otherwise.
- column `rasterCell`: equivalent numbering of the tiles according to the package `raster`.

Then, the probabilities are obtained and the emission matrix is built as follows:

```
emissionProbs.dt <- RSS.dt[
  , watt := 10**((RSS - 30) / 10 )][
      , eventLoc := watt / sum(watt, na.rm = TRUE), by = 'rasterCell'][
is.na(eventLoc), eventLoc := 0][
      , watt := NULL]
emissionProbs.dt <- emissionProbs.dt[
    , c("antennaID", "rasterCell", "eventLoc"), with = FALSE][
order(antennaID, rasterCell)]

frmla <- paste0(c('rasterCell', 'antennaID'), collapse = ' ~ ')
emissionProbs.mat <- as.matrix(
dcast(emissionProbs.dt,  as.formula(frmla), value.var = 'eventLoc')[
    , rasterCell := NULL]
  )
dimnames(emissionProbs.mat) <- list(
as.character(unique(emissionProbs.dt[['rasterCell']])),
as.character(unique(emissionProbs.dt[['antennaID']])))
dim(emissionProbs.dt)
#> [1] 112000      3
emissionProbs.dt
#>          antennaID rasterCell eventLoc
#>       1:        01          1        1
#>       2:        01          2        1
```

```
#>       3:         01           3         1
#>       4:         01           4         1
#>       5:         01           5         1
#>      ---
#> 111996:         70        1596         0
#> 111997:         70        1597         0
#> 111998:         70        1598         0
#> 111999:         70        1599         0
#> 112000:         70        1600         0
```

The number of rows arise from the number of different events (70 different antennas) and the number of tiles (1600). The inclusion of missing values for the time padding is dealt with internally during the fitting. The assignment to the model is immediate.

```
emissions(model) <- emissionProbs.mat
```

Of course, in practice, models will have many states and will be created automatically. While the purpose of the package `destim` is estimation and not automatic modeling (at least for the moment), some functions have been added to ease the construction of example models.

A very simple function to create emissions matrices is also provided. It is called `createEM` and the observation events are just connections to a specific antenna. The input parameters are the dimensions of the rectangle, the location of towers (in grid units) and the distance decay function of the signal strength (Tennekes et al., 2020). In this case, each tile is required to be able to connect to at least one antenna, so no out-of-coverage tiles are allowed. Note that this is not a requirement for the model, just a limitation of the function `createEM`.

If the case were a network of 7 antennas, the creation of the emission matrix can be done as follows:

```
tws <- matrix(c(3.2, 6.1, 2.2, 5.7, 5.9, 9.3, 5.4,
4.0, 2.9, 8.6, 6.9, 6.2, 9.7, 1.3),
nrow = 2, ncol = 7)
S <- function(x) if (x > 5) return(0) else return(20*log(5/x))
emissionProbs.mat2 <- createEM(c(nrow_grid, ncol_grid), tws, S)
dim(emissionProbs.mat2)
#> [1] 1600    7
```

4.2.4. Construction of the transition model

Now we specify a model for the transition between states (tiles in our simple rectangular model). Let $A = [a_{ij}]$ be the transition matrix, with $a_{ij} = \mathbb{P}\left(T_{jt} | T_{it}\right)$. In order to obtain the elements of this matrix, we make use of our preceding imposition by which an individual can at most reach a contiguous tile in each contiguous time. Then, to model these transitions rectangular isotropic conditions are imposed. Let θ_1 be the probability of vertical/horizontal transition and θ_2 the probability of diagonal transition, as represented in Figure˜4.1. Moreover, row-stochasticity conditions have to be fulfilled as well.

All these conditions lead to having a highly sparse transition matrix A with up to 4 terms equal to θ_1 and θ_2 (each) per row and diagonal entries guaranteeing row-stochasticity.

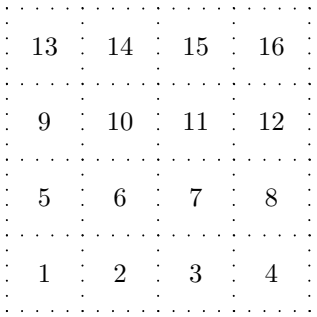


Figure 4.1: Example with a regular square grid of dimensions 4×4.

For a detailed explanation of the elements of the transition matrix (see Appendix A of Salgado et al., 2020).

Returning to the code, we can see that there are as many states as tiles (nrows*ncols) in the grid and the corresponding transitions to all possible movements in the grid, consecutive tiles.

```
nstates(model)
#> [1] 1600
ntransitions(model)
#> [1] 13924
```

The transitions with non zero probability are represented by an integer matrix with two rows, where each column is a transition. The first row is the initial state and the second the final state. Of course, the states are represented by an integer number. The columns of the matrix are ordered first by initial state and then by final state.

```
transitions(model)[1:2, 1:10]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10]
#> [1,]    1    1    1    1    2    2    2    2    2     2
#> [2,]    1    2   41   42    1    2    3   41   42    43
```

The constraints can be shown by using `constraints(model)`. As we have not specified any constraints, one constraint by state is introduced, the sum of the transition probabilities for a given initial state has to be one (row-stochasticity of the transition matrix). Otherwise, the transition matrix would not be stochastic. In general, the package adjusts this specific kind of constraints automatically.

The constraints are represented as the augmented matrix of a linear system of equations. The transition probabilities must fulfill the equations, with the same order as shown in transitions function. So, the first coefficient in each row is for the transition probability of the transition shown in the first row of the matrix of transitions, and so on.

Both transitions and constraints can be specified as parameters when creating the model. It is also possible to add transitions and constraints later. Let us suposse that we add the following transitions:

```
model0 <- addtransition(model, c(1,22))
model0 <- addtransition(model0, c(2,33))
transitions(model0)[, 1:12]
#>      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
```

```
#> [1,]    1    1    1    1    1    2    2    2    2    2    2    2
#> [2,]    1    2   22   41   42    1    2    3   33   41   42   43
```

Now it becomes possible to transition from state 1 to state 22, and from state 2 to state 33.

Moreover, we can add constraints to the model. The constraints matrix is a row major sparse matrix. The function to add new constraints is `addconstraint` whose second argument can be a vector or a matrix. If it is a vector, it is expected to be a set of transition probabilities indexed as in field transitions of the model. In this case the constraint added is the equality between the referred probabilities of transition. The purpose of these *equality constraints* is to improve performance as they might be a lot and can be treated easily.

If the second argument is a matrix, it is expected to be a system of additional linear equalities that the model must fulfill. Thus, the new equations are added to the field constraints of the model. While it is possible to use a matrix to add equality constraints, it is not recommended because of performance. In any case, previous constraints of the model are preserved.

Now, an example of how an equality constraint is added. In this case the second transition probability is equal to the fourth one. In the matrix of transitions we can see that those transitions represent: transition 2 is from state 1 to state 2 and transition 3 is from state 1 to state 22. Then, to add the equality constraint that relate these two transitions is done as follows:

```
dim(constraints(model0))
#> [1] 13922 13927
model0 <- addconstraint(model0, c(2, 3))
dim(constraints(model0))
#> [1] 13923 13927
```

Once the model is fitted, the values of the transition matrix can be obtained from the HMM object in the element names as `model$parameters$transitions`. This is a vector with the values corresponding to each column of the matrix `transitions(model)`.

4.3. Fitting the model

Once we have defined an appropriate model for our problem, the next step is to estimate the free parameters. As it has been already stated, emissions are known, so there are no emission parameters to fit. The initial state is either fixed or set to the steady state, thus the only parameters to fit in practice are the transition probabilities.

The method used to estimate the parameters is maximum likelihood, and the forward algorithm computes the (minus) log-likelihood. A constrained optimization is then done. Note that the EM algorithm is generally not a good choice for constrained problems, so it is not used in the package `destim`. Let us see in detail how the model is fitted.

4.3.1. Parameter estimation

The estimation of the unknown parameters $\boldsymbol{\theta} = (\theta_1, \theta_2$ is conducted maximizing the likelihood. The restrictions coming from the transition model makes the optimization problem not trivial. Notice that the EM algorithm is not useful. Instead, we provide a taylor-made solution seeking for future generalizations with more realistic choices of transition probabilities incorporating land use information. Formally, the optimization problem is given by:

$$\begin{aligned} \max \quad & h(\mathbf{a}) \\ \text{s.t.} \quad & C \cdot \mathbf{a} = \mathbf{b} \ , \\ & \mathbf{a} \in [0,1]^d, \end{aligned} \tag{4.2}$$

where $\mathbf{a}$ stands for the nonnull entries of the transition probability matrix A, the objective function $h(\mathbf{a})$ is derived from the likelihood L, see the following section for more detail, expressed in terms of the nonnull entries of the transition matrix A, and the system $C \cdot \mathbf{a} = \mathbf{b}$ expresses the sets of restrictions from the transition model (see Appendix A of Salgado et al., 2020).

The number of restrictions n_r not involving zeroes depends very sensitively on the particular transition model chosen for the displacements. Then, we have that $C \in \mathbb{R}^{n_r \times d}$ and $\mathbf{b} \in \mathbb{R}^d$. The objective function $h(\mathbf{a})$ is indeed a polynomial in the non-null entries $\mathbf{a}$.

This problem can be further simplified using the QR matrix decomposition. Write $C = Q \cdot R$, where Q is an orthogonal matrix of dimensions $n_r \times n_r$ and R is an upper triangular matrix of dimensions $n_r \times d$. Then we can rewrite the linear system as $R \cdot \mathbf{a} = Q^T \cdot \mathbf{b}$ and we can linearly solve variables $a_1, \ldots, a_{n_r}$ in terms of variables $a_{n_r+1}, \ldots, a_d$:

$$\begin{pmatrix} a_1 & \cdots & a_{n_r} \end{pmatrix}^T = \tilde{C}_{n_r \times (d-n_r)} \begin{pmatrix} a_{n_r+1} & \cdots & a_d \end{pmatrix}^T .$$

The system (4.2) then reduces to

$$\begin{aligned} \max \quad & \tilde{h}(a_{n_r+1}, \ldots, a_d) \\ \text{s.t.} \quad & 0 \leq \tilde{C} \cdot \begin{pmatrix} a_{n_r+1} & \cdots & a_d \end{pmatrix}^T \leq 1. \end{aligned} \tag{4.3}$$

The solution $\mathbf{a}^*$ to problem (4.2) will be introduced in the transition probability matrix, which will thus be denoted by A^*.

In terms of optimization, all we have to do is a linear constrained non-linear optimization in the same space. The linear constraints may seem to be a lot, but in practice, a good modeling will make most of the constraints equal, as most of the transition probabilities are going to be equal.

Usually, algorithms for constrained optimization will require an initial value in the interior of the feasible region. To get such initial value, the following algorithm is used:

1. Set transition probabilities to independent uniform $(0, 1)$ random variables.
2. Now the constraints do not hold, so the closest point in the constrained space is got through Lagrange multipliers.
3. Now some of the probabilities might be greater than one or smaller than zero. Those are set once again to independent uniforms.
4. Repeat steps 2 and 3 till all transition probabilities are between zero and one.

As already stated, the initial state is set to steady if not fixed. The steady state is calculated as the (normalized to sum up one) solution to $(A - I)x = 0$, where I the identity and the last component of x is set to one divided by its dimension. This should be enough because these Markov chains are expected to be both irreducible and aperiodic, otherwise we would have strange movement restrictions.

Returning to the code, the next step is to estimate the parameters of the model, by constrained maximum likelihood. But first, as already said, the optimizer usually requires an initial guess, so the function initparams obtains an initial random set of parameters.

```
model <- initparams(model)
all(model$parameters$transitions < 1)
#> [1] TRUE
all(model$parameters$transitions > 0)
#> [1] TRUE
range(constraints(model) %*% c(model$parameters$transitions, -1))
#> [1] 0.000000e+00 4.440892e-16
```

All transition probabilities are between zero and one and the constraints hold, but no observed data is still used.

The function minparams reduces the number of parameters of the model to the number of free parameters, as already explained. In the present example, the model has 13924 transitions but the number of parameters is two.

```
model <- minparams(model)
rparams(model)
#> [1] 0.33528506 0.06178254
```

Notice that it does not matter the size of the problem, only two parameters are really needed. It is possible to assign values with `rparams`, as the optimizer does, but some transition probability might move outside the interval $[0, 1]$. The optimization process avoids this problem constraining by linear inequalities.

Now the model is ready to be fitted. Of course, the observed events are needed. Since we have the emissions matrix in the model, the observed events is just an integer vector, that refers to the appropriate column of the emissions matrix. The length of that vector is the number of observed times in a device. It is possible to introduce missing values for the observations as `NA`, obviously when at a time there is no event.

```
obs <- sapply(antennas_deviceID_pad,
function(x) ifelse(!is.na(x),
which (x == colnames(emissionProbs.mat)), NA))
model_dev <- fit(model, obs)
#> Loading required package: Rsolnp
rparams(model_dev)
#> [1] 0.9910131 0.9820262
```

4.3.2. Computation of the likelihood

The likelihood is trivially computed using the numerical proviso of setting emission probabilities equal to 1 when there is a missing value in the observed variables. The general expression

for the likelihood is

$$L(\mathbf{E}) = \sum_{i_0=1}^{N_T} \cdots \sum_{i_T=1}^{N_T} \mathbb{P}\left(T_{t_0} = i_0\right) \prod_{n=1}^{N} \mathbb{P}\left(T_{t_n} = i_n | T_{t_{n-1}} = i_{n-1}\right) \mathbb{P}\left(E_{t_n} \middle| T_{t_n} = i_n\right) \quad (4.4a)$$

$$= \sum_{i_0=1}^{N_T} \cdots \sum_{i_T=1}^{N_T} \mathbb{P}\left(T_{t_0} = i_0\right) \prod_{n=1}^{N} a_{i_{n-1} i_n}(\boldsymbol{\theta}) b_{i_n a_{t_n}} \quad (4.4b)$$

Notice that the emission probabilities only contribute numerically providing no parameter whatsoever to be estimated.

Returning to the code, the function to compute the likelihood for a model and a vector of given observations of events is `logLik`. Despite the name, logLik returns minus the log-likelihood, so the smaller the better.

```
logLik(model, obs)
#> [1] 26.29721
logLik(model_dev, obs)
#> [1] 11.57194
```

4.3.3. Posterior location probabilities estimation

Once the HMM has been fitted, we can readily apply the well-known forward-backward algorithm (Bishop, 2006) to compute the target probabilities γ_{dti} and γ_{dtij} (see equations (4.1)). No novel methodological content is introduced at this point. For our implementation, as suggested by Bishop (2006), we have used the scaled version of the algorithm.

We can estimate the smooth states by means of the forward-backward algorithm. The smooth states are the mass probability function of the states given the observed data (and the model), thus they summarize all the information available for a given time t. So one of the outputs of the package are the smooth states, that can be aggregated to get a space distribution of the number of devices as explained in (section 4.2 of Salgado et al., 2020).

The other main output of the package is the posterior joint mass probability function for two consecutive instants $t, t + \Delta t$ of the states. As it is a posterior probability, it is once again conditioned on all the information available, but it is more dynamic because its time reference is now an interval. A possible analogy would be the smooth positions and speeds of a particle. The former would correspond to position and the later to speed.

These target probabilities are the main output of the geolocation estimation. Both outputs are needed to estimate the target population in next steps of the process as it is shown in the following sections of this document.

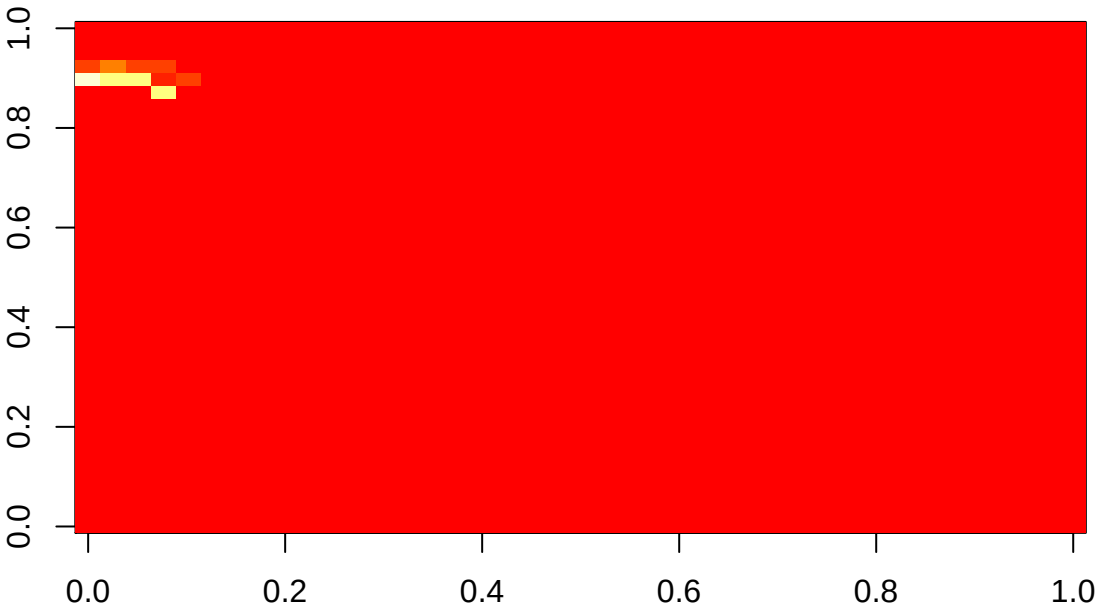
Returning to the code, the function `sstates` returns the smooth states, i.e. the estimation of the posterior location probabilities. The output is given as a matrix of *number of states* $\times$ *number of observations* (missing values included) dimensions, i.e. *number of raster cells* $\times$ *times*. So each column represents the space distribution in its corresponding time slot.

```
postLocP <- sstates(model_dev, obs)

dim(postLocP)
#> [1] 1600  270

image(matrix(postLocP[, 4], ncol = ncol_grid))
```

The function scpstates returns the (smooth) joint probability mass function for consecutive states, analogous to the usually denoted ξ_{ij} probabilities in the Baum-Welch algorithm (once convergence is achieved). The result is a matrix with the raster cells in the rows and the raster cells per time in the columns. Then, each set of columns corresponding to the same time represents a space bi-variant distribution matrix. The probability of the consecutive pair of states (i, j) from time t to $t + \Delta t$ can be found in the row i and column $(t - 1) * N_T + j$. The transition matrix only allows transitions to contiguous points, so it is *almost* diagonal per blocks of times.

```
postJointLocP <- scpstates(model, obs)
dim(postJointLocP)
#> [1]   1600 430400
```

It is difficult to visualize these probabilities in two dimensions.



4.3.4. The initial probability distribution

The initial probability distribution $\mathbb{P}(T_{t_0})$ has not been specified yet. With abundance of data, it has very little incidence on the final results. In our implementation two options are provided: (i) the stationary state, i.e. the eigenvector of A with eigenvalue 1 and (ii) any distribution provided by the user. The difference will be ultimately in terms of computational cost (provided

we have abundance of data).

Returning to the code, let us see in the present example how to fit the model with two different initial probability distribution: the default uniform distribution and the so-called network distribution (see Tennekes et al., 2020). The uniform is equivalent to the previous executions and the network is obtained by using the information in the network about the signal strength of the antennas.

First, we prepare the initial distribution vectors.

```
nTiles <- ncol_grid * nrow_grid
initialDistr_RSS_uniform.vec <- rep(1 / nTiles, nTiles)

initialDistr_RSS_network.dt <- RSS.dt[
  , watt := 10**( (RSS - 30) / 10 )][
    , total := sum(watt, na.rm = TRUE)][
      , list(num = sum(watt, na.rm = TRUE), total = unique(total)),
                                                    by = 'rasterCell'][
        , prior_network := num / total][
order(rasterCell)]
initialDistr_RSS_network.vec <- initialDistr_RSS_network.dt$prior_network
```

Then, we create both models and assign the corresponding initial distributions.

```
model_network <- model
model_uniform <- model

istates(model_network) <- initialDistr_RSS_network.vec
istates(model_uniform) <- initialDistr_RSS_uniform.vec
```

4.4. An end to end example

We provide below an integrated script that exemplifies how to use this package to produce the location probabilities starting from the input data. To keep the size of the script reasonable small we've made some simplifying assumptions: we considered that the emission probabilities are computed using the signal strength and we used uniform prior location probabilities. There are also two functions that we used but we didn't provide here their code: `tileEquivalence()` and `transform_postLoc()`. The first function builds a table of equivalence between the numbering system used by the simulation software for tiles and the one used by the `raster` package. The second one mainly transforms the dense format of the matrices storing the location probabilities and joint location probabilities into the sparse matrix format already described in chapter 2. The input data used by this script are provided by the simulation software. We use the same file names as described in table 2.2.

```
library(data.table)
library(tidyr)
library(destim)
library(stringr)
library(Matrix)
library(xml2)

source('transform_postLoc.R')
```

```
source('tileEquivalence.R')

# set file names
fileGridName       <- 'grid.csv'
fileEventsInfoName <- 'AntennaInfo_MNO_MNO1.csv'
signalFileName <- 'SignalMeasure_MNO1.csv'
simulationFileName <- 'simulation.xml'

# read simulation params
simulation.xml  <- as_list(read_xml(simulationFileName))
simulation.xml <- simulation.xml$simulation
start_time <- as.numeric(simulation.xml$start_time)
end_time <- as.numeric(simulation.xml$end_time)
time_increment <- as.numeric(simulation.xml$time_increment)
times <-
  seq(from = start_time,
        to = (end_time - time_increment),
        by = time_increment)
sigMin <- as.numeric(simulation.xml$conn_threshold)

# read grid params
gridParam <-   fread( 'grid.csv', sep = ',', header = TRUE,
                      stringsAsFactors = FALSE)
ncol_grid  <- gridParam[['No Tiles Y']]
nrow_grid  <- gridParam[['No Tiles X']]
tile_sizeX <- gridParam[['X Tile Dim']]
tile_sizeY <- gridParam[['Y Tile Dim']]
ntiles     <- ncol_grid * nrow_grid

# tile-rasterCell equivalence
tileEquiv.dt <- data.table(tileEquivalence(ncol_grid, nrow_grid))

# read Received Signal Strength file and compute emission probabilities
RSS <-
  fread(signalFileName, sep = ",", header = TRUE, stringsAsFactors = FALSE )
setnames(RSS, c('antennaID', 0:(ntiles - 1)))
RSS <- melt(RSS,id.vars = 'antennaID',variable.name = 'tile',
               variable.factor = FALSE,value.name = 'RSS')
RSS[, RSS := ifelse(RSS < sigMin, NA, RSS)]

# compute event location (emission probabilities)
RSS <-
  RSS[, eventLoc := 10 ** RSS / sum(10 ** RSS, na.rm = TRUE), by = 'tile']
RSS <- RSS[is.na(eventLoc), eventLoc := 0]
RSS[, tile := as.numeric(tile)]
RSS <- RSS[tileEquiv.dt, on = 'tile'][, tile := NULL]
RSS <-
  dcast(RSS, rasterCell ~ antennaID, value.var = 'eventLoc')[, rasterCell :=
 NULL]
emissionProbs <- Matrix(data = as.matrix(RSS))
dimnames(emissionProbs)[[1]] <-as.character(1:dim(emissionProbs)[1])

# read and process network event data
allEvents.dt <- fread( fileEventsInfoName,sep = ',',stringsAsFactors = FALSE,
                       colClasses = c('integer','character','character',
                       'character','numeric','numeric','character'))
```

```
allEvents.dt <- allEvents.dt[!duplicated(allEvents.dt)]
setnames(allEvents.dt ,
c('time', 'antennaID', 'eventCode', 'device', 'x', 'y', 'tile'))
allEvents.dt[, obsVar := do.call(paste, c(.SD, sep = "-")),
             .SDcols = c('antennaID', 'eventCode')]
events.dt <- allEvents.dt[eventCode %in% c('0', '2', '3')]
events.dt_noDup <- copy(events.dt)[, list(eventCode =
                as.character(min(as.numeric(eventCode)))),
                by = c("time", "device")]
events.dt <- merge(events.dt_noDup, events.dt,by = names(events.dt_noDup),
                all.x = TRUE)
events.dt <- events.dt[!duplicated(events.dt, by =
                c("time", "device", "eventCode"))][,
                .(time, device, eventCode, antennaID, obsVar)][order(time)]

# Set maximum velocity (from an external source)
vMax_ms <- 16
# Set time padding params
distMax <- vMax_ms * time_increment
pad_coef <- as.integer(ceiling(distMax / max(tile_sizeX, tile_sizeY)))
pad_coef <- pad_coef + 1

# Initial state distribution (PRIOR)

# Prepare prior_network distribution (uniform prior)
prior_network <- rep(1 / ntiles, ntiles)

# Initialize HMM
model <- HMMrectangle(nrow_grid, ncol_grid)
emissions(model) <- emissionProbs

model <- initparams(model)   # initialize transition prob
model <- minparams(model)    # parameter reduction according to restrictions
istates(model) <- prior_network

# compute posterior location probabilities
deviceIDs <- sort(unique(events.dt$device))

# for each device
for (i in seq(along = deviceIDs)) {
  devID <- deviceIDs[i]
  cat(paste0('    device ', devID,'...\n'))
  cat(' Selecting network events...')
  events_device.dt <- events.dt[device == devID, .(device, time, antennaID)]
                              [order(device, time)]

  antennas_deviceID  <- unlist(events_device.dt[, c("antennaID")])
  if (!all(is.na(antennas_deviceID))) {
    # Fit and compute HMM model
    observedValues_pad <- rep(NA, pad_coef * length(antennas_deviceID))
    observedValues_pad[seq(1, length(observedValues_pad), by = pad_coef)] <-
      antennas_deviceID
    colEvents <- sapply(observedValues_pad,function(x) ifelse(!is.na(x),
                    which(x == colnames(emissionProbs)), NA))

# Fit HMM - ML estimation of transition probabilities
```

```
    fitTry <- try(model_devID <- fit(model, colEvents, init = TRUE))
    if (inherits(fitTry, "try-error")) {
      stop("Fit model fails")
    }
    ssTry <- try(A <- sstates(model_devID, colEvents))
    if (inherits(ssTry, "try-error")) {
      stop("[compute_HMM] Smooth States fails")
    }
    B <- scpstates(model_devID, colEvents)
# Transform output of the HMM model to sparse matrix file format
    transform_output <- transform_postLoc(
                postLocP = A, postLocJointP = B,
                observedValues = antennas_deviceID,
                times = times,t_increment = time_increment,
                ntiles = ntiles,pad_coef = pad_coef,
                tileEquiv.dt = tileEquiv.dt,
                devID = devID,sparse_postLocP = TRUE,
                sparse_postLocJointP = TRUE)
    rm(A, B)
    gc()
    fwrite(transform_output$postLocProb[, .(tile , time, postLocProb)],
        paste0('postLocProb_', devID,'.csv'),col.names = FALSE,
        row.names = FALSE,sep = ',')
    transform_output$postLocJointProb[, time_to            :=
    time_from + time_increment]
    fwrite(transform_output$postLocJointProb[, .(time_from, time_to,
        tile_from, tile_to, postLocProb)],
        paste0('postLocJointProb_', devID,'.csv'), col.names =FALSE,
        row.names = FALSE,sep = ',')
  }
}
```

4.5. Some remarks about computational efficiency

The package has some degree of optimization, as it uses `Rcpp` and `RcppEigen` (for sparse linear algebra) in some critical functions and the difference in execution speed between C++ code and pure R code is well-known. We choose to use C++ for some computational intensive operations (based on level 3 BLAS operations) like LU factorizations or QR decompositions. For other packages in our hierarchy that also work with (sparse) matrices use the `Matrix` R package because they only perform simple manipulations of rows or columns of these matrices which run fast enough.

It can handle fairly well models with around 10^7 states in a desktop computer (if enough RAM is provided). Some faster sparse linear algebra library (for example Intel MKL) might improve a little bit the performance of such operations. Also, we are going to comment the possibility of improve the performance using parallel computing.

4.5.1. Model construction

As has been already stated, the package is not really ready for model construction, except for the function HMMrectangle, which are very basic models. While it is a rather fast function, its performance can be easily improved as it is an embarrassingly parallel algorithm. This also allows to use a cluster to generate the model.

4.5.2. Model initialization and parametrization

The algorithm used to find an initial value for the optimizer, solves a linear system of equations at each step. While the order of the system grows with the number of transitions and constraints, in practice, most constraints state the equality between two transition probabilities. It is not difficult to get rid of one of the transitions and the constraint in those cases, so in practice the process scales very well for parsimonious models.

Mostly all said for initialization also goes for parametrization, where the QR decomposition is the *slow* step.

4.5.3. Forward-Backward algorithm

This amounts mostly to multiplying sparse matrices, which relies on another library (currently Eigen). Eigen is not the faster library at this moment even on a desktop computer but the performance is not so bad. In the future Intel MKL might be a good choice, and it can also work in distributed mode.

4.5.4. Likelihood optimization

The purpose of all the previous steps is to make easier the task of the optimizer, so it should not be a problem if everything else is fine. Transition probabilities are required to be between zero and one, what in general means O(n) inequality constraints. A well specified parsimonious model, will often have a lot less constraints, as most of them are duplicated. As a reference, an HMMrectangle(20,20) has 3364 transitions and only 5 constraints are needed in practice.

Equalities between transition probabilities would generate duplicated rows in the matrix of inequality constraints which are eliminated before calling the optimizer.

4.5.5. Optimization algorithm

Before fitting the model there is another possibility to make faster the computation. There is a parameter in the function `fit`, named `init` which is logical with FALSE as default. In this case, there is an assignment of the steady state in each evaluation of the optimization. If we assign the steady state to the initial state of the model with the function `inisteady`, and use the argument `init = TRUE` in the fit of the model, there is just one assignment, so it is faster. The code is as simple as follows.

```
model_network <- initsteady(model_network)
model_uniform <- initsteady(model_uniform)

model_devID <- fit(model_network, obs, init = TRUE)
model_devID <- fit(model_uniform, obs, init = TRUE)
```

The optimization algorithm to be used is set in the function `fit` with the argument `method`, which is set by default to `solnp` from package Rsolnp. The other possible choice is `constrOptim` from package stats.

In order to avoid giving a local minimum as solution, there is another parameter that allows the user to execute the optimization several times. The optimizer will be launched with different initial parameters as many times as the number in the argument `retrain`. The model with higher likelihood will be returned.

5

The deduplication layer

5.1. Introduction

In this chapter, it is shown how to deal with the duplicity problem about the unknown fraction of mobile subscribers carrying more than one device. It also contains a brief explanation about the intended use of the R package `deduplication` (Oancea et al., 2020b) and provides a short introduction to the underlaying methodology. The goal will be to compute a device-multiplicity probability $p_d^{(n)}$ for each mobile device d, i.e. the probability that a device d is carried by an individual carrying n devices. A detailed description of the methodological approach implemented by this package is provided by Salgado et al. (2020) and Salgado et al. (2020). To fully understand the theory behind this package it is recommended to read the above mentioned papers.

We start by first presenting a brief theoretical introduction of the methods used to compute the duplicity probabilities (subsections)5.1.1, 5.1.2 and 5.1.3) and then we provide examples on how to use `deduplication` package, step by step, in section 5.2. We also provide an example that shows the easiest way of using this package, mainly by one single function call (`computeDuplicity()`) in subsection 5.3.1. All the examples provided here use some input files that come from the `destim` package (the location probabilities for mobile devices) and from the simulation software (files with the networks events, the signal strength for each tile, the boundary of each cell, the grid paramaters, general simulation parameters). These files are provided with the `deduplication` package but they can be replaced by users with their own files. The name of the files coming from the simulation software are the same as those already presented in table 2.2.

5.1.1. Device duplicity problem

The problem of device multiplicity comes from the fact that the statistical unit of analysis with mobile network data is the individual of a target population, not a mobile device. Since an individual can carry more than one device with him/her, this introduces the problem of multiple counting. For simplicity we make the simplifying assumption that each individual can carry at most 2 devices.

The main purpose is to classify each device d in a dataset as corresponding to an individual with only one device (1:1 correspondence between devices and individuals) or as corresponding to an individual with two devices (2:1 correspondence between devices and individuals). This classification will be probabilistic, thus assigning a probability $p_d^{(n)}$ of duplicity to each device d carrying $n = 1, 2$ devices. The generalization to more devices is just a matter of computational

complexity of this same approach.

Three methodological approaches have been developed and implemented in the `deduplication` package, two approaches based on network events and another based on the distance between centers of location probabilities which compares trajectories. Let see a brief explanation before using the code.

5.1.2. Bayesian approaches based on network events

5.1.2.1. The one-to-one approach

We shall follow a Bayesian hypothesis testing approach. In this case, for each device d we shall consider the disjoint set of hypotheses $\{H_{dd'}\}_{d'=1,\dots,D}$ meaning that the devices d and d' are carried by the same individual. When $d = d'$ this reduces to mobile device d being the only mobile device carried by its corresponding individual. We focus on computing

$$p_d^{(1)} = \mathbb{P}\left(H_{dd} \middle| \mathbf{E}_{d1:T}, \mathbf{I}^{\text{aux}}\right), \tag{5.1}$$

where we are using the same notation as in chapter 4. Since the entire event set Ω_d for device d can be decomposed as $\Omega_d = \bigcup_{d'=1}^{D} H_{dd'}$, we can make use of Bayes' theorem to write:

$$p_d^{(1)} = 1 - \frac{1}{1 + \sum_{d' \neq d} \alpha_{dd'} \cdot \exp\left(\ell_{dd'} - \ell_d\right)}$$

where ℓ_d is the log-likelihood for a single device d and $\ell_{dd'}$ for two devices d and d' and $\alpha_{dd'} = \frac{1-P_1}{P_1}$, P_1 is the a priori probability of 1:1 correspondence for all devices.

The log-likelihood ℓ_d for a single device d corresponds to the HMM model shown in the geolocation chapter. The log-likelihood $\ell_{dd'}$ for two devices d and d' is computed according to the HMM duplicity model represented where the emission probabilities are computed as the product of the original single-device emission probabilities for d and d'.

For the specification of priors the key is the available auxiliary information $\mathbf{I}^{\text{aux}}$. For example, if some auxiliary information at the device level is available (for instance from the Customer Relationship Management database) showing that devices d and any other d' reside in far away locations, then naturally $\mathbb{P}\left(H_{dd'} | \mathbf{I}^{\text{aux}}\right) \approx 0$ so that $p_d^{(1)} \approx 1$, as expected.

If we denote $\lambda_d^{(1)} = \frac{\mathbb{P}(D_{dd}|\mathbf{I}^{\text{aux}})}{1-\mathbb{P}(D_{dd}|\mathbf{I}^{\text{aux}})}$ the prior odds ratio which gives how much more probable is that an individual carries a priori only one device d than another device together with d, considering that apriori any other device d' can be the second device so that $\mathbb{P}\left(D_{dd'} | \mathbf{I}^{\text{aux}}\right)$ is constant for any other device d' and $\mathbb{P}\left(D_{dd} | \mathbf{I}^{\text{aux}}\right) + (N_D - 1) * \mathbb{P}\left(D_{dd'} | \mathbf{I}^{\text{aux}}\right) = 1$, where N_D is the total number of devices, we arrive at the following formula for the probability of duplicity:

$$p_d^{(1)} = 1 - \frac{1}{1 + \frac{\exp(-\ell_d)}{\lambda_d \times (N_D - 1)} \sum_{d' \neq d} \exp\left(\ell_{dd'}\right)}.$$

Thus, depending on the available information, if there is information at the device level that can be used to evaluate λ_d, the latter formula can be used to compute the duplicity probability, otherwise, the former formula with a single value of α for all devices is used. More detailed about this approach is provided by Salgado et al. (2020).

5.1.2.2. The pair approach

This approach is explained in detail in Salgado et al. (2020). Here there are some notes to understand what is computing. Denoting by $D_{dd'}$ the event which has the meaning "devices d and d' are carried by the same individual" and by $D^c_{dd'}$ the event with the meaning "devices d and d' are not carried by the same individual" the duplicity probability for device d is the pair duplicity probability $p_{dd'} \equiv \mathbb{P}(D_{dd'}|\mathbf{E}, \mathbf{I}^{\text{aux}})$ corresponding to device d' more similar to d and we can write $p_d^{(2)} = \max_{d' \neq d} \mathbb{P}\left(D_{dd'}|\mathbf{E}, \mathbf{I}^{\text{aux}}\right)$. Obviously, $p_{dd'} = 0$ for all $d = d'$.

We compute the pair-duplicity probabilities $p_{dd'}$ for two devices d and d' using the Bayes theorem:

$$\mathbb{P}\left(D^c_{dd'}|\mathbf{E}, \mathbf{I}^{\text{aux}}\right) = \frac{\mathbb{P}\left(\mathbf{E}|D^c_{dd'}, \mathbf{I}^{\text{aux}}\right)\mathbb{P}\left(D^c_{dd'}|\mathbf{I}^{\text{aux}}\right)}{\mathbb{P}\left(\mathbf{E}|D_{dd'}, \mathbf{I}^{\text{aux}}\right)\mathbb{P}\left(D_{dd'}|\mathbf{I}^{\text{aux}}\right) + \mathbb{P}\left(\mathbf{E}|D^c_{dd'}\mathbf{I}^{\text{aux}}\right)\mathbb{P}\left(D^c_{dd'}|\mathbf{I}^{\text{aux}}\right)} = \frac{1}{1 + \frac{\mathbb{P}(D_{dd'}|\mathbf{I}^{\text{aux}})}{\mathbb{P}\left(D^c_{dd'}|\mathbf{I}^{\text{aux}}\right)} \times \frac{\mathbb{P}(\mathbf{E}|D_{dd'}, \mathbf{I}^{\text{aux}})}{\mathbb{P}\left(\mathbf{E}|D^c_{dd'}, \mathbf{I}^{\text{aux}}\right)}}$$

Here $\mathbb{P}\left(D_{dd'}|\mathbf{I}^{\text{aux}}\right)$ and $\mathbb{P}\left(D^c_{dd'}|\mathbf{I}^{\text{aux}}\right)$ are the prior probabilities for the duplicity and non-duplicity events and $\mathbb{P}\left(\mathbf{E}|D_{dd'}, \mathbf{I}^{\text{aux}}\right)$ and $\mathbb{P}\left(\mathbf{E}|D^c_{dd'}, \mathbf{I}^{\text{aux}}\right)$ stands for the likelihoods under each hypothesis $D_{dd'}$ and $D^c_{dd'}$, respectively.

After some mathematical manipulations we arrive at the following formula:

$$p_d^{(2)} = \max_{d \neq d'} \left(\frac{1}{\left(1 + \alpha * \exp\left(\ell_{dd'} - \ell_d - \ell_{d'}\right)\right)} \right),$$

where $\alpha = \frac{P_2}{P_1}$, P_1 is the a priori probability of duplicity for a device and $P_2 = 1 - P_1$.

5.1.3. The trajectory approach

This approach also follows a Bayesian philosophy, but instead of using network event variables $\mathbf{E}$ we will use properties of the trajectories derived from the HMMs, i.e. the location probability distributions $\{\gamma_{dt}\}$ of all devices d.

Applying the Bayes theorem again we have:

$$\mathbb{P}\left(D^c_{dd'}|\mathbf{X}, \mathbf{I}^{\text{aux}}\right) = \frac{1}{1 + \frac{\mathbb{P}(D_{dd'}|\mathbf{I}^{\text{aux}})}{\mathbb{P}\left(D^c_{dd'}|\mathbf{I}^{\text{aux}}\right)} \times \frac{\mathbb{P}(\mathbf{X}|D_{dd'}, \mathbf{I}^{\text{aux}})}{\mathbb{P}\left(\mathbf{X}|D^c_{dd'}, \mathbf{I}^{\text{aux}}\right)}},$$

where $\mathbf{X}$ is a variable related to the estimated trajectories in terms of posterior location probabilities.

To apply this idea we compute the probability distribution of the signed distance between the x- and y-axis position of each pair of devices (we denote these random variables by $\Delta_{x,dd't} = X_{dt} - X_{d't}$ and $\Delta_{y,dd't} = Y_{dt} - Y_{d't}$) and count how many times the mode of these distributions are less than a predefined quantity ($\xi \times \max\left(r_{dt}, r_{d't}\right)$. If a device d corresponds to an individual with two devices (2:1), there will be another device d' such that their distance will be significatively close to 0 along their trajectories.

We define:

$$\hat{p}^{\text{mode}}_{dd'} \equiv \mathbb{P}\left(\mathbf{X}|D_{dd'}, \mathbf{I}^{\text{aux}}\right) = \frac{\#\{t = 1, \ldots, T : |\delta^*_{xt}| \leq \xi \cdot \max\{rd_{dt}, rd_{d't}\}, |\delta^*_{yt}| \leq \xi \cdot \max\{rd_{dt}, rd_{d't}\}\}}{T}, \tag{5.2}$$

where δ^*_{xt} and δ^*_{yt} are the mode of the $\Delta_{x,dd't}$ and $\Delta_{y,dd't}$ variables. The duplicity probability will be given by:

$$p_d^{(2)} = \max_{d \neq d'} \left(1 - \frac{1}{1 + \alpha \times \frac{\hat{p}^{\text{mode}}_{dd'}}{1 - \hat{p}^{\text{mode}}_{dd'}}} \right)$$

where $\alpha = \frac{P_1}{1-P_1}$, P_1 being the a priori probability of duplicity.

5.2. Syntax step by step

This section explains briefly the main functions of the package and how to use each method of computing the duplicity probability implemented in the `deduplication` package. In all the examples below we will use the data set included in this package. This data set was generated using the simulation software. The first step will be to set the path to the data:

```
library(deduplication)
path_root <- 'extdata'
```

Then, some information which is needed whatever the duplicity method is computed. Read the information about the territory, data from the simulation: general parameters, antennas information and events. Let us see the input parameters:

```
gridParams <-readGridParams(system.file(path_root, 'grid.csv',
   package = 'deduplication'))
```

`gridParams` is a list that contains the number of rows and columns of the grid and the tile dimensions along OX and OY axes.

Since we will work with simulated data in our example, we need some parameters that were used to generate the data set: the probability of a person to have two mobile devices (needed for the a priori duplicity probability) and the minimum value of the signal strength/quality to allow a connection between a mobile device and an antenna. These two values are read from the `simulation.xml` file:

```
simParams <-readSimulationParams(system.file(path_root, 'simulation.xml',
   package = 'deduplication'))
```

We also need to read the network events:

```
events <- readEvents(system.file(path_root, 'AntennaInfo_MNO_MNO1.csv',
   package = 'deduplication'))
```

From the `events` table we can easily build a list of devices present in the current data set and a table with the antenna IDs where these devices are connected for every time instant:

```
devices <- getDeviceIDs(events)
connections <- getConnections(events)
```

`devices` is a (sorted) list of the IDs of all devices detected by the network and `connections` is a matrix with each row corresponding to a device and the elements on the columns corresponding to the IDs of the antenna where the device is connected at a every time instant.

The next step will be the computation of the emission probabilities for the individual HMM models (for each device) and for the joint models (for pairs of devices). Since the emission probabilities are computed for each tile in the grid we need the number of rows and columns of the grid and also the file with the signal strength/quality. We also need the minimum value of the signal strength/quality that allows a connection between a mobile device and an antenna and we will use it to set to 0 the signal strength/quality for each tile where the actual value is below this threshold.

```
sgFileName <-  system.file(path_root, 'SignalMeasure_MNO1.csv',
   package = 'deduplication')
emissionProbs <- getEmissionProbs(nrows = gridParams$nrow,
   ncols = gridParams$ncol,
   signalFileName = sgFileName,
   sigMin = simParams$conn_threshold)

jointEmissionProbs <- getEmissionProbsJointModel(emissionProbs)
```

Using the emission probablities we can build the generic HMM model (for each individual device) and the joint HMM model (for pairs of devices):

```
model <- getGenericModel(nrows = gridParams$nrow,
                         ncols = gridParams$ncol,
                         emissionProbs = emissionProbs)
modelJ <- getJointModel(nrows = gridParams$nrow,
                        ncols = gridParams$ncol,
                        jointEmissionProbs = jointEmissionProbs)
```

We can fit now the individual models:

```
ll <- fitModels(length(devices), model, connections)
```

`fitModels` calls the `fit` function from `destim` package to do this task. Being a time consuming operation, it builds a cluster of working nodes and spreads the computations for subsets of devices to these nodes. The number of working nodes equals the number of logical cores of the computer. On Windows the cluster is a **SOCK** one while on Unix-like operating systems (Linux and MacOS) it is a **FORK** cluster, taking advantage of its higher speed.

Now, let us see the computation of each method.

5.2.1. The Bayesian approach with network events - the one-to-one method

This method needs a complete list of pairs of devices and it also uses as an input parameter the apriori probability for one-to-one correspondence between devices and owners.

Now, we compute the a priori probability for one-to-one correspondence and build the pairs of devices:

```
Pii <- apriorioneDeviceProb(prob2Devices = simParams$prob_sec_mobile_phone,
                            ndevices = length(devices))
pairs4dup <- computePairs(connections = connections,
                          ndevices = length(devices),
                          oneToOne = TRUE)
```

Finally, we call the `computeDuplicityBayesian` function by using the one-to-one method: `method = "1to1"`.

```
probDup1 <- computeDuplicityBayesian(method = "1to1",
                                     deviceIDs = devices,
                                     pairs4dupl = pairs4dup,
                                     modeljoin = modelJ,
                                     llik = ll,
                                     P1 = NULL,
                                     Pii = Pii)
```

```
probDup1[]
#>       deviceID       dupP
#>    1:       73 0.00000000
#>    2:       78 1.00000000
#>    3:       79 1.00000000
#>    4:       83 0.07203531
#>    5:       85 0.00000000
#>   ---
#> 214:      776 1.00000000
#> 215:      777 1.00000000
#> 216:      779 0.00000000
#> 217:      782 0.00000000
#> 218:      787 0.00000000
```

`probDup1` is a data.table where in the first column we have the deviceID and in the second column we have the corresponding duplicity probability.

If we have the value of the `lambda` parameter for each device (or a single value for all devices) we can call the same function but instead of providing the a priori probability for one-to-one correspondence, we can provide the value of `lambda` (the value given here is only for convenience):

```
probDup2 <- computeDuplicityBayesian("1to1", devices, pairs4dup,
                                     modelJ, ll, P1 = NULL, Pii = NULL,
                                     init = TRUE, lambda = 0.67)
```

5.2.2. The Bayesian approach with network events - the pairs method

The `pairs` method needs to receive a list of pairs of devices and the corresponding antennas where they are connected at every time instant. This list depends on the number of devices and could be very large which means a long execution time. To shorten the execution time we can exclude from the list of pairs the devices that are impossible to belong to the same person. For this, we first build a list of neighbouring antennas, considering that two antennas are neighbours if their coverage areas (cells) have a non void intersection. Then, this list will be used to retain only those devices connected to neighboring antennas most of the time.

```
coverarea <- readCells(system.file(path_root, 'AntennaCells_MNO1.csv',
                                   package = 'deduplication'))
antennaNeigh <- antennaNeighbours(coverarea)
```

The a priori probability of duplicity is simply given by:

```
P1 <- aprioriDuplicityProb(prob2Devices = simParams$prob_sec_mobile_phone,
                           ndevices = length(devices))
```

We can build now the pairs of devices needed to compute the duplicity probabilities:

```
pairs4dup <- computePairs(connections = connections,
                          ndevices = length(devices),
                          oneToOne = FALSE,
                          P1 = P1,
                          limit = 0.05,
                          antennaNeighbors = antennaNeigh)
```

Note that we set `oneToOne = FALSE` to build the *reduced* list of pairs of devices that takes into consideration the exclusion criterion mentioned above.

The duplicity probability for each devices is now computed as:

```
probDup3 <- computeDuplicityBayesian(method = "pairs",
                                     deviceIDs = devices,
                                     pairs4dupl = pairs4dup,
                                     modeljoin = modelJ,
                                     llik = ll,
                                     P1 = P1)
```

`probDup3` is a data.table where in the first column we have the deviceID and in the second column we have the corresponding duplicity probability.

5.2.3. The trajectory approach

The trajectory method needs a path to the files with the posterior location probabilities. These files should have the following name convention: `postLocDevice_` + `deviceID` + `.csv`. The files with the posterior location probabilities are obtained with the `destim` package. We provide all the files needed to run this example.

Below is the sequence of instructions to compute the duplicity probabilities using the trajectory method. As we have done in the previous methods, there is some information from the simulation but in this case it is needed to read the network events file only to obtain the list of devices and sequence of time instants. If they are available separately they can be provided without the need of the events file. To shorten the execution time we have made use of the same technique to reduce the number of the pairs of devices as in the case of the `pairs` method.

```
ntimes <- nrow(unique(events[,1]))
```

```
P1a <- aprioriDuplicityProb(prob2Devices = simParams$prob_sec_mobile_phone,
                            ndevices = length(devices))
```

```
pairs4dup <- computePairs(connections = connections,
                          ndevices = length(devices),
                          oneToOne = FALSE,
                          antennaNeighbors = antennaNeigh)
```

```
probDup4 <- computeDuplicityTrajectory(path = path_root,
                                       devices = devices,
                                       gridParams = gridParams,
                                       pairs = pairs4dup,
                                       P1 = P1a,
                                       T = ntimes,
                                       gamma = 0.5)
```

The `computeDuplicityTrajectory` function uses a cluster of working nodes to parallelize the computations. As in the Bayesian approach, the number of nodes equals the number of logical cores. The structure of the result is the same as in the previous examples: a table where we have the device IDs on the first column and the corresponding duplicity probability on the second column. The value of the argument `gamma` is the value of ξ explained before (see equation˜5.2).

5.3. Some remarks

5.3.1. Basic use in the easy way

As one can notice, arriving at the final duplicity probability table involves several intermediate steps. In order to hide all these details from the user we provide the function `computeDuplicity` that is easier to use. Below we show a full example with all the method computed by using this function.

Firstly, we set the folder where the necessary input files are stored:

```
path_root <- 'extdata'
```

Next, we set the grid file name, i.e. the file where the grid parameters are found:

```
gridfile <- system.file(path_root, 'grid.csv', package = 'deduplication')
```

Then we set the events file name, i.e. the file with network events registered during a simulation:

```
eventsfile <- system.file(path_root, 'AntennaInfo_MNO_MNO1.csv',
                          package = 'deduplication')
```

We also need to set the signal file name, i.e. the file where the signal strength/quality for each tile in the grid is stored:

```
signalfile <- system.file(path_root, 'SignalMeasure_MNO1.csv',
                          package = 'deduplication')
```

The antenna cells file is needed to build the list of neighboring antennas. This file is needed only if the duplicity probabilities are computed using `pairs` or `trajectory` methods:

```
antennacellsfile <- system.file(path_root, 'AntennaCells_MNO1.csv',
                                package = 'deduplication')
```

Finally, we set the simulation file name, i.e. the file with the simulation parameters used to produce the data set:

```
simulationfile <- system.file(path_root, 'simulation.xml',
                              package = 'deduplication')
```

Now we can compute the duplicity probabilities using one of the three methods:

1. Using the `1to1` method:

```
out1 <- computeDuplicity(method = "1to1",
                         gridFileName = gridfile,
                         eventsFileName = eventsfile,
                         signalFileName = signalfile,
                         simulatedData = TRUE,
                         simulationFileName = simulationfile)
```

Using the `1to1` method with `lambda` parameter (note that the value given here is for convenience):

```
out1p <- computeDuplicity(method = "1to1",
                          gridFileName = gridfile,
                          eventsFileName = eventsfile,
                          signalFileName = signalfile,
                          simulatedData = TRUE,
                          simulationFileName = simulationfile,
                          lambda = 0.67)
```

2. Using the `pairs` method:

```
out2 <- computeDuplicity(metho = "pairs",
                         gridFileName = gridfile,
                         eventsFileName = eventsfile,
                         signalFileName = signalfile,
                         antennaCellsFileName = antennacellsfile,
                         simulationFileName = simulationfile)
```

3. Using the `trajectory` method:

```
out3 <- computeDuplicity(method = "trajectory",
                         gridFileName = gridfile,
                         eventsFileName = eventsfile,
                         signalFileName = signalfile,
                         antennaCellsFileName = antennacellsfile,
                         simulationFileName = simulationfile,
                         path= path_root)
```

5.3.2. A note on building the HMM models

The HMM models (both individual ones and the joint models) are built storing the steady state as fixed initialization by default. This is achieved by setting the default value of the `initSteady` parameter : `initSteady = TRUE`. If a user wants to use some specific a priori probabilities this can be done as in the following sequence:

```
aprioriProbModel <- matrix (1 / (gridParams$nrow * gridParams$ncol),
                            nrow = gridParams$nrow, ncol = gridParams$ncol)
model <- getGenericModel(nrows = gridParams$nrow,
                         ncols = gridParams$ncol,
                         emissionProbs = emissionProbs,
                         initSteady = FALSE,
                         aprioriProb = aprioriProbModel)
modelJ <- getJointModel(nrows = gridParams$nrow,
                        ncols = gridParams$ncol,
                        jointEmissionProbs = jointEmissionProbs,
                        initSteady = FALSE,
                        aprioriJointProb = aprioriProbModel)
```

5.3.3. Notes about computational efficiency

The most computational intensive functions of the package (`computeDuplicity`, `computeDuplicityBayesian` and `computeDuplicityTrajectory`) use parallel computations to decrease the execution time. Parallelization is done using the standard techniques found in the `parallel` package: first the above mentioned functions build a cluster of working nodes, exports the variables needed for computations to all nodes and then distribute the computations equally among these nodes. While executing the parallel code, all the logical cores of the computer are used. Even using these parallel computations techniques, the execution time could be high, depending on the size of the input data. The most demanding method from the execution time point of view is the `trajectory` method.

6

The aggregation layer

6.1. Introduction

In this chapter, we illustrate the aggregation process through the corresponding implementation in the R package `aggregation` (Oancea et al., 2020a). The main purpose is to present some technical details of its implementation and provide examples on how to use this package. Some basic knowledge about `destim` and `deduplication` packages would be useful to understand how this package works (see previous chapters). A detailed description of the methodological approach implemented by this package is provided by Salgado et al. (2020) and Salgado et al. (2020).

The aggregation process connects the number of devices detected by the network with the number of individuals in the network (the whole territory or a partition). There are two main goals in this process:

1. The number of detected individuals.
2. The origin - destination matrix.

Let us see a brief description of the underlaying methodology and the steps to solve them with the implementation done in the aggregation package.

We are under the assumption that the goal is the whole population, so there is no need of statistical filtering before computing the aggregation process. In case that the target population would be a subset such as: domestic tourists, inbound tourists, commuters, etc., a process of statistical filtering must be applied before doing the aggregation. The main idea would be to identify groups of devices through their patterns of movement. We have identify several indicators and propose some possible methods (see Salgado et al., 2020). However, we have not developed a specific methodology for that process since in our simulated data there is currently no pattern apart from random walks (with or without drift). In fact, in the following sections the example is shown through the same simulation of previous chapters.

The rest of the chapter is organized as follows. Section 6.2 presents the method of computing the number of detected individuals. It starts with a brief introduction into the methodological approach (subsection 6.2.1) and continues with an example of using the `aggregation` package to compute this number (subsection 6.2.2) where it presents the function `rNentEvent()`. This function generates random variates according to a Poisson multinomial distribution which can be used to compute a point estimation (mean, mode) of the number of individuals. Section 6.3 is dedicated to the origin-destination matrix. Again, we start with a short introduction of the methodological approach and then we present an example of using function `rNnetEventOD()` to compute the origin-destination matrix in subsection 6.3.1.

6.2. The number of detected individuals

6.2.1. Brief methodological description

The main objective of the aggregation is to estimate the number of detected individuals starting from the number of detecting devices and making use of the duplicity probability for each device.

For this purpose, it uses a probabilistic approach in order to carry forward the uncertainty already present in the preceding stages all along the end-to-end process. The geolocation of network events is conducted with certain degree of uncertainty (due to the nature itself of the process – see chapter 4) and the duplicity of a given device (carried by an individual with another device) is also probabilistic in nature (see chapter 5), therefore, a priori it is impossible to provide a certain number of individuals in a given territorial unit.

For this reason the methodology behind this process focuses on the probability distribution of the number of individuals detected by the network. Having a probability distribution amounts to having all statistical information about the random phenomenon and one can choose any point estimation (mean, median, mode) together with uncertainty measures (coefficient of variation, credible intervals).

The aggregation procedure is strongly based on the results of preceding modules (geolocation and duplicity) avoiding any extra hypothesis.

We define the vectors $\mathbf{e}_i^{(1)} = \mathbf{e}_i$ and $\mathbf{e}_i^{(2)} = \frac{1}{2}\mathbf{e}_i$, where $\mathbf{e}_i$ is the canonical unit vector in $\mathbb{R}^{N_T}$ (with N_T the number of tiles in the reference grid).

Next, we define the random variable $\mathbf{T}_{dt} \in \{\mathbf{e}_i^{(1)}, \mathbf{e}_i^{(2)}\}_{i=1,\ldots,N_T}$ with probability mass function $\mathbb{P}\left(\mathbf{T}_{dt}|\mathbf{E}_{1:D}\right)$ given by

$$\mathbb{P}\left(\mathbf{T}_{dt} = \mathbf{e}_i^{(1)}|\mathbf{E}_{1:D}\right) = \gamma_{dti} \times (1 - p_d^{(2)})$$
$$\mathbb{P}\left(\mathbf{T}_{dt} = \mathbf{e}_i^{(2)}|\mathbf{E}_{1:D}\right) = \gamma_{dti} \times p_d^{(2)},$$

where $p_d^{(2)}$ is the device duplicity probability computed with `deduplication` package (named as $p_d^{(2)}$ in chapter 5) and γ_{dti} denote the location probability of device d at time t and tile i computed with `destim` package. It can be easily observed that this is a categorical or multinoulli random variable.

Finally, we define the multivariate random variable $\mathbf{N}_t^{\text{net}}$ providing the number of individuals N_{ti}^{net} detected by the network at each tile $i = 1, \ldots, N_T$ at time instant t:

$$\mathbf{N}_t^{\text{net}} = \sum_{d=1}^{D} \mathbf{T}_{dt}.$$

The random variable $\mathbf{N}_t^{(\text{net})}$ is a Poisson multinomial distributed random variable. The properties and software implementation of this distribution are not trivial and we use a Monte Carlo simulation method by convolution to generate random variates according to this distribution.

Another interesting issue is to consider the computation of the distribution of the number of detected individuals at a region/zone level. Let us consider a combination of tiles that we can

called regions. We shall denote them as $\bar{T}_r = \bigcup_{i \in \mathcal{I}_r} T_i$, where $\mathcal{I}_r$ denotes the set of tile indices composing region r. If the independence assumption still holds (because the size of the region is still small enough), then we can reproduce the whole derivation above just by defining the location probability $\bar{\gamma}_{dtr}$ at region r as

$$\bar{\gamma}_{dtr} = \sum_{i \in \mathcal{I}_r} \gamma_{dti}. \tag{6.1}$$

The subsequent elaboration to build the final Poisson-multinomial-distributed number of detected individuals is completely similar. Notice again that there exists a limitation in the sum of device-level distributions put by the size of the underlying region breakdown. The random vector $\bar{\mathbf{N}}_t^{\text{net}}$ of individuals per region in terms of the deduplicated location $\bar{\mathbf{T}}_{dt}$ per region would be also expressed as a sum:

$$\bar{\mathbf{N}}_t^{\text{net}} = \sum_{d=1}^{D} \bar{\mathbf{T}}_{dt}. \tag{6.2}$$

Notice that this decomposition allows us to write straightforwardly the mean vector and the covariance matrix for $\bar{\mathbf{N}}_t^{\text{net}}$. Define the deduplicated location probabilities per region as $\bar{\gamma}_{dtr}^{\text{dedup}} \equiv (1 - \frac{p_d^{(2)}}{2}) \cdot \bar{\gamma}_{dtr}$ for all regions $r = 1, \ldots, R$. Then

$$\mathbb{E}\left[\bar{\mathbf{N}}_t^{\text{net}}\right] = \sum_{d=1}^{D} \sum_{r=1}^{R} \bar{\gamma}_{dtr}^{\text{dedup}} \mathbf{e}_r, \tag{6.3}$$

$$\mathbb{V}\left[\bar{\mathbf{N}}_t^{\text{net}}\right] = \sum_{d=1}^{D} \sum_{r=1}^{R} \bar{\gamma}_{dtr}^{\text{dedup}} \cdot (1 - \bar{\gamma}_{dtr}^{\text{dedup}}) E_{rr}. \tag{6.4}$$

In the following, we show how to obtain in practice all these concepts.

6.2.2. The `rNnetEvent()`

The `aggregation` package provides a single function to generate random variates according to the Poisson multinomial distribution: `rNnetEvent()`. Thus, all the details about intermediate computations are hidden from the users. The input data needed by this function are:

- `n`: the number of the random values to be generated,
- `dupFileName`: the file with the duplicity probabilities for each device,
- `regsFileName`: the file defining the geographical regions where we intend to aggregate the number of individuals,
- `postLocPath`: the path to the directory where the files with the posterior location probabilities for each device are found,
- `prefix`: the name prefix of these files (which are the output of the `destim` package),
- `times`: a vector with the values of time instants.

There is also an optional argument called `seed`, the seed needed to initialize the random number generator. In the example below we use the default value of this argument.

We provide a complete set of files with example data in the `extdata` folder of this package. The raw data used to produce these files are given by our simulation software. If the user wants to work with real data reading of the `simulation.xml` (see code below) will be skipped, and

instead a vector with all the time instants when the network events were registered should be build and provided.

The duplicity file is a simple .csv file which is the main result of the `deduplication` package. It is a simple table with two columns, namely `deviceID` and `duplicityProbability`:

```
dupProb <- read.csv(file = system.file('extdata/duplicity.csv',
   package = 'aggregation'))
head(dupProb)
#>   deviceID       dupP
#> 1       73 0.00000000
#> 2       78 1.00000000
#> 3       79 1.00000000
#> 4       83 0.05141439
#> 5       85 0.00000000
#> 6       90 0.06842542
```

The regions file is also a simple .csv file defined by the user. It contains two columns: the tile number and the region number. Normally, all tiles in the grid should be part of a region.

```
regions <- read.csv(file = system.file('extdata/regions.csv',
   package = 'aggregation'))
head(regions)
#>   tile region
#> 1 1560      3
#> 2 1561      3
#> 3 1562      3
#> 4 1563      3
#> 5 1564      3
#> 6 1565      3
```

The third parameter that should be passed to this function is the path where the files with the posterior location probabilities are found. There should be one file for each device in the whole set of devices. A file contains a table with the posterior location probabilities for a device. It has three columns: tile, time, probL. It contains only the entries corresponding to nonzero values of the posterior location probability (probL column). The file extension is .csv.

Below we show a simple example of how to use this function and its result.

```
# set the folder where the necessary input files are stored
path      <- 'extdata'

prefix = 'postLocDevice'

# get the series of time instants from the simulation.xml file.
simParamsFileName <- system.file(path, 'simulation.xml',
   package = 'aggregation')
simParams <- deduplication::readSimulationParams(simParamsFileName)
time_from <- simParams$start_time
time_to   <- simParams$end_time
time_incr <- simParams$time_increment
times     <- seq(from = time_from, to = time_to-time_incr, by = time_incr)
```

```
# set the duplicity probabilities file name,
#i.e. the file with duplicity probability for each device
dpFile <- system.file(path, 'duplicity.csv', package = 'aggregation')

# set the regions file name, i.e. the file defining the regions for which
# we need the estimation of the number of individuals detected by network.
rgFile <- system.file(path, 'regions.csv', package = 'aggregation')

# set the path to the posterior location probabilities files
pathLoc <- system.file(path, package = 'aggregation')

# set the number of random values to be generated
n <- 1e3

# call rNnetEvent
nNet <- rNnetEvent(n = n,
   dupFileName = dpFile,
   regsFileName = rgFile,
   postLocPath = pathLoc,
   prefix = prefix,
   times = times)

head(nNet)
```

```
time region  N iter
1:    1      1 11    1
2:    1      1 11    2
3:    1      1 10    3
4:    1      1 13    4
5:    1      1 10    5
6:    1      1 12    6
```

The result nNet is a data.table object with 4 columns: time, region, N, iter. For each distinct combination of time-region this table contains n randomly generated values. The last column, iter, contains the index of the random value (given in column N) generated for each time, instant and region.

One can use the mean, mode or median to obtain an estimation of the number of individuals at each time instants in each region. Below is an example of how to do this.

```
# print the mean number of detected individuals
# for each region, for each time instant
regions <- as.numeric(unique(nNet$region))
times <- unique(nNet$time)

for(r in regions) {

   print(paste0("region: ", r))
   for(t in times) {

     print(paste0("time instant: ", t,
     " number of individuals: " ,
     round(mean(nNet[region == r][time ==t]$N))))
```

```
    }
}
```

6.3. The origin destination matrix

6.3.1. Brief methodological description

The construction of the probability distribution for the number of individuals $\bar{\mathbf{N}}_t^{\text{net}}$ detected by the network can be easily generalized to the number of individuals $\bar{N}_{t,\cdot\cdot}^{\text{net}}$ detected by the network moving between territorial units. We begin by defining matrices $E_{rs}^{(1)} = E_{rs}$ and $E_{rs}^{(2)} = \frac{1}{2}E_{rs}$, where E_{rs} are the Weyl matrices of dimension $R \times R$. Next, we define the matrix random variable $E_{dt} \in \{E_{rs}^{(1)}, E_{rs}^{(2)}\}_{r,s=1\ldots,R}$ with probability mass function given by

$$\mathbb{P}\left(E_{dt} = E_{rs}^{(1)}\right) = \tilde{\gamma}_{dt,sr} \cdot p_d^{(1)}, \tag{6.5a}$$

$$\mathbb{P}\left(E_{dt} = E_{rs}^{(2)}\right) = \tilde{\gamma}_{dt,sr} \cdot p_d^{(2)}, \tag{6.5b}$$

where $\gamma_{dt,sr}$ stands for the joint location probabilities computed in the geolocation module aggregated to the regions $r, s = 1, \ldots, R$. Notice that, although matrix-valued, this is still a categorical or multinoulli random variable. Then, we can define the origin-destination matrix between regions of individuals detected by the network by

$$\bar{\mathbf{N}}_t^{\text{net}} = \sum_{d=1}^{D} E_{dt}, \tag{6.6}$$

which, as before, distributes according to a multinomial-Poisson distribution. Again, we shall use Monte Carlo techniques to deal with it. If we define the deduplicated joint location probabilities $\tilde{\gamma}_{dt,sr}^{\text{dedup}} = \left(1 - \frac{p_d^{(2)}}{2}\right) \cdot \tilde{\gamma}_{dt,sr}$, then the mean origin-destination matrix is given by

$$\mathbb{E}\left[\bar{\mathbf{N}}_t^{\text{net}}\right] = \sum_{d=1}^{D} \sum_{r,s=1}^{R} \tilde{\gamma}_{dt,sr}^{\text{dedup}} \, E_{rs}. \tag{6.7}$$

Once we have posterior distributions we can also compute credible intervals for each region and each time instant.

6.3.2. The `rNnetEventOD()` function

Again, the `aggregation` package provides a single function to generate random variates that can be used then to compute an estimation of the number of individuals moving from one region to another. The parameters of this function are:

- `n`: the number of the random values to be generated,
- `dupFileName`: the file with the duplicity probabilities for each device,
- `regsFileName`: the file defining the geographical regions where we intend to aggregate the number of individuals,
- `postLocJointPath`: the path to the directory where the files with the posterior joint location probabilities for each device are found,
- `prefix`: the name prefix of these files.

There is also an optional argument, `seed`, the seed needed to initialize the random number generator. In the example below we use the default value of this argument.

The files containing the joint probabilities are also a result of the `destim` package. We provide a complete set of files with example data in the `extdata` folder of this package. The raw data used to produce these files are given by our simulation software.

```
# For the origin-destination matrix we proceed as follows
# set the folder where the necessary input files are stored
path      <- 'extdata'

postLocJointPath <- system.file(path, package = 'aggregation')
prefixJ <- 'postLocJointProbDevice'

# set the duplicity probabilities file name,
# i.e. the file with duplicity probability for each device
dpFile <- system.file(path, 'duplicity.csv', package = 'aggregation')

# set the regions file name, i.e. the file defining the regions for which
# we need the estimation of the number of individuals detected by network.
rgFile <- system.file(path, 'regions.csv', package = 'aggregation')

# generate n random values
n <- 1e3

nnetOD <- rNnetEventOD(n = n,
   dupFileName = dpFile,
   regsFileName = rgFile,
   postLocJointPath = postLocJointPath,
   prefix = prefixJ)

head(nnetOD)
```

```
time_from time_to region_from region_to Nnet iter
1:         0      10           1         1 18.0    1
2:         0      10           1         1 18.5    2
3:         0      10           1         1 19.0    3
4:         0      10           1         1 18.0    4
5:         0      10           1         1 19.0    5
6:         0      10           1         1 18.0    6
```

For each pair(time_from-time_to, region_from-region_to) there are `n` random values in the last but one column. One can use again the mean, mode or median to have an estimate of the number of individuals moving from one region to another at a certain time.

The following code shows how to compute the the origin-destination matrix for the time interval (0,10).

```
t_from <-0
t_to <- 10


regions_from <- sort(as.numeric(unique(nnetOD$region_from)))
regions_to <- sort(as.numeric(unique(nnetOD$region_to)))
```

```
ODmat <- matrix(nrow = length(regions_from), ncol = length(regions_to))
for(r1 in regions_from) {

for(r2 in regions_to) {

      aux <- nnetOD[time_from == t1][time_to == t2][
        region_from == r1][region_to == r2]$Nnet

          ODmat[r1,r2] <- round(mean(aux))

          }

  }
ODmat
```

6.4. Some remarks about computational efficiency

The most computational intensive functions of the package (`rNnetEvent`, `rNnetEventOD`) use parallel computations to decrease the execution time. Parallelization is done using the standard techniques found in the `parallel` package: firstly, the above mentioned functions build a cluster of working nodes, exports the variables needed for computations to all nodes and then distribute the computations equally among these nodes. While executing the parallel code, all the logical cores of the computer are used. Even using these parallel computations techniques, the execution time could be high, depending on the size of the input data. The cluster used for parallel computations is a SOCK one under the Windows operating system and a FORK one under Unix-like operating systems.

7

The inference layer

7.1. Introduction

In this chapter, the process on the inference layer is illustrated. The inference process connects the number of individuals in the network with the number of individual in the target population. The main goal is the computation of the probability distribution for the number of individuals in the target population conditioned on the number of individuals detected by the network and some auxiliary information which is absolutely necessary to provide a meaningful inference on the target population. The auxiliary information is provided by the penetration rates (ratio of number of devices to number of individuals in the target population) P_r^{net} of the MNO and the register-based population N_r^{reg} at each region r.

We propose a two-staged modelling exercise. Firstly, we assume that there exists an initial time instant t_0 in which both the register-based target population and the actual population can be assimilated in terms of their physical location. We can assume, e.g., that at 6:00am all devices stay physically at the residential homes declared in the population register. This assumption will trigger the first stage in which we compute a probability distribution for the number of individuals $\mathbf{N}_{t_0}$ of the target population in all regions in terms of the number of individuals $\mathbf{N}_0^{\text{net}}$ detected by the network and the auxiliary information. Secondly, we proceed with the dynamical part for what we assume that individuals displace over the geographical territory independently of the MNO, i.e. subscribers of MNO 1 will show a displacement pattern similar to those of MNO 2. This assumption will trigger the second stage in which we provide a probability distribution for the number of individuals $\mathbf{N}_t$ for later times $t > t_0$.

Regarding the origin-destination matrix, we can use the same assumptions to infer the number of individuals moving from one region to another at time instant t, also providing credible intervals as an accuracy indicator.

A detailed description of the methodological approach implemented is provided by Salgado et al. (2020) and Salgado et al. (2020).

This chapter is divided in three main parts:

- Population at the initial time t_0.
- The dynamical approach: population at $t > t_0$.
- Origin-destination matrices.

Inside each section, we show a brief methodological description that can be extended with the material by Salgado et al. (2020) and Salgado et al. (2020) and the implementation step by

step that has been done in the R package `inference` (Oancea et al., 2020c). Thus, in section 7.2 we treated the problem of estimating the population count at t_0. We started by presenting a short methodological overwiew (subsection 7.2.1) and then we presented a detailed example on using the function that performs this estimation `computeInitialPopulation()` in subsection 7.2.2. In section 7.3, we presented the estimation of the population count at successive time instants $t > t_0$ in the same way: a short introduction to the methodological background is given in subsection 7.3.1 and an example on how to use `computePopultionT()` function is given in subsection 7.3.2. The origin-destination matrix estimation is presented in section7.4 with a outline of the method used in subsection 7.4.1 and details on how to estimate this matrix with `computePopulationOD()` function in subsection 7.4.2. This chapter ends with the presentation of an add-on functionality of it, namely a REST AP, in section 7.5.

7.2. Population at the initial time t_0

7.2.1. Brief methodological description

In this section we focus on the present population at the initial time t_0. Then, for ease of notation we shall drop the time index. We shall combine the number of individuals in the network per region, N_r^{net}, the penetration rates per region, P_r, and the register-based population per region N_r^{reg} to produce the probability distribution for $\mathbf{N} = (N_1, \ldots, N_R)^T$ for all R regions.

We follow the approach used in the species abundance problem in Ecology by Royle and Dorazio (2009). This approach clearly distinguishes between the state and the observation process. The state process is the underlying dynamical process of the population and the observation process is the procedure by which we get information about the location and timestamp of each individual in the target population. The different available auxiliary information will be integrated using different levels in the hierarchy of the statistical model.

7.2.1.1. Observation process

The first level makes use of the detection probability p_r of individuals of a network in each region r. We shall concentrate first on the observation process. We model

$$N_r^{\text{net}} \simeq \text{Binomial}\left(N_r, p_r\right). \tag{7.1}$$

This model makes the only assumption that the probability of detection p_r for all individuals in region r is the same. We approximate it using the penetration rate P_r of the MNO in region r. The posterior probability distribution for N_r in terms of N_r^{net} will be given by

$$\mathbb{P}\left(N_r | N_r^{\text{net}}\right) = \begin{cases} 0 & \text{if } N_r < N_r^{\text{net}}, \\ \text{negbin}\left(N_r - N_r^{\text{net}}; 1 - p_r, N_r^{\text{net}} + 1\right) & \text{if } N_r \geq N_r^{\text{net}}, \end{cases}$$

where negbin denotes the probability mass function of a negative binomial random variable. Once we have a distribution, we can provide a point estimators, a posterior variance, a posterior coefficient of variation, a credible interval, and as many indicators as possible computed from the distribution. In our implementation we compute the mean, mode and median as point estimators, the standard deviation, coefficient of variation the first and third quartile, the interquartile range and the credible intervals.

We introduce now the second level and model the detection probability p_{kr} per individual k in the target population as $p_{kr} = p_r + noise$. We propose to implement this idea modeling

$p_r \simeq \text{Beta}\,(\alpha_r, \beta_r)$ and choosing the hyperparameters α_r and β_r according to the penetration rates P_r^{net} and the register-based population figures N_r^{reg}. The penetration rate is also subjected to the problem of device deduplication. We define:

$$\Omega_r^{(1)} = \frac{\sum_{d=1}^{D} \bar{\gamma}_{dr} \cdot p_d^{(1)}}{\sum_{d=1}^{D} \bar{\gamma}_{dr}}, \tag{7.2}$$

$$\Omega_r^{(2)} = \frac{\sum_{d=1}^{D} \bar{\gamma}_{dr} \cdot p_d^{(2)}}{\sum_{d=1}^{D} \bar{\gamma}_{dr}}, \tag{7.3}$$

with $p_d^{(i)}$ being the duplicity probabilities (computed in chapter 6 under the same assumptions about at most two devices per individual) and $\bar{\gamma}_{dr}$ the posterior location probabilities in region r for device d. The deduplicated penetration rate is defined as:

$$\tilde{P}_r^{\text{net}} = \left(\Omega_r^{(1)} + \frac{\Omega_r^{(2)}}{2} \right) \cdot P_r^{\text{net}}. \tag{7.4}$$

Let us make the following assumptions:

- On average, we assume that detection takes place with probability $\tilde{P}_r^{\text{net}}$.
- Detection is undertaken over the register-based population. We assume some coherence between the official population count and the network population count.
- The penetration rates P_r^{net} and the official population counts N_r^{reg} come without error. Should this not be attainable or realistic, we would need to introduce a new hierarchy level to account for this uncertainty (see below).
- The deduplicated penetration rates are computed as a deterministic procedure (using a mean point estimation), i.e. the deduplicated penetration rates are also subjected to uncertainty, thus we should also introduce another hierarchy level to account for this uncertainty.

Then, we fix the following: $\alpha_r + \beta_r = N_r^{\text{reg}}$, $\frac{\alpha_r}{\alpha_r + \beta_r} = \tilde{P}_r^{\text{net}}$, which immediately implies that

$$\alpha_r = \tilde{P}_r^{\text{net}} \cdot N_r^{\text{reg}}, \tag{7.5a}$$

$$\beta_r = \left(1 - \tilde{P}_r^{\text{net}}\right) \cdot N_r^{\text{reg}}. \tag{7.5b}$$

Now, we can readily compute the posterior distribution for N_r:

$$\mathbb{P}\left(N_r | N_r^{\text{net}}\right) = \begin{cases} 0 & \text{if } N_r < N_r^{\text{net}}, \\ \text{betaNegBin}\left(N_r - N_r^{\text{net}}; N_r^{\text{net}} + 1, \alpha_r - 1, \beta_r\right) & \text{if } N_r \geq N_r^{\text{net}}. \end{cases} \tag{7.6}$$

It is a displaced beta negative binomial distribution. Again, we can provide point estimates as well as posterior variances, credible intervals, etc.

Notice that when $\alpha_r, \beta_r \gg 1$ (i.e., when $\min(\tilde{P}_r^{\text{net}}, 1 - \tilde{P}_r^{\text{net}}) \cdot N_r^{\text{reg}} \gg 1$) the beta negative binomial distribution (7.6) reduces to the negative binomial distribution

$$\mathbb{P}\left(N_r|N_r^{\text{net}}\right) = \begin{cases} 0 & \text{if } N_r < N_r^{\text{net}}, \\ \text{negbin}\left(N_r - N_r^{\text{net}}; \frac{\beta_r}{\alpha_r+\beta_r-1}, N_r^{\text{net}}+1\right) & \text{if } N_r \geq N_r^{\text{net}}. \end{cases}$$

Note also that $\frac{\beta_r}{\alpha_r+\beta_r-1} \approx 1 - \tilde{P}_r^{\text{net}}$ so that in this case we do not need the register-based population (this is similar to dropping out the finite population correction factor in sampling theory for large populations).

So far, the inference has been conducted independently in each region r. We can introduce another layer in the hierarchy by modelling also the hyperparameters (α_r, β_r) so that the relationship between these parameters and the external data sources (penetration rates and register-based population counts) is also uncertain.

7.2.1.2. State process

Finally, we can also introduce the state process. The system is a human population and we can make a common modelling hypothesis to represent the number of individuals N_r in region r of the target population as a Poisson-distributed random variable in terms of the population density, i.e.

$$N_r \simeq \text{Poisson}\left(A_r\sigma_r\right), \tag{7.7}$$

where σ_r stands for the population density of region r and A_r denotes the area of region r. We choose to model N_r in terms of the population density to make an auxiliary usage of some results already found in the literature (see e.g. Deville et al., 2014).

Similarly to the observation process, we introduce the following hierarchy:

$$\begin{aligned} N_r^{\text{net}} &\simeq \text{Bin}\left(N_r, p_r\right), \quad \text{for all } r = 1, \ldots, R, && \text{(7.8a)} \\ N_r &\simeq \text{Poisson}\left(A_r\sigma_r\right), \quad \text{for all } r = 1, \ldots, R, && \text{(7.8b)} \\ p_r &\simeq \text{Beta}\left(\alpha_r, \beta_r\right), \quad \text{for all } r = 1, \ldots, R, && \text{(7.8c)} \\ \sigma_r &\simeq \text{Gamma}\left(1+\zeta_r, \theta_r\right), \quad \text{for all } r = 1, \ldots, R, && \text{(7.8d)} \end{aligned}$$

where the hyperparameters will express the uncertainty about the register-based population and the detection probability. The values for α_r and β_r are taken from (7.5). Regarding the hyperparameters θ_r and ζ_r, notice that the modes of the gamma distributions are at $\tau_r = \zeta_r \cdot \theta_r$ and the variances are given by $\mathbb{V}\left(\tau_r\right) = \left(\zeta_r + 1\right) \cdot \theta_r^2$. We shall parameterise these gamma distributions in terms of the register-based population densities σ_r^{reg} as

$$\begin{aligned} \zeta_r \cdot \theta_r &= \sigma_r^{\text{reg}} + \Delta\sigma_r, \\ \sqrt{\left(\zeta_r + 1\right) \cdot \theta_r^2} &= \epsilon_r \cdot \sigma_r^{\text{reg}}, \end{aligned}$$

where ϵ_r can be viewed as the coefficient of variation for σ_r^{reg} and $\Delta\sigma_r$ can be interpreted as the bias for σ_r^{reg}. This parametrization implies that

$$\begin{aligned}\theta_r(\Delta\sigma_r,\epsilon_r) &= \frac{\sigma_r^{\text{reg}}}{2}\left(1+\frac{\Delta\sigma_r}{\sigma_r^{\text{reg}}}\right)\left[\sqrt{1+\left(\frac{2\epsilon_r}{1+\frac{\Delta\sigma_r}{\sigma_r^{\text{reg}}}}\right)^2}-1\right],\\ \zeta_r(\Delta\sigma_r,\epsilon_r) &= \frac{2}{\sqrt{1+\left(\frac{2\epsilon_r}{1+\frac{\Delta\sigma_r}{\sigma_r^{\text{reg}}}}\right)^2}-1}.\end{aligned} \tag{7.9}$$

Under assumptions (7.8) and assuming $\alpha_r, \beta_r \gg 1$, as above, we get

$$\mathbf{P}\left(\mathbf{N}|\mathbf{N}^{\text{net}}\right) = \prod_{r=1}^{R} \text{negbin}\left(N_r - N_r^{\text{net}}; \frac{\beta_r}{\alpha_r+\beta_r}\cdot Q(\theta_r), N_r^{\text{net}}+1+\zeta_r\right) \tag{7.10}$$

where $Q(\theta_r) \equiv \frac{A_r\theta_r}{1+A_r\theta_r}$. The interpretation of this hierarchy is also simple. It is just a Poisson-gamma model in which the gamma parameters have been chosen so that we account for the uncertainty in the register-based population figures N_r^{reg}.

Usual point estimators are easily derived from (7.10) as well as accuracy indicators such as posterior variance or credible intervals are computed from the distribution (7.10).

Expression (7.10) contains the uncertainty of both the observation and the state processes.

7.2.2. Implementation step by step

Let us see now how to the methodology using functions from the the `inference` package. First, the input files are read and the deduplication factors calculated as it is shown in the following code. The input files in this stage comes from the `deduplication` package (`duplicity.csv`), `destim` package (the location probabilities files) and an from external source (the `regions.csv` file).

In these lines the steps are: set the folder where the location probabilities files are stored and the prefix of these input file names, read the other input files (duplicity and regions) and then compute the deduplication factors.

```
library(inference, warn.conflicts = FALSE)

path   <- 'extdata'
prefix <- 'postLocDevice'

postLocPath <- system.file(path, package = 'inference')
dpFileName  <- system.file(path, 'duplicity.csv', package = 'inference')
rgFileName  <- system.file(path, 'regions.csv', package = 'inference')

omega_r <- computeDeduplicationFactors(dupFileName = dpFileName,
   regsFileName = rgFileName,
   postLocPrefix = prefix,
   postLocPath = postLocPath)

head(omega_r)
```

```
   region    omega1     omega2
1:      4 0.9786578 0.02134223
2:      6 0.7116936 0.28830636
3:      9 0.6520971 0.34790293
4:      3 0.7876368 0.21236317
5:     10 0.7199611 0.28003894
6:      8 0.8367990 0.16320103
```

Then, we can compute the parameters needed by the distribution functions used to estimate the target population count. The `computeDistrParams()` function computes the parameters needed by all three distributions presented in the previous subsection: α_r, β_r, θ_r and ζ_r. The computations are performed under the assumption that $\Delta\sigma_r = 0$ and $\epsilon_r = 10^{-5}$ unless the user specifies other values for them. The input files needed in this step are: `nnet.csv` which is one of the outputs of the `aggregation` package containing the random variates generated for each region, the file with the population count for each geographical region (named here `pop_reg.csv`) which can be taken from a population register, the penetration rates of the MNO in each of the geographical regions (named in our example `pnt_rates.csv`) which can be obtained from the MNO itself or from another telecommunication authority and the parameters of the grid (`grid.csv`). In the code presented below we used the files included in the `inference` package, but they can be replaced by the user with his/her own files easily.

```
nFileName     <- system.file(path, 'nnet.csv', package = 'inference')
nnet          <- readNnetInitial(nFileName)
pRFileName    <- system.file(path, 'pop_reg.csv', package = 'inference')
pRateFileName <- system.file(path, 'pnt_rate.csv', package = 'inference')
grFileName    <- system.file(path, 'grid.csv', package = 'inference')
params        <- computeDistrParams(omega = omega_r,
   popRegFileName = pRFileName,
   pntRateFileName = pRateFileName,
   regsFileName = rgFileName,
   gridFileName = grFileName)
head(params)
```

```
   region    omega1     omega2   pntRate regionArea_km2 N0 dedupPntRate
1:      1 0.6878592 0.31214077 0.3684211           10.5 38    0.3109215
2:      2 0.8991648 0.10083522 0.4000000            7.5 55    0.3798330
3:      3 0.7876368 0.21236317 0.4153846           12.0 65    0.3712784
4:      4 0.9786578 0.02134223 0.4615385           10.0 39    0.4566134
5:      5 0.6734889 0.32651114 0.3666667           10.0 60    0.3068063
6:      6 0.7116936 0.28830636 0.3720930           12.5 43    0.3184546
      alpha     beta        theta       zeta       Q
1: 11.81502 26.18498 3.619048e-10 9999999173 3.8e-09
2: 20.89081 34.10919 7.333334e-10 9999999173 5.5e-09
3: 24.13310 40.86690 5.416667e-10 9999999173 6.5e-09
4: 17.80792 21.19208 3.900000e-10 9999999173 3.9e-09
5: 18.40838 41.59162 6.000000e-10 9999999173 6.0e-09
6: 13.69355 29.30645 3.440000e-10 9999999173 4.3e-09
```

Then, the population count distribution at t_0 is computed. As it has been explained before, three distributions can be used: Beta Negative Binomial, Negative Binomial or the state process Negative Binomial. The distribution used to compute the population count is specified using the `popDistr` parameter which can have three values `BetaNegBin`, `NegBin` or `STNegBin`. This function also needs the population count detected by the network computed using the `aggregation` package and read from a `csv` file. The result of the `computeInitialPopulation`

is a list object with one or two elements. If the parameter `rndVal` is `FALSE` the list will have a single element with descriptive statistics for the population count, which is a data.table object with the following columns: `region, Mean, Mode, Median, Min, Max, Q1, Q3, IQR, SD, CV, CI_LOW, CI_HIGH`. If `rndVal` is `TRUE` the list will have a second element which is a data.table object containing the random values generated for each region. The name of the two list elements giving the descriptive statistics and random values for time t are `stats` and `rnd_values`.

```
# Beta Negative Binomial distribution
n_bnb <- computeInitialPopulation(nnet = nnet,
   params = params,
   popDistr = 'BetaNegBin',
   rndVal = TRUE)

head(n_bnb$stats)
```

```
     region Mean Mode Median Min Max Q1 Q3 IQR    SD    CV CI_LOW CI_HIGH
[1,]      1   43   41     39  13 136 31 50  19 17.74 41.55  22.00   77.00
[2,]      2   60   57     58  24 142 49 69  20 16.19 26.98  38.00   87.53
[3,]      3   80   68     77  42 176 66 92  25 19.32 24.07  54.97  113.50
[4,]      4   38   33     37  14 102 30 44  14 11.41 29.86  23.50   58.00
[5,]      5   77   64     73  26 182 62 89  28 23.19 30.02  47.97  120.06
[6,]      6   49   36     46  14 140 36 58  22 18.41 37.59  26.00   82.03
```

```
head(n_bnb$rnd_values)
```

```
   region    N NPop
1:      1 11.0 46.0
2:      1  9.0 42.0
3:      1 13.0 52.0
4:      1 12.0 33.0
5:      1 12.0 35.0
6:      1 12.5 30.5
```

Here `N` is the population count detected by the network and `NPop` is the target population count.

```
# Negative Binomial distribution
n_nb <- computeInitialPopulation(nnet = nnet,
   params = params,
   popDistr = 'NegBin',
   rndVal = TRUE)

head(n_nb$stats)
```

```
     region Mean Mode Median Min Max Q1 Q3 IQR    SD    CV CI_LOW CI_HIGH
[1,]      1   40   34     39  12  82 32 46  14 11.23 28.40  23.94   59.00
[2,]      2   58   51     57  27 100 50 65  15 11.89 20.46  41.00   80.00
[3,]      3   79   76     78  48 130 70 86  16 12.63 16.08  60.00  100.03
[4,]      4   37   36     36  17  66 32 42  10  7.95 21.52  25.00   50.50
[5,]      5   75   75     74  33 128 64 84  20 15.10 20.21  51.50  100.50
[6,]      6   44   43     44  18  84 36 51  14 10.82 24.41  28.00   62.50
```

```
head(n_nb$rnd_values)
```

```
   region    N NPop
1:      1 11.0 24.0
2:      1  9.0 33.0
3:      1 13.0 61.0
4:      1 12.0 32.0
5:      1 12.0 49.0
6:      1 12.5 79.5
```

```
# State process Negative Binomial distribution
n_stnb <- computeInitialPopulation(nnet = nnet,
   params = params,
   popDistr= 'STNegBin',
   rndVal = TRUE)

head(n_stnb$stats)
```

```
     region Mean Mode Median Min Max Q1 Q3 IQR   SD    CV CI_LOW CI_HIGH
[1,]      1   37   36     37  22  55 34 41   8 5.45 14.71  29.00   45.53
[2,]      2   55   54     54  36  73 51 59   8 6.09 11.10  45.00   64.50
[3,]      3   69   68     68  49  96 64 74   9 6.72  9.74  58.00   80.00
[4,]      4   37   36     37  22  56 33 40   7 5.13 13.95  29.00   45.00
[5,]      5   63   62     63  42  88 58 68   9 6.89 10.91  52.00   74.50
[6,]      6   42   40     42  26  60 38 46   8 5.51 13.05  33.97   51.00
```

```
head(n_stnb$rnd_values)
```

```
   region    N NPop
1:      1 11.0 36.0
2:      1  9.0 33.0
3:      1 13.0 40.0
4:      1 12.0 42.0
5:      1 12.0 36.0
6:      1 12.5 36.5
```

7.3. The dynamical approach: population at $t > t_0$

7.3.1. Brief methodological description

In this section we focus on the probability distributions for the number of individuals N_{tr} in the target population at region r for times $t > t_0$, then the dynamical component is taken into consideration. Currently, we consider only **closed** populations, i.e. neither individuals nor devices enter into or leave the territory under analysis along the whole time period.

Our reasoning tries to introduce as less assumptions as possible. Thus, we begin by considering a balance equation. Let us denote by $N_{t,rs}$ the number of individuals moving from region s to region r in the time interval $(t-1, t)$. Then, we can write:

$$\begin{aligned} N_{tr} &= N_{t-1r} + \sum_{\substack{r_t=1 \\ r_t \neq r}}^{N_T} N_{t,rr_t} - \sum_{\substack{r_t=1 \\ r_t \neq r}}^{N_r} N_{t,r_t r} \\ &= \sum_{r_t=1}^{N_T} \tau_{t,rr_t} \cdot N_{t-1r_t}, \end{aligned} \tag{7.11}$$

where we have defined $\tau_{t,rs} = \frac{N_{t,rs}}{N_{t-1s}}$ (0 if $N_{t-1s} = 0$). Notice that $\tau_{t,rs}$ can be interpreted as an aggregate transition probability from region s to region r at time interval $(t-1, t)$ in the target population.

We make the assumption that individuals detected by the network move across regions in the same way as individuals in the target population. Thus, we can use $\tau^{\text{net}}_{t,rs} \equiv \frac{N^{\text{net}}_{t,rs}}{N^{\text{net}}_{t-1s}}$ to model $\tau_{t,rs}$. In particular, as our first choice we shall postulate $\tau_{t,rs} = \tau^{\text{net}}_{t,rs}$.

The probability distributions of N^{net}_{st-1} and $[\mathbf{N}^{\text{net}}_t]_{sr} = N^{\text{net}}_{t,rs}$ were indeed already computed in the aggregation layer (see chapter 6).

7.3.2. Implementation step by step

Now, we show the implementation of the dynamical procedure by computing the population count distribution at time instants $t > t_0$. As it was done for the hierarchical model, we show the three distributions: Beta Negative Binomial, Negative Binomial and the state process Negative Binomial.

The target population distribution is computed using `computePopulationT()` function. As inputs, it needs the population distribution at t_0 (here we will use all three previous results), the file with the population detected by the network moving from one region to another (an output of the `aggregation` package) and an optional parameter `rndVal`. The result of this function is a list with one element for each time instant (including t_0). Each element of the list is also a list with one or two elements, depending on the value of the `rndVal` parameter. If `rndVal` is `TRUE` there are two elements in the list corresponding to time instant t. The first one is a `data.table` object with some descriptive statistics for the population count at time t, containing the following columns:`region, Mean, Mode, Median, Min, Max, Q1, Q3, IQR, SD, CV, CI_LOW, CI_HIGH`. The second one is a `data.table` object with the random values for population count generated for each region, with the following columns: `region, iter, NPop`. If `rndVal` is `FALSE` the list for time instant t contains only the first element previously mentioned. The name of the list element corresponding to time instant t is `t` and the name of the two list elements giving the descriptive statistics and random values are `stats` and `rnd_values`.

First, we set the name of the file with the population detected by the network moving from one region to another (output of the `aggregation` package (see chapter 6 and Oancea et al. (2020a)). Notice that this file is stored as a zip archive because it could be very large. Then we call `computePopulationT()` function to obtain the population count estimates at $t > t_0$.

```
nnetODFile <- system.file(path, 'nnetOD.zip', package = 'inference')
```

```
# Beta Negative Binomial distribution
nt_bnb <- computePopulationT(nt0 = n_bnb$rnd_values,
   nnetODFileName = nnetODFile,
   rndVal = TRUE)
```

To display the results we select a random time instant first and then display the results for it:

```
times <- names(nt_bnb)
t     <- sample(1:length(times), size = 1)
t
head(nt_bnb[[t]]$stats)
```

```
     region Mean Mode Median Min Max  Q1  Q3 IQR    SD    CV CI_LOW CI_HIGH
[1,]      1   35   33     33   9  88  27  41  14 11.89 34.35     18      56
[2,]      2   67   60     65  31 142  57  76  19 14.82 22.16     46      93
[3,]      3  166  161    164  96 259 150 181  31 23.38 14.11    131     205
[4,]      4   41   32     40  14  93  33  48  15 11.08 27.09     25      60
[5,]      5   81   80     80  45 137  70  89  19 15.07 18.70     58     106
[6,]      6   23   19     22   2  52  17  27  10  7.66 33.73     12      36
```

```
head(nt_bnb[[t]]$rnd_values)
```

```
   region iter NPop
1:      1    1   52
2:      2    1   57
3:      3    1  184
4:      4    1   49
5:      5    1   80
6:      6    1   33
```

The `iter` column shows the index of the random value generated for a region. The total number of random values generated for each region equals the same number used in the `aggregation` package that provides the input for this function.

```
# Negative Binomial distribution
nt_nb <- computePopulationT(nt0 = n_nb$rnd_values,
   nnetODFileName = nnetODFile,
   rndVal = TRUE)

# to display results, select a random time instant
times <- names(nt_nb)
t <- sample(1:length(times), size = 1)
t
head(nt_nb[[t]]$stats)
```

```
     region Mean Mode Median Min Max Q1  Q3 IQR    SD    CV CI_LOW CI_HIGH
[1,]      1   36   35     35  11  80 28  42  14 10.62 29.84     20   54.00
[2,]      2   58   52     57  26 110 50  65  15 11.93 20.71     40   77.06
[3,]      3  103  105    102  66 155 92 112  20 15.40 14.97     80  130.00
[4,]      4   42   39     42  13  80 36  48  12  9.64 22.67     28   58.06
[5,]      5   72   69     70  33 129 61  81  20 14.63 20.40     50   97.00
[6,]      6   35   32     34  11  66 29  40  11  8.51 24.49     22   49.00
```

```
head(nt_nb[[t]]$rnd_values)
```

```
   region iter NPop
1:      1    1   38
2:      2    1   44
3:      3    1   92
4:      4    1   43
5:      5    1   64
6:      6    1   23
```

```
# State process Negative Binomial distribution
nt_stnb <- computePopulationT(nt0 = n_stnb$rnd_values,
nnetODFileName = nnetODFile,
rndVal = TRUE)

# to display results, select a random time instant
times <- names(nt_stnb)
t <- sample(1:length(times), size = 1)
t
head(nt_stnb[[t]]$stats)
```

```
     region Mean Mode Median Min Max  Q1  Q3 IQR    SD    CV CI_LOW CI_HIGH
[1,]      1   32   26     32   9  62  26  38  12  9.17 28.26     19      48
[2,]      2   63   57     62  33 109  55  71  16 12.02 19.07     45      84
[3,]      3  149  149    149  86 201 138 160  22 15.86 10.61    126     175
[4,]      4   41   42     41  19  81  35  47  12  9.16 22.23     27      57
[5,]      5   61   58     61  31 100  53  68  15 11.26 18.36     44      80
[6,]      6   20   18     19   4  44  15  24   9  6.54 33.12     11      31
```

```
head(nt_stnb[[t]]$rnd_values)
```

```
   region iter NPop
1:      1    1   35
2:      2    1   53
3:      3    1  152
4:      4    1   48
5:      5    1   51
6:      6    1   27
```

7.4. Origin-destination matrices

7.4.1. Brief methodological description

The inference of the origin-destination matrices for the target population is more delicate than the present population because auxiliary information from population registers do not contain this kind of information. Therefore, the statistical models proposed above for the present population estimation cannot be applied. As a first important conclusion we point out that, in our view, National Statistical Plans should start considering what kind of auxiliary information is needed to make a more accurate use of Mobile Network Data and new digital data, in general.

We can provide a simple argument extending the above model to produce credible intervals for the origin-destination matrices. If N_{tr} and $\tau_{t,rs}$ denote the number of individuals of the target population at time t in region r and the aggregate transition probability from region s to region

r at the time interval $(t-1,t)$, then we can simply define $N_{t,rs} = N_{t-1s} \times \tau_{t,rs}$ and trivially build the origin-destination matrix for each time interval $(t-1,t)$. Under the same general assumption as before, if individuals are to move across the geographical territory independently of their mobile network operator (or even not being a subscriber or carrying two devices), we can postulate as a first simple choice $\tau_{t,rs} = \tau^{\text{net}}_{t,rs}$, as before.

7.4.2. Implementation step by step

As final step, the origin-destination matrices for all pairs of time instants `time_from-time_to` are computed. We follow the implementation in the R package `inference` and the three distributions: Beta Negative Binomial, Negative Binomial and the state process Negative Binomial.

This computation is performed by `computePopulationOD()` function which takes the same input parameters as `computePopulationT()`. The result of this function is again a list with one element for each pair of `time_from-time_to`. Each element of the list is also a list with one or two elements, depending on the value of the `rndVal` parameter. If `rndVal` is `TRUE` there are two elements in the list corresponding to a time instant pair (`time_from, time_to`). The first one is a data.table object with some descriptive statistics for the origin-destination matrix, containing the following columns: `region_from, region_to, Mean, Mode, Median, Min, Max, Q1, Q3, IQR, SD, CV, CI_LOW, CI_HIGH`. The second one is a data.table object with the random values for origin-destination matrix generated for each pair of time instants `time_from-time_to` and each pair of regions `region_from-region_to`, with the following columns: `region_from, region_to, iter, NPop`. If `rndVal` is `FALSE` the list for a pair of time instants `time_from-time_to` contains only the first element previously mentioned. The name of the list element corresponding to a pair of time instants is `time_from-time_to` and the name of the two list elements giving the descriptive statistics and random values are `stats` and `rnd_values`.

```
# Beta Negative Binomial distribution
OD_bnb <- computePopulationOD(nt0 = n_bnb$rnd_values,
   nnetODFileName = nnetODFile,
   rndVal = TRUE)

# to display results, select a random time instant
time_pairs <- names(OD_bnb)
i          <- sample(1:length(time_pairs), size = 1)
time_pairs[i]
head(OD_bnb[[i]]$stats)
```

```
     region_from region_to Mean Mode Median Min Max Q1 Q3 IQR    SD
[1,]           1         1   34   28     33   6  95 26 41  15 11.81
[2,]           1         2    1    0      0   0  12  0  0   0  1.35
[3,]           1         3    0    0      0   0   0  0  0   0  0.00
[4,]           1         4    0    0      0   0   5  0  0   0  0.50
[5,]           1         5    0    0      0   0   0  0  0   0  0.00
[6,]           1         6    0    0      0   0   0  0  0   0  0.00
          CV CI_LOW CI_HIGH
[1,]  34.50  17.96   56.00
[2,] 259.79   0.00    3.64
[3,]    NaN   0.00    0.00
[4,] 665.94   0.00    0.00
```

```
[5,]    NaN   0.00    0.00
[6,]    NaN   0.00    0.00
```

```
head(OD_bnb[[i]]$rnd_values)
```

```
   region_from region_to iter NPop
1:           1         1    1   63
2:           1         2    1    0
3:           1         3    1    0
4:           1         4    1    0
5:           1         5    1    0
6:           1         6    1    0
```

```
# Negative Binomial distribution
OD_nb <- computePopulationOD(nt0 = n_nb$rnd_values,
   nnetODFileName = nnetODFile,
   rndVal = TRUE)

# to display results, select a random time instant
time_pairs <- names(OD_nb)
i <- sample(1:length(time_pairs), size = 1)
time_pairs[i]
head(OD_nb[[i]]$stats)
```

```
     region_from region_to Mean Mode Median Min Max Q1 Q3 IQR   SD      CV
[1,]           1         1   32   30     31   5  79 25 38  13 9.99   30.85
[2,]           1         2    0    0      0   0   9  0  0   0 1.25  253.77
[3,]           1         3    0    0      0   0   0  0  0   0 0.00     NaN
[4,]           1         4    0    0      0   0   5  0  0   0 0.49  667.92
[5,]           1         5    0    0      0   0   0  0  0   0 0.00     NaN
[6,]           1         6    0    0      0   0   0  0  0   0 0.00     NaN
     CI_LOW CI_HIGH
[1,]     18   50.00
[2,]      0    3.45
[3,]      0    0.00
[4,]      0    0.00
[5,]      0    0.00
[6,]      0    0.00
```

```
head(OD_nb[[i]]$rnd_values)
```

```
   region_from region_to iter NPop
1:           1         1    1   31
2:           1         2    1    0
3:           1         3    1    0
4:           1         4    1    0
5:           1         5    1    0
6:           1         6    1    0
```

```
# State process Negative Binomial distribution
OD_stnb <- computePopulationOD(nt0 = n_stnb$rnd_values,
nnetODFileName = nnetODFile,
rndVal = TRUE)
```

```
# to display results, select a random time instant
time_pairs <- names(OD_stnb)
i <- sample(1:length(time_pairs), size = 1)
time_pairs[i]
head(OD_stnb[[i]]$stats)
```

```
     region_from region_to Mean Mode Median Min Max Q1 Q3 IQR   SD     CV
[1,]           1         1   30   32     30   8  60 24 36  12 8.83  29.17
[2,]           1         2    0    0      0   0   8  0  0   0 1.17 252.68
[3,]           1         3    0    0      0   0   0  0  0   0 0.00    NaN
[4,]           1         4    0    0      0   0   5  0  0   0 0.44 664.15
[5,]           1         5    0    0      0   0   0  0  0   0 0.00    NaN
[6,]           1         6    0    0      0   0   0  0  0   0 0.00    NaN
     CI_LOW CI_HIGH
[1,]  17.19   45.00
[2,]   0.00    3.25
[3,]   0.00    0.00
[4,]   0.00    0.00
[5,]   0.00    0.00
[6,]   0.00    0.00
```

```
head(OD_stnb[[i]]$rnd_values)
```

```
   region_from region_to iter      NPop
1:           1         1    1 37.846154
2:           1         2    1  3.153846
3:           1         3    1  0.000000
4:           1         4    1  0.000000
5:           1         5    1  0.000000
6:           1         6    1  0.000000
```

7.5. The inference REST API

7.5.1. A conceptual overview

The `inference` package can also expose its main functions as a `http REST API` implemented using the `plumber` package (Trestle Technology, LLC, 2018). We have to mention from the beginning that this feature is an add-on, i.e. `inference` package can be used without this interface as presented in the previous sections. By adding this extra-functionality we wanted to open a new development track for future versions of our packages because it presents a series of advantages. Exposing the functionalities of this package as a `http API` has several advantages:

- `APIs` are flexible, easy to deploy and maintain, and they are accessible by multiple clients at the same time;
- `APIs` can be accessed via Internet by anyone without install any `R` package on his/her computer (`destim`, `deduplication`, `aggregation`, `inference`), so, our software is easily accessible;
- a user can write not only `R` code to access the functions exposed by the `inference` package, but he/she can use any language (Java, Python, etc.) capable of sending `API` requests over Internet;

- for large datasets, the functions from the `inference` package can take a long time to compute their results. In this case the `inference` package can be installed on a powerful computer that makes public its `API` to all the users, saving thus further investments in infrastructure;

Using a `http REST API` to access the processing functions in the `inference` package is in line with the proposed models of mobile phone data usage: the data sets stays in the MNO premises and the statisticians perform their data analyses calling functions from the available `API`. Of course, the functions available through the API should be first agreed between the MNOs and statistical offices. In a real environment, more precaution should be taken, i.e. using encrypted connections or even VPNs.

In figure 7.1 we have a representation of the interaction between a client and the `inference` API.

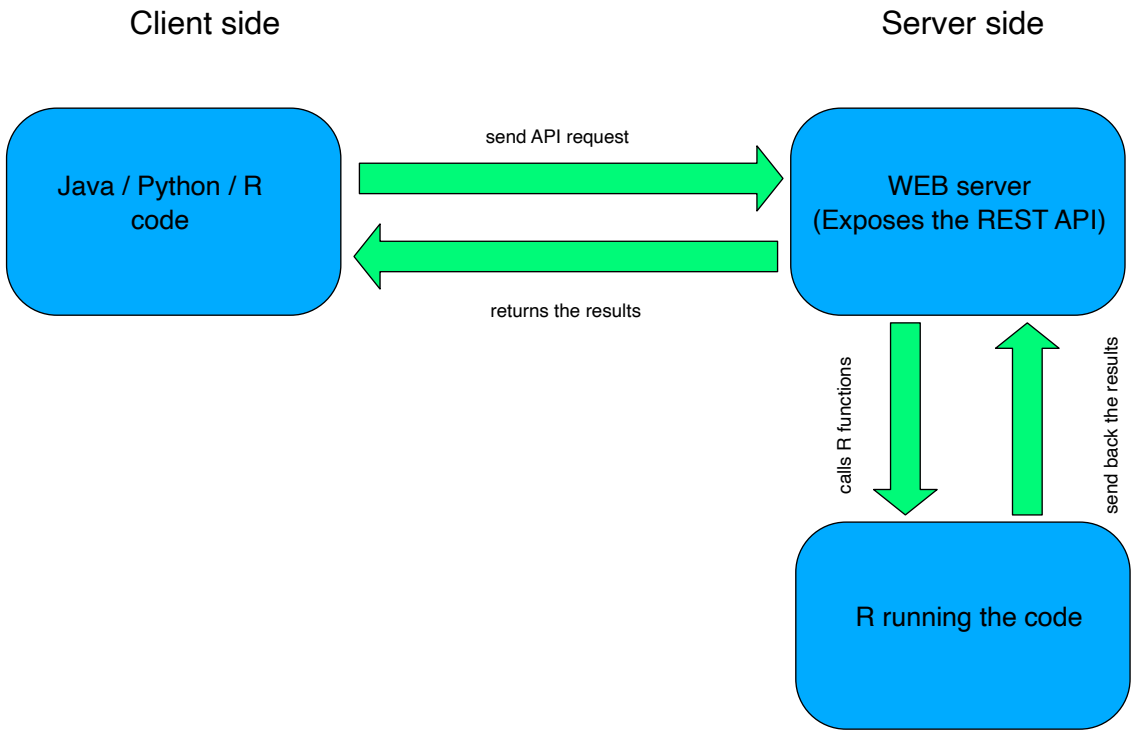


Figure 7.1: The client-server architecture of `inference`.

A client that can be a script/program written in `R`, `Python`, `Java` or any other language sends a request to the Web server exposing the `API`. In turn, the server calls the specific R functions invoked by the `API` sending them the parameters extracted from the body of the request. An `R` instance runs the function and sends back the results to the server. The server packs the results in a supported format (JSON for example) and sends the response to the client which unpacks the body of the response to get the requested data.

7.5.2. API example step by step

We implemented this feature using the `plumber` R package. The code presented below is the equivalent of the previous examples, but it uses the `API` to call functions of the `inference` package. The first step is to install the `inference` package on the server which can be the local

computer (as we will use in our examples) or another true Web server accessible via Internet.

In our examples we use the same computer as client and server and we need to run two instances of R. In one instance we will start the `http API`:

```
library(plumber)
pathPL <-'plumber'
initPop_api <- plumber::plumb(system.file(pathPL, 'plumb.R',
                                          package = 'inference'))
initPop_api$run(host = '127.0.0.1', port = 8000)
```

The address 127.0.0.1 can be changed with the address of any other server. After running these lines of code, if we access the localhost at port 8000 we will see the interface shown in figure 7.2.

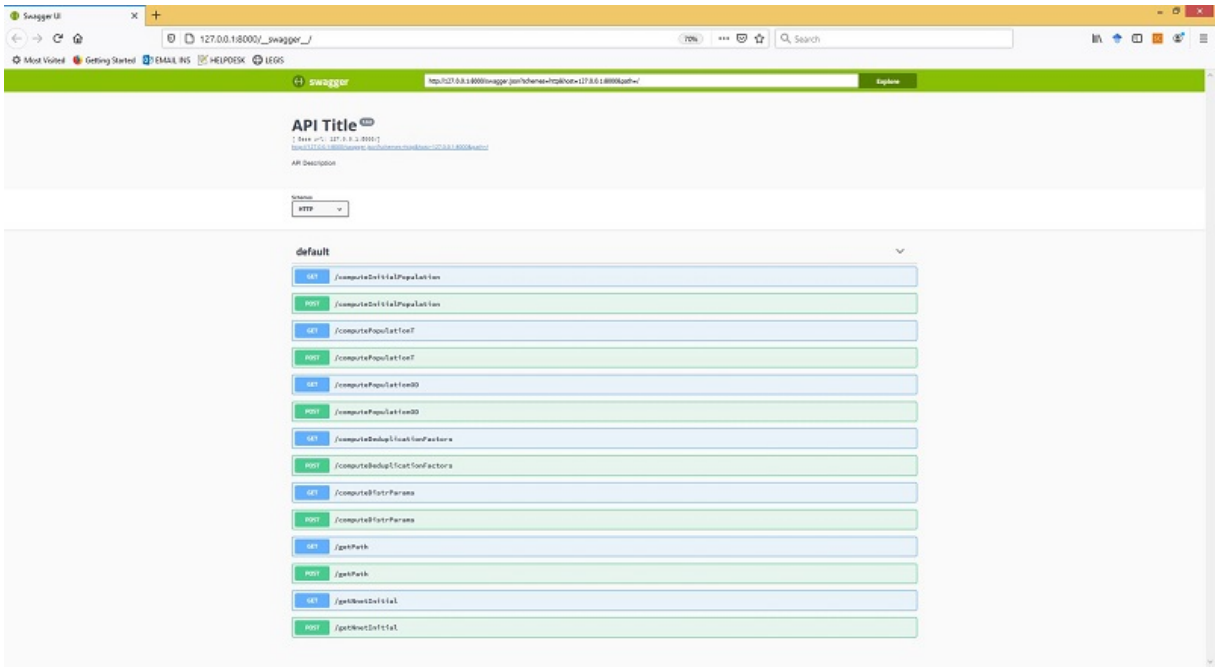


Figure 7.2: The client-server architecture of inference.

Here we can see the names of the endpoints of our API as well as the methods that can be used to access them (in our case `GET` and `POST`). Our `API` exposes the `computeDeduplicationFactors()`, `computeDistrParams()`,`computeInitialPopulation()`,`computePopulationT()` and `computePopulationOD()` as main processing functions and `getPath()` and `readNnetInitial()` needed for intermediate steps. The end points of the `API` have the same names as the functions they make public.

Now we have to switch to the other `R` instance which will act as a client. First we have to set the folder where the file with duplicity probabilities (`duplicity.csv`, comming from `deduplication` package) and the file defining the regions (`regions.csv`, defined by the user) are stored and the prefix of the posterior location probabilities files for all devices (files that are the output of the `destim` package). These example files are provided in the `inference` package but the user can change them with his/her own files.

Please note that if you run this example using a true client-server configuration, where the client and the server reside on different machines, in the same or different networks, the IP addresses should be updated accordingly. The path of the files needed for computation should be also updated according to their actual location.

```
library(httr)
library(jsonlite)
library(data.table)

# Set the folder where the necessary input files are stored and
# the prefix of the input file names.
path      <- 'extData'
prefix <- 'postLocDevice'
dpFileName <- system.file(path, 'duplicity.csv',
                          package = 'inference')
rgFileName <- system.file(path, 'regions.csv',
                          package = 'inference')
```

Next, we compute the deduplication factors. For this we have prepare the body of the `http` request, set the `API` path, set the `url` of the `API` and then send the request. In our example we used the `POST` method to send this request. The body of the `http` request contains the parameters needed by the `R` function that computes the deduplication factors. They are sent packing them in `JSON` format.

```
# prepare the body of the http request
body <- list(
 .dupFileName = dpFileName,
 .regsFileName = rgFileName,
 .postLocPrefix = prefix,
 .postLocPath = postLocPath
)

# set API path
pathDedup <- 'computeDeduplicationFactors'

# send POST Request to API
url <- "http://127.0.0.1:8000"
raw.result <- POST(url = url,
                   path = pathDedup,
                   body = body,
                   encode = 'json')
```

Now we obtained the result. First, we check that everything went OK (we have to obtain code 200) and then unpack it from `JSON` format back to an `R` object:

```
# check status code
raw.result$status_code

# transform back the results from json format
omega_r <- as.data.table(fromJSON(rawToChar(raw.result$content)))
```

Next, we compute the parameters of the posterior distribution of the population count using a similar approach: prepare the input data and build the body of the `http` request, set the `API`

path and then send the request. After the API send back the response we check the status code (it should be 200 if all went OK) and unpack the response from JSON to an R object.

```
# Compute the parameters of the distribution
# First reads the number of individuals detected by network
nFileName <- system.file(path, 'nnet.csv', package = 'inference')
nnet <- readNnetInitial(nFileName)

pRFileName <- system.file(path, 'pop_reg.csv', package = 'inference')
pRateFileName <- system.file(path, 'pnt_rate.csv', package = 'inference')
grFileName <- system.file(path, 'grid.csv', package = 'inference')

# prepare the body of the http request
body <- list(
 .omega = omega_r,
 .popRegFileName = pRFileName,
 .pntRateFileName  = pRateFileName,
 .regsFileName = rgFileName,
 .gridFileName = grFileName,
 .rel_bias = 0,
 .cv = 1e-5
)

# set API path
pathDistr <- 'computeDistrParams'

# send POST Request to API
raw.result <- POST(url = url,
                   path = pathDistr,
                   body = body,
                   encode = 'json')

# check status code
raw.result$status_code

# transform back the results from json format
params <- as.data.table(fromJSON(rawToChar(raw.result$content)))
```

We can compute now the population at initial time. In our example we will use only the Beta Negative Binomial distribution. A similar approach should be followed for the other two distributions.

```
# Compute the population count distribution at t0
# using the Beta Negative Binomial distribution

# prepare the body of the http request
body <- list(
 .nnet = nnet,
 .params = params,
 .popDistr = 'BetaNegBin',
 .rndVal = TRUE,
 .ciprob = 0.95,
 .method = 'ETI'
)
```

```
# set API path
pathInit <- 'computeInitialPopulation'

# send POST Request to API
raw.result <- POST(url = url,
                   path = pathInit,
                   body = body,
                   encode = 'json')

# check status code
raw.result$status_code

# transform back the results from json format
n_bnb <- fromJSON(rawToChar(raw.result$content))

# display results
n_nb$stats
head(n_nb$rnd_values)
```

Computing the population at time instants $t > t_0$ is performed as follows:

```
# Compute the population count distribution at time instants t > t0
# using the Beta Negative Binomial distribution
# first set the name of the file with the population moving
# from one region to another (output of the aggregation package)
nnetODFile <- system.file(path, 'nnetOD.zip', package = 'inference')

# prepare the body of the http request
body <- list(
 .nt0 = as.data.table(n_bnb$rnd_values),
 .nnetODFileName = nnetODFile,
 .zip = TRUE,
 .rndVal = TRUE,
 .ciprob = 0.95,
 .method = 'ETI'
)

# set API path
pathT <- 'computePopulationT'

# send POST Request to API
raw.result <- POST(url = url,
                   path = pathT,
                   body = body,
                   encode = 'json')

# check status code
raw.result$status_code

# transform back the results from json format
nt_bnb <- fromJSON(rawToChar(raw.result$content))

# display results
# first, select a random time instant
times <- names(nt_bnb)
t <- sample(1:length(times), size = 1)
```

```
t
nt_bnb[[t]]$stats
head(nt_bnb[[t]]$rnd_values)
```

Finally, we show how to compute the origin-destination matrix:

```
# Compute the Origin-Destination matrices for all pairs of time
# instants time_from-time_to using the Beta Negative Binomial distribution

# prepare the body of the http request
body <- list(
 .nt0 = as.data.table(n_bnb$rnd_values),
 .nnetODFileName = nnetODFile,
 .zip = TRUE,
 .rndVal = TRUE,
 .ciprob = 0.95,
 .method = 'ETI'
)

# set API path
pathOD <- 'computePopulationOD'

# send POST Request to API
raw.result <- POST(url = url,
                   path = pathOD,
                   body = body,
                   encode = 'json')

# check status code
raw.result$status_code

# transform back the results from json format
OD_bnb <- fromJSON(rawToChar(raw.result$content))

# display results
time_pairs <- names(OD_bnb)
# first, select a random time instants pair
i <- sample(1:length(time_pairs), size = 1)
time_pairs[i]
OD_bnb[[i]]$stats
head(OD_bnb[[i]]$rnd_values)
```

The `http REST API` of the inference can be called from any programming language or programs (like `curl` for example) capable of sending `http` requests. We show here a small `Python` script that demonstrates how to use the `R` inference `API` from another programming language. In this example we show only how to compute the population at initial time, but the rest of the computations are done in a similar way. The steps are the same as in the preceding example with two exceptions: we need to know the path where the input files are stored and we call `getPath API` method and to read the number of individuals detected by the network for which we called `getNnetInitial API` method. These two intermediate `API` calls were not necessary in the `R` example since they are available as functions of the `plumber` package.

```
""import requests
import simplejson
import pandas as pd
```

```
4
5  data = {"path": "extData"}
6  data_json = simplejson.dumps(data)
7
8  session = requests.Session()
9  session.trust_env = False
10 r = session.post("http://127.0.0.1:8000/getPath",
11                  data = data_json )
12
13 path = simplejson.loads(r.content)[0]
14 prefix = 'postLocDevice'
15 postLocPath = path
16 dpFileName = path +"/" + "duplicity.csv"
17 rgFileName = path + "/" + "regions.csv"
18
19 body = {\
20         ".dupFileName":dpFileName,\
21         ".regsFileName":rgFileName,\
22         ".postLocPrefix":prefix,\
23         ".postLocPath":path\
24 }
25
26 body_json = simplejson.dumps(body)
27 r = session.post("http://127.0.0.1:8000/computeDeduplicationFactors",
28                  data = body_json )
29
30 omega_r = simplejson.loads(r.content)
31 omega_r_df = pd.read_json(r.content)
32
33 omega_r_df
34
35 pRFileName = path +"/" + "pop_reg.csv"
36 pRateFileName = path +"/" + "pnt_rate.csv"
37 grFileName = path +"/" + "grid.csv"
38
39 body = { \
40         ".omega" :omega_r, \
41         ".popRegFileName" : pRFileName, \
42         ".pntRateFileName" : pRateFileName, \
43         ".regsFileName" : rgFileName, \
44         ".gridFileName" : grFileName, \
45         ".rel_bias" : 0, \
46         ".cv" :1e-5 \
47 }
48
49 body_json = simplejson.dumps(body)
50 r = session.post("http://127.0.0.1:8000/computeDistrParams",
51                  data = body_json )
52
53 params = simplejson.loads(r.content)
54 params_df = pd.read_json(r.content)
55
56 params_df
57
58 nnetFileName = path +"/" + "nnet.csv"
59 body = {".nnetFileName":nnetFileName}
60 body_json = simplejson.dumps(body)
61 r = session.post("http://127.0.0.1:8000/getNnetInitial",
62                  data = body_json )
63 nnet_r = simplejson.loads(r.content)
64
65 body = {\
66         ".nnet"  :  nnet_r, \
67         ".params" : params, \
68         ".popDistr" : 'BetaNegBin',\
69         ".rndVal" : True,\
70         ".ciprob" : 0.95,\
71         ".method" : 'ETI'\
72 }
73 body_json = simplejson.dumps(body)
74 r = session.post("http://127.0.0.1:8000/computeInitialPopulation",
```

```
                  data = body_json )

popInitStats = simplejson.loads(r.content)['stats']
popInitVals = simplejson.loads(r.content)['rnd_values']

stats = pd.DataFrame(popInitStats)
vals = pd.DataFrame(popInitVals)

stats
vals
%\end{verbatim}
```

7.6. Some remarks about computational efficiency

Functions in this package make use of the processing features of the data.table package which implements them very efficiently. Since population at t depends on population at $t-1$, the computation of the target population distributions at different time instants is inherently sequential. Functions that takes a longer time to execute display a progress bar to show how the computations advance.

In the API mode, the computational efficiency could be supported by a powerful server machine. Moreover, parallelization of the computations is achieved on server if several clients call in the same time different functions from API. For a real production environment a load balancer could be added too (available in `nginx` or one can use a docker-based solution **?**).

8

Further developments

This chapter is devoted to gather some reflections and conclusions for future work which will be part of the national efforts of the authors of this document and of the activity of the future ESS Task Force on MNO data. The following steps can be mainly divided in two approaches: the methodological modules and the computational implementation.

In the case of the methodological part, several branches to follow have been pointed out in the section about future prospects on the deliverable of methodology (Salgado et al., 2020). In summary, the methodological framework proposed does not intend to provide closed and definitive methods, but to put in place a first concrete substantiation of the ESS Reference Methodological Framework for Mobile Network Data. Much work remains to be done in the future. Results are encouraging, since we achieve modularity and evolvability, as well as rigorous accuracy indicators, giving a first solution to the main problem that comprise all the modules of the process.

Regarding the computational issues, we have developed all the implementation needed to execute the methods of the whole process. This implementation has been done in `R` which is a free software environment focus on statistical computing. Then, all the code is open, available and free to be used. Following the modularity ideas, an `R` package has been developed for each module of the process:

Module	**R package**
Geolocation	destim
Deduplication	deduplication
Aggregation	aggregation
Inference	inference

Regarding the future prospects about the organization of the developed software, we expect to connect all these packages with the aim to make them more user-friendly. The idea is to make another layer over these packages with some high level functions available to the user. These functions are devoted to obtain the final results executed in the inference layer which are the goal of the process. Then, they will call some functions from the
textttinference package which in turn will call functions from the `aggregation` package which will call functions from the `deduplication` package which will call functions from the `destim` package. The results will go back to the calling functions until they will reach again the top of the hierarchy and the users will have the answers to their query. The user requests go from the top of the hierarchy to the bottom and the answers go back from the bottom layer to the top. These calls will be optimized (borrowing the principle used by cache memories), for example

if a new inference problem implies the same geolocation problem and the results are already available, they will be not be computed again but provided from the storage. Of course, these optimizations will require some changes of the existing code with a considerable effort but will make all the intermediate steps transparent to users. The current interface will still be available, though.

In terms of computational efficiency, although several improvements have been done, there is a lot of work to upgrade the current implementation. Let see some possibilities:

Geolocation layer: There are some ideas about parallelization and a possible migration to take advantage of some highly optimized linear algebra libraries such as Intel Math Kernel Library (MKL). From now on, we have given priority to the idea of being able to distribute the software fully free with GPL license. At present, the estimation is done individually per device, efficiency can be substantially improved if it would be done for the whole set of the device all at once. Other high performance versions of the BLAS library can be considered too as alternatives to Intel MKL: OpenBLAS (Qian et al., 2013), GotoBLAS or GoToBLAS2 (Goto and van de Geijn, 2008), ATLAS (Whaley et al., 2001; Whaley and Dongarra, 1999).

Deduplication layer: All the improvements achieved in the geolocation layer will cause an improvement in the efficiency of the Bayesian approaches to execute deduplication. In relation to the trajectory approach, as well as in the majority of the processes, it has been taken into account the sparsity of the matrices of distances to speed up the executions. One computational intensive step of the trajectory method consist in computing the dispersion radius which involves the calculation of the (Euclidean) distances between the rows of a data matrix. For this specific step we use the standard `dist` function but in the future we can consider replacing it with `rpuDist` from `rpud` package (Yau, 2010) or `gpuDist` from `gputools` package (Buckner et al., 2010) which uses GPU to speed-up the computations. However, the increase in the speed of execution comes with the cost of decreasing the portability of the `deduplication` package since both `rpud` and `gputools` requires CUDA (Cook, 2012).

Aggregation layer: The aggregation module is base on a Poisson multinomial distribution and to increase the speed of execution the generation of random values from a Poisson multinomial distribution should be improved. Now we use a Monte Carlo approach to generate these values but wiser method could greatly improve the speed.

Inference layer: The computations performed in this layer are inherently serial, since the population at t depends on population at $t-1$, thus parallelization is not straightforward here. In case of very large data sets, some performance tests should be run to test if parallelization of computations inside a time iteration by dividing the datasets into several chunks and assigning them to different processors is efficient. Each processor should have enough computations to perform in order to overcome the overhead of setting up the cluster of processors.

For all packages in our software stack the parallelization is implemented using the standard `parallel` package available for `R`. We plan to test if other parallelization techniques and `R` packages can provide higher speedups and less memory requirements. To be more specific we intend to test `Rth` package (Matloff and Schmidt, 2015) the provides a function to compute the distance between rows of a matrix and has also parallel implementations for random number generators. Comparing to other GPU-oriented packages mentioned before, `Rth` support several parallel backends: CUDA, OpenMP or Intel TBB. So, if an NVIDIA card is not available to work

with CUDA, `Rth` functions uses the multithreading capabilities offered by OpenMP or TBB libraries. Another package that we intend to use in our performance tests is `Rdsm` (Matloff, 2014) which offers a shared-memory approach to parallel processing saving memory and execution time compared with the standard `parallel` package, although it is available only on Unix-like operating systems.

At this moment, only the `inference` package has a WEB REST API that allow calling its functions remotely. This decision was based on the fact that it is the package that provides the highest level functions to users: population estimations for different geographical areas. We intend to add such APIs to all packages developed so far, thus letting statisticians perform different data analysis at various levels of the methodological stack remotely.

Moreover, all the proposed methodology is supported by the results obtained from simulations due to the simulator (see Oancea et al., 2019), and all the implementation done in packages. In relation to the simulations, the future work is focused on testing different scenarios and compare the results to have a better understanding of the end-to-end process.

In conclusion, the whole methodology for the use of mobile network data in official statistical production needs further research and testing. In our view, Official Statistics should avoid past errors and struggle for a process-oriented approach to production. Concentrating on statistical domains with an abuse of one-off use cases will bring the risk of growing silos again in the production. In our view, the construction of this process-oriented statistical process with mobile network data should be made in partnerships with MNOs clearly identifying those critical elements in the methodology (which data to access and how to process them). The process must be end-to-end so that the production of official statistics can be openly disseminated.

In the same way as it is said for the methodology part, the implementation has to be done following the modularity of the process and with the aim to avoid developing software just for some specific statistical domain. The main result of this work is not in the details themselves of each module but on the whole process as a modular structure.

Appendix A

Reference manual for the `inference` package

Package 'inference'

October 28, 2020

Type Package

Title R package for computing the number of individuals in the target population conditioned on the number of individuals detected by the MNO and auxiliary information.

Version 0.1.0

Author Bogdan Oancea <bogdan.oancea@gmail.com>, David Salgado <david.salgado.fernandez@ine.es> Sandra Barragan <sandra.barragan.andres@ine.es>

Maintainer Bogdan Oancea <bogdan.oancea@gmail.com>

Description R package for computing the number of individuals in the target population conditioned on the number of individuals detected by the mobile network and some auxiliary information

License GPL3, EUPL

Imports data.table,
deduplication,
Matrix,
doParallel,
parallel,
extraDistr

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Suggests knitr,
rmarkdown

VignetteBuilder knitr

Collate 'buildCluster.R'
'computeDeduplicationFactors.R'
'computeDistrParams.R'
'utils.R'
'computeInitialPopulation.R'
'computeTau.R'
'computeStats.R'
'computePopulationOD.R'
'computePopulationT.R'
'computeRegionAreas.R'
'example.R'
'exampleAPI.R'

'inference.R'
'readNnetInitial.R'

R topics documented:

`computeDeduplicationFactors`
Computes the deduplication factors for each region.

Description

Computes the deduplication factors for each region of the map. For a complete description of these factors an interested reader can consult the description of the methodological framework https://webgate.ec.europa.eu/fpfis/mwikis/essnetbigdata/images/f/fb/WPI_Deliverable_I3_A_proposed_production_framework_with_mobile_network_data_2020_05_31_draft.pdf.

Usage

```
computeDeduplicationFactors(
  dupFileName,
  regsFileName,
  postLocPrefix,
  postLocPath
)
```

Arguments

`dupFileName`	The name of the file with the duplicity probabilities. This file is the output of the `deduplication` package.
`regsFileName`	The name of the .csv file defining the regions. It has two columns: `tile,region`. The first column contains the IDs of each tile in the grid while the second contains the number of a region. This file is defined by the user and it can be created with any text editor.
`postLocPrefix`	The file name prefix of the files with posterior location probabilities for each device. The whole file name is composed by a concatenation of `prefixName`, _ and `deviceID`. The extension of these files is `.dt.csv`
`postLocPath`	The path to the location where the posterior location probabilities are stored.

Value

A data.table object with the deduplication factors for each region.

References

https://github.com/MobilePhoneESSnetBigData

`computeDistrParams` *Computes the parameters of the population counts distributions.*

Description

Computes a series of parameters needed to build the target population counts distribution. For a complete description of these parameters an interested reader can consult the description of the methodological framework https://webgate.ec.europa.eu/fpfis/mwikis/essnetbigdata/images/f/fb/WPI_Deliverable_I3_A_proposed_production_framework_with_mobile_network_data_2020_05_31_draft.pdf.

Usage

```
computeDistrParams(
  omega,
  popRegFileName,
  pntRateFileName,
  regsFileName = NULL,
  gridFileName = NULL,
  rel_bias = 0,
  cv = 1e-05
)
```

Arguments

`omega`	The deduplication factors. They are computed by `computeDeduplicationFactors` function and it is a data.table object with the deduplication factors for each region.
`popRegFileName`	The name of the file with the population counts for each region taken from a population register. It has 2 columns: `region,N0`.
`pntRateFileName`	The name of the file with the penetration rates for each region. It has 2 columns: `region,pntRate`.
`regsFileName`	The name of the .csv file defining the regions. It has two columns: `tile,region`. The first column contains the IDs of each tile in the grid while the second contains the number of a region. This file is defined by the user and it can be created with any text editor. It is required only for the state process negative binomial distribution.
`gridFileName`	The name of the .csv file with the grid parameters. It is required only for the state process negative binomial distribution.
`rel_bias`	The value of the relative bias for the population density of each region. The default value is 0.
`cv`	The coefficient of variation for the population density of each region. The default value is 0.

Value

A data.table object with the following columns region,omega1,omega2,pnrRate,regionArea_km2, N0,dedupPntRate,alpha,beta. If regsFileName and gridFileName are not NULL the result will have 3 more columns:region,omega1,omega2,pnrRate,regionArea_km2,N0,dedupPntRate, alpha,beta,theta,zeta,Q. They are needed only for the state process negative binomial distribution.

References

https://github.com/MobilePhoneESSnetBigData

---

computeInitialPopulation

Computes the distribution of the population count at initial time instant.

Description

Computes the distribution of the population count at initial time instant using one of the three distributions: Negative Binomial, Beta Negative Binomial or State Process Negative Binomial. For details of the theoretical background behind this distribution an interested reader can consult the description of the methodological framework https://webgate.ec.europa.eu/fpfis/mwikis/essnetbigdata/images/f/fb/WPI_Deliverable_I3_A_proposed_production_framework_with_mobile_network_data_2020_05_31_draft.pdf.

Usage

```
computeInitialPopulation(
  nnet,
  params,
  popDistr,
  rndVal = FALSE,
  ciprob = NULL,
  method = "ETI"
)
```

Arguments

nnet	The random values generated with aggregation package for the number of individuals detected by the network.
params	The parameters of the distribution. It should be a data.table object with the following columns: region,omega1,omega2,pnrRate,regionArea_km2,N0, dedupPntRate,alpha,beta,theta,zeta,Q.
popDistr	The distribution to be used for population count. This parameter could have one of the following values: NegBin (negative binomial distribution), BetaNegBin (beta negative binomial distribution) or STNegBin (state process negative binomial distribution).

rndVal	If FALSE the result return by this function will be a list with a single element, a data.table object with the following columns: region,Mean,Mode,Median,SD, Min,Max,Q1,Q3,IQR,CV,CI_LOW,CI_HIGH. If TRUE the list will have a second element which is a data.table object containing the random values generated for each region.
ciprob	Value of probability of the CI (between 0 and 1) to be estimated. If NULL the default value is 0.89.
method	The method to compute credible intervals. It could have 2 values, 'ETI' or 'HDI'. The default value is 'ETI.

Value

A list object with one or two elements. If rndVal is FALSE the list will have a single element with descriptive statistics for the population count, which is a data.table object with the following columns: region,Mean,Mode,Median,Min,Max,Q1,Q3,IQR,SD,CV, CI_LOW,CI_HIGH. If rndVal is TRUE the list will have a second element which is a data.table object containing the random values generated for each region. The name of the two list elements giving the descriptive statistics and random values for time t are 'stats' and 'rnd_values'.

References

https://github.com/MobilePhoneESSnetBigData

---

computePopulationOD *Computes the origin-destination matrices.*

Description

Computes the origin-destination matrices for all pairs of time instants time_from-time_to. For details of the theoretical background of the origin-destination matrices computation an interested reader can consult the description of the methodological framework https://webgate.ec.europa.eu/fpfis/mwikis/essnetbigdata/images/f/fb/WPI_Deliverable_I3_A_proposed_production_framework_with_mobile_network_data_2020_05_31_draft.pdf.

Usage

```
computePopulationOD(
  nt0,
  nnetODFileName,
  zip = TRUE,
  rndVal = FALSE,
  ciprob = NULL,
  method = "ETI"
)
```

Arguments

nt0	The population at t0.
nnetODFileName	the name of the file where the population moving from one region to another is stored. This is an output of the aggregation package.

zip	If TRUE the file where where the population moving from one region to another is stored is a zipped csv file, otherwise it is simple csv file.
rndVal	Controls if the random values generated for each t are returned or not in the result of this function. If TRUE, the random values generated according to the corresponding distribution are returned in the results, if FALSE only the summary statistics for each t and region are returned.
ciprob	Value of probability of the CI (between 0 and 1) to be estimated. If NULL the default value is 0.89.
method	The method to compute credible intervals. It could have 2 values, 'ETI' or 'HDI'. The default value is 'ETI.

Value

A list with one element for each pair of time_from-time_to. Each element of the list is also a list with one or two elements, depending on the value of the rndVal parameter. If rndVal is TRUE there are two elements in the list corresponding to time instant a pair time_from-time_to. The first one is a data.table object with some descriptive statistics for the origin-destination matrix, containing the following columns:`region_from`,`region_to`,`Mean`,`Mode`,`Median`,`Min`,`Max`,`Q1`,`Q3`,`IQR`,`SD`,`CV`, `CI_LOW`,`CI_HIGH`. The second one is a data.table object with the random values for origin-destination matrix generated for each pair of time instants time_from-time_to and each pair of regions region_from-region_to, with the following columns: `region_from`,`region_to`,`iter`,`NPop`. If rndVal is FALSE the list for a pair of time instants time-from-time_to contains only the first element previously mentioned. The name of the list element corresponding to a pair of time instants is 'time_from-time_to' and the name of the two list elements giving the descriptive statistics and random values are 'stats' and 'rnd_values'.

References

https://github.com/MobilePhoneESSnetBigData

---

computePopulationT *Computes population counts at time instants t >t0.*

Description

Computes the distribution of the population counts for all times instants t > t0. For details of the theoretical background behind this distribution an interested reader can consult the description of the methodological framework https://webgate.ec.europa.eu/fpfis/mwikis/essnetbigdata/images/f/fb/WPI_Deliverable_I3_A_proposed_production_framework_with_mobile_network_data_2020_05_31_draft.pdf.

Usage

```
computePopulationT(
  nt0,
  nnetODFileName,
  zip = TRUE,
  rndVal = FALSE,
  ciprob = NULL,
  method = "ETI"
)
```

Arguments

nt0	The population at t0.
nnetODFileName	the name of the file where the population moving from one region to another is stored. This is an output of the aggregation package.
zip	If TRUE the file where where the population moving from one region to another is stored is a zipped csv file, otherwise it is simple csv file.
rndVal	Controls if the random values generated for each t >t0 are returned or not in the result of this function. If TRUE, the random values generated according to the corresponding distribution are returned in the results, if FALSE only the summary statistics for each t>t0 and region are returned.
ciprob	Value of probability of the CI (between 0 and 1) to be estimated. If NULL the default value is 0.89.
method	The method to compute credible intervals. It could have 2 values, 'ETI' or 'HDI'. The default value is 'ETI.

Value

A list with one element for each time instant (including t0). Each element of the list is also a list with one or two elements, depending on the value of the rndVal parameter. If rndVal is TRUE there are two elements in the list corresponding to time instant t. The first one is a data.table object with some descriptive statistics for the population count at time t, containing the following columns:region,Mean,Mode,Median,Min,Max,Q1,Q3,IQR,SD,CV,CI_LOW,CI_HIGH. The second one is a data.table object with the random values for population count generated for each region, with the following columns: region,iter,NPop. If rndVal is FALSE the list for time instant t contains only the first element previously mentioned. The name of the list element corresponding to time instant t is 't' and the name of the two list elements giving the descriptive statistics and random values for time t are 'stats' and 'rnd_values'.

References

https://github.com/MobilePhoneESSnetBigData

---

example *Example of using the inference package*

Description

This is just an example on how to use this package to generate the distribution of the population count.

Usage

```
example()
```

Details

This is a script that shows how to use the functions of this package to compute the distribution of the initial target population count, the distribution of the population count at successive time instants and the origin-destination matrix.

References

https://github.com/MobilePhoneESSnetBigData

Examples

```
# set the folder where the necessary input files are stored and the prefix of the input file names.
path      <- 'extData'

prefix <- 'postLocDevice'

# compute the deduplication factors
dpFileName <- system.file(path, 'duplicity.csv', package = 'inference')
rgFileName <- system.file(path, 'regions.csv', package = 'inference')

omega_r <- computeDeduplicationFactors(dpFileName, rgFileName, prefix,
system.file(path, package = 'inference'))

# reads the number of individuals detected by network
nFileName <- system.file(path, 'nnet.csv', package = 'inference')
nnet <- readNnetInitial(nFileName)

# compute the parameters of the distribution
pRFileName <- system.file(path, 'pop_reg.csv', package = 'inference')
pRateFileName <- system.file(path, 'pnt_rate.csv', package = 'inference')
grFileName <- system.file(path, 'grid.csv', package = 'inference')
params <- computeDistrParams(omega_r, pRFileName, pRateFileName, rgFileName, grFileName)

# A. Compute the population count distribution at t0
# compute the population count distribution using the Beta Negative Binomial distribution
n_bnb <- computeInitialPopulation(nnet, params, popDistr = 'BetaNegBin', rndVal = TRUE)

# display results
n_bnb$stats
head(n_bnb$rnd_values)


# compute the population count distribution using the Negative Binomial distribution
n_nb <- computeInitialPopulation(nnet, params, popDistr = 'NegBin', rndVal = TRUE)

# display results
n_nb$stats
head(n_nb$rnd_values)


# compute the population count distribution using the state process Negative Binomial distribution
n_stnb <- computeInitialPopulation(nnet, params, popDistr= 'STNegBin', rndVal = TRUE)

# display results
n_stnb$stats
head(n_stnb$rnd_values)


# B. compute the population count distribution at time instants t > t0
# first set the name of the file with the population moving from one region
# to another (output of the aggregation package)
```

```
nnetODFile <- system.file(path, 'nnetOD.zip', package = 'inference')

# 1.Using the Beta Negative Binomial distribution
nt_bnb <- computePopulationT(n_bnb$rnd_values, nnetODFile, rndVal = TRUE)


# display results
# first, select a random time instant
times <- names(nt_bnb)
t <- sample(1:length(times), size = 1)
t
nt_bnb[[t]]$stats
head(nt_bnb[[t]]$rnd_values)


# 2.Using the Negative Binomial distribution
nt_nb <- computePopulationT(n_nb$rnd_values, nnetODFile, rndVal = TRUE)

# display results
# first, select a random time instant
times <- names(nt_nb)
t <- sample(1:length(times), size = 1)
t
nt_nb[[t]]$stats
head(nt_nb[[t]]$rnd_values)
# 3.Using the state process Negative Binomial distribution
nt_stnb <- computePopulationT(n_stnb$rnd_values, nnetODFile, rndVal = TRUE)

# display results
# first, select a random time instant
times <- names(nt_stnb)
t <- sample(1:length(times), size = 1)
t
nt_stnb[[t]]$stats
head(nt_stnb[[t]]$rnd_values)

# C. compute the origin-destination matrices for all pairs of time instants time_from-time_to
# first set the name of the file with the population moving from one region
# to another (output of the aggregation package)
nnetODFile <- system.file(path, 'nnetOD.zip', package = 'inference')

# 1.Using the Beta Negative Binomial distribution
OD_bnb <- computePopulationOD(n_bnb$rnd_values, nnetODFile, rndVal = TRUE)

# display results
time_pairs <- names(OD_bnb)
# first, select a random time instants pair
i <- sample(1:length(time_pairs), size = 1)
time_pairs[i]
OD_bnb[[i]]$stats
head(OD_bnb[[i]]$rnd_values)

# 2.Using the Negative Binomial distribution
OD_nb <- computePopulationOD(n_nb$rnd_values, nnetODFile, rndVal = TRUE)

# display results
time_pairs <- names(OD_nb)
```

```
# first, select a random time instants pair
i <- sample(1:length(time_pairs), size = 1)
time_pairs[i]
OD_nb[[i]]$stats
head(OD_nb[[i]]$rnd_values)

# 3.Using the  state process Negative Binomial distribution
OD_stnb <- computePopulationOD(n_stnb$rnd_values, nnetODFile, rndVal = TRUE)

# display results
time_pairs <- names(OD_stnb)
# first, select a random time instants pair
i <- sample(1:length(time_pairs), size = 1)
time_pairs[i]
OD_stnb[[i]]$stats
head(OD_stnb[[i]]$rnd_values)
```

`exampleAPI` *Example of using the API inference*

Description

This is just an example on how to use the REST API of this package to generate the distribution of the population count.

Usage

```
exampleAPI()
```

Details

This is a script that shows how to use the REST API of this package to compute the distribution of the initial target population count, the distribution of the population count at successive time instants and the origin-destination matrix.

References

https://github.com/MobilePhoneESSnetBigData

Examples

```
########################################
# First, in a separate R console run the following instructions that start the http API
# on your local computer
# One can replace 127.0.0.1 with the API address of another Web server
library(plumber)
pathPL <-'plumber'
initPop_api <- plumber::plumb(system.file(pathPL, 'plumb.R', package = 'inference'))
initPop_api$run(host = '127.0.0.1', port = 8000)
########################################

library(httr)
```

```
library(jsonlite)
library(data.table)

# set the folder where the necessary input files are stored and the prefix of the input file names.
path      <- 'extData'
prefix <- 'postLocDevice'
postLocPath <- system.file(path, package = 'inference')

# compute the deduplication factors
dpFileName <- system.file(path, 'duplicity.csv', package = 'inference')
rgFileName <- system.file(path, 'regions.csv', package = 'inference')

# prepare the body of the http request
body <- list(
  .dupFileName = dpFileName,
  .regsFileName = rgFileName,
  .postLocPrefix = prefix,
  .postLocPath = postLocPath
)

# set API path
pathDedup <- 'computeDeduplicationFactors'

# send POST Request to API
url <- "http://127.0.0.1:8000"
raw.result <- POST(url = url, path = pathDedup, body = body, encode = 'json')

# check status code
raw.result$status_code

# transform back the results from json format
omega_r <- as.data.table(fromJSON(rawToChar(raw.result$content)))

# Compute the parameters of the distribution
# First reads the number of individuals detected by network
nFileName <- system.file(path, 'nnet.csv', package = 'inference')
nnet <- readNnetInitial(nFileName)

pRFileName <- system.file(path, 'pop_reg.csv', package = 'inference')
pRateFileName <- system.file(path, 'pnt_rate.csv', package = 'inference')
grFileName <- system.file(path, 'grid.csv', package = 'inference')

# prepare the body of the http request
body <- list(
   .omega = omega_r,
  .popRegFileName = pRFileName,
  .pntRateFileName  = pRateFileName,
  .regsFileName = rgFileName,
  .gridFileName = grFileName,
  .rel_bias = 0,
  .cv = 1e-5
)

# set API path
pathDistr <- 'computeDistrParams'

 # send POST Request to API
```

```
raw.result <- POST(url = url, path = pathDistr, body = body, encode = 'json')

# check status code
raw.result$status_code

# transform back the results from json format
params <- as.data.table(fromJSON(rawToChar(raw.result$content)))

# Compute the population count distribution at t0 using the Beta Negative Binomial distribution

# prepare the body of the http request
body <- list(
  .nnet = nnet,
  .params = params,
  .popDistr = 'BetaNegBin',
  .rndVal = TRUE,
  .ciprob = 0.95,
  .method = 'ETI'
)

# set API path
pathInit <- 'computeInitialPopulation'

 # send POST Request to API
raw.result <- POST(url = url, path = pathInit, body = body, encode = 'json')

# check status code
raw.result$status_code

# transform back the results from json format
n_bnb <- fromJSON(rawToChar(raw.result$content))

# display results
n_bnb$stats
head(n_bnb$rnd_values)

# Compute the population count distribution at time instants t > t0 using the
# Beta Negative Binomial distribution
# first set the name of the file with the population moving from one region
# to another (output of the aggregation package)
nnetODFile <- system.file(path, 'nnetOD.zip', package = 'inference')

# prepare the body of the http request
body <- list(
  .nt0 = as.data.table(n_bnb$rnd_values),
  .nnetODFileName = nnetODFile,
  .zip = TRUE,
  .rndVal = TRUE,
  .ciprob = 0.95,
  .method = 'ETI'
)

# set API path
pathT <- 'computePopulationT'

 # send POST Request to API
raw.result <- POST(url = url, path = pathT, body = body, encode = 'json')
```

```
# check status code
raw.result$status_code

# transform back the results from json format
nt_bnb <- fromJSON(rawToChar(raw.result$content))

# display results
# first, select a random time instant
times <- names(nt_bnb)
t <- sample(1:length(times), size = 1)
t
nt_bnb[[t]]$stats
head(nt_bnb[[t]]$rnd_values)


# Compute the Origin-Destination matrices for all pairs of time instants
# time_from-time_to using the Beta Negative Binomial distribution

# prepare the body of the http request
body <- list(
  .nt0 = as.data.table(n_bnb$rnd_values),
  .nnetODFileName = nnetODFile,
  .zip = TRUE,
  .rndVal = TRUE,
  .ciprob = 0.95,
  .method = 'ETI'
)

# set API path
pathOD <- 'computePopulationOD'

 # send POST Request to API
raw.result <- POST(url = url, path = pathOD, body = body, encode = 'json')

# check status code
raw.result$status_code

# transform back the results from json format
OD_bnb <- fromJSON(rawToChar(raw.result$content))

# display results
time_pairs <- names(OD_bnb)
# first, select a random time instants pair
i <- sample(1:length(time_pairs), size = 1)
time_pairs[i]
OD_bnb[[i]]$stats
head(OD_bnb[[i]]$rnd_values)
```

---

inference	*inference: A package for computing the distribution of the number of individuals in the target population conditioned on the number of individuals detected by MNO.*

Description

This package contains functions to compute the distribution of the number of individuals in the target population conditioned on the number of individuals detected by MNO. For an example on how to use this package please read example or exampleAPI.

`readNnetInitial` *Reads the number of individuals detected by network at initial time.*

Description

Reads the number of individuals detected by network at initial time instant, as they are generated by the `aggregation` package.

Usage

```
readNnetInitial(nnetFileName)
```

Arguments

`nnetFileName`	The file name of the random values generated by the `aggregation` package for the number of individuals detected by network for each region and each time instant.

Value

A data.table object with two columns: `region,N`

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Appendix B

Reference manual for the `aggregation` package

Package 'aggregation'

October 28, 2020

Type Package

Title R package for aggregation of device numbers into population number

Version 0.1.0

Author Bogdan Oancea <bogdan.oancea@gmail.com>, David Salgado <david.salgado.fernandez@ine.es> Sandra Barragan <sandra.barragan.andres@ine.es>

Maintainer Bogdan Oancea <bogdan.oancea@gmail.com>

Description R package for aggregation of the number of devices detected by mobile network into the number of individuals.

License GPL3, EUPL

Imports data.table,
deduplication,
Matrix,
doParallel,
parallel,
extraDistr

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Suggests knitr,
rmarkdown

VignetteBuilder knitr

Collate 'aggregation.R'
'buildCluster.R'
'buildPostLocJointProbs.R'
'rNnet_Event.R'
'doAggr.R'
'example.R'
'nIndividuals.R'
'nIndividuals3.R'
'rNnetEvent.R'
'rNnetJoint_Event.R'
'rNnetEventOD.R'

R topics documented:

`aggregation` *aggregation: A package for computing the number of individuals detected by the network.*

Description

This package contains functions to compute the number of individuals detected by the network in each geogrphical region as well as the number of individuals detected by the network moving from one region to another at successive time instants. For an example on how to use this package please read example.

`example` *Example of using the aggregation package*

Description

This is just an example on how to use this package to generate random values from a Poisson multinomial distribution in order to obtain a point estimate of the number of individuals detected by mobile network in a region.

Usage

```
example()
```

Details

This is a script that shows how to use the functions of this package to compute a point estimate of the number individuals detected by the network in each region and the number of individuals moving from one region to another. From the set of random values one can obtain any point estimate: mean. mode, median.

References

https://github.com/MobilePhoneESSnetBigData

Examples

```
# set the folder where the necessary input files are stored and the prefix of
# the input file names.
path      <- 'extdata'

prefix='postLocDevice'

# gets the series of time instants from the simulation.xml file.
simParams <-deduplication::readSimulationParams(system.file(path,
'simulation.xml', package = 'aggregation'))
time_from <- simParams$start_time
time_to <- simParams$end_time
time_incr <- simParams$time_increment
times<-seq(from=time_from, to=time_to-time_incr, by = time_incr)

# set the grid file name, i.e. the file the parameters of the grid
grFile <- system.file(path, 'grid.csv', package = 'aggregation')

# set the duplicity probabilities file name, i.e. the file with duplicity
# probability for each device
dpFile<-system.file(path, 'duplicity.csv', package = 'aggregation')

# set the regions file name, i.e. the file defining the regions for which we
# need the estimation of the number of individuals detected by network.
rgFile<-system.file(path, 'regions.csv', package = 'aggregation')

# generate n random values
n <- 1e3
nNet <- rNnetEvent(n, grFile, dpFile, rgFile, system.file(path,
package = 'aggregation'), prefix, times = times)

# print the mean number of detected individuals for each region, for each
# time instant
regions <- as.numeric(unique(nNet$region))
times <- unique(nNet$time)

for(r in regions) {
    print(paste0("region: ", r))
    for(t in times) {
        print(paste0("time instant: ", t, " number of individuals: " ,
        round(mean(nNet[region == r][time ==t]$N))))
    }
}


# For the origin-destination matrix we proceed in a similar way
prefixJ <- 'postLocJointProbDevice'
nnetOD <- rNnetEventOD(n, dpFile, rgFile, system.file(path,
package = 'aggregation'), prefixJ)

# The origin-destination matrix can be computed now very simple
# First we choose two consecutive time instants
t1 <- 0
t2 <- 10
# The we extract the regions:
```

```
regions_from <- sort(as.numeric(unique(nnetOD$region_from)))
regions_to <- sort(as.numeric(unique(nnetOD$region_to)))

# Now we compute the origin-destination matrix:
ODmat <- matrix(nrow = length(regions_from), ncol = length(regions_to))
for(r1 in regions_from) {
   for(r2 in regions_to) {
       ODmat[r1,r2] <-
       round(mean(nnetOD[time_from==t1][time_to==t2][region_from==r1][region_to==r2]$Nnet))
   }
}
ODmat
```

`rNnetEvent` *Generates random values according to a Poisson multinomial probability distribution.*

Description

Generates random values according to a Poisson multinomial probability distribution. A point estimation derived from this distribution (mean, mode) represents an estimation of the number of individuals detected by the network in a region. Regions are composed as a number of adjacent tiles. This is the only one function of this package available to users to compute an estimation of the number of detected individuals. For a theoretical background an interested reader can find more details in the methodological framework available here: https://webgate.ec.europa.eu/fpfis/mwikis/essnetbigdata/images/f/fb/WPI_Deliverable_I3_A_proposed_production_framework_with_mobile_network_data_2020_05_31_draft.pdf

Usage

```
rNnetEvent(
  n,
  gridFileName,
  dupFileName,
  regsFileName,
  postLocPath,
  prefix,
  times,
  seed = 123
)
```

Arguments

`n`	The number of random values to be generated.
`gridFileName`	The name of the .csv file with the grid parameters.
`dupFileName`	The name of the .csv file with the duplicity probability for each device. This is an output of the `deduplication` package.

regsFileName	The name of the .csv file defining the regions. It has two columns: tile,region. The first column contains the IDs of each tile in the grid while the second contains the number of a region. This file is defined by the user and it can be created with any text editor.
postLocPath	The path where the files with the posterior location probabilities for each device can be found. A file with the location probabilities should have the name prefix_ID.csv where ID is replaced with the device ID and prefix is given as a parameter to this function.
prefix	A prefix that is used to compose the file name with posterior location probabilities.
times	A vector with the time instants when the events were registered.
seed	The value of the random seed to be used by the random number generator.

Value

A data.table object with the following columns: time,region,N,iter. The last column contains the index of the random value (given in column N) generated for each time instant and region.

---

rNnetEventOD *Generates random value according to a Poisson multinomial distribution needed to estimate the origin destination matrices.*

Description

Generates random value according to a Poisson multinomial distribution needed to estimate the origin destination matrices. This is a high level function, the only one to be called by users to estimate the number of individuals going from one region to another. For a theoretical background an interested reader can find more details in the methodological framework available here: https://webgate.ec.europa.eu/fpfis/mwikis/essnetbigdata/images/f/fb/WPI_Deliverable_I3_A_proposed_production_framework_with_mobile_network_data_2020_05_31_draft.pdf The actual omputations are performed using a parallelization (transparent to the users) which uses the whole number of (logical) cores.

Usage

```
rNnetEventOD(
  n,
  dupFileName,
  regsFileName,
  postLocJointPath,
  prefix,
  seed = 123
)
```

Arguments

n	The number of random values to be generated.
dupFileName	The name of the .csv file with the duplicity probability for each device. This is an output of the deduplication package.

regsFileName — The name of the .csv file defining the regions. It has two columns: tile,region. The first column contains the IDs of each tile in the grid while the second contains the number of a region. This file is defined by the user and it can be created with any text editor.

postLocJointPath — The path where the files with the posterior location probabilities for each device can be found. A file with the location probabilities should have the name prefix_ID.csv where ID is replaced with the device ID and prefix is given as a parameter to this function.

prefix — A prefix that is used to compose the file name with posterior location probabilities.

Value

A data table object with the following columns: time_from,time_to,region_from,region_to,Nnet,iter. The number of detected individuals moving from a region to another between two succesive time instants is given in column Nnet while the last column gives the index of the random value generated for this number.

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Appendix C

Reference manual for the `deduplication` package

Package 'deduplication'

October 30, 2020

Type Package

Title R package for computing the duplicity probility for each mobile device.

Version 0.1.0

Author Bogdan Oancea <bogdan.oancea@gmail.com>, David Salgado <david.salgado.fernandez@ine.es> Sandra Barragan <sandra.barragan.andres@ine.es>

Maintainer Bogdan Oancea <bogdan.oancea@gmail.com>

Description R package for computing the duplicity probility for each mobile device, i.e. the probability of a device to be in a 2-to-1 correspondence with its owner.

License GPL3, EUPL

Imports data.table,
destim,
Matrix,
doParallel,
parallel,
rgeos,
stringr,
xml2,
Rsolnp

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Suggests knitr,
rmarkdown

VignetteBuilder knitr

Collate 'antennaNeighbours.R'
'aprioriDuplicityProb.R'
'aprioriOneDevice.R'
'buildCentroidProbs.R'
'buildCentroids.R'
'buildCluster.R'
'buildDeltaProb.R'
'buildDeltaProb2.R'
'buildDuplicityTable1to1.R'
'buildDuplicityTablePairs.R'
'centerOfProbabilities.R'

'checkConnections_step1.R'
'tileEquivalence.R'
'distance_coverArea.R'
'checkConnections_step2.R'
'computeDuplicity.R'
'computeDuplicityBayesian.R'
'dispersionRadius.R'
'readPostLocProb.R'
'computeDuplicityTrajectory.R'
'computePairs.R'
'deduplication.R'
'example1.R'
'example2.R'
'example3.R'
'fitModels.R'
'getDeviceIDs.R'
'getConnections.R'
'getEmissionProbs.R'
'getEmissionProbsJointModel.R'
'getGenericModel.R'
'getJointModel.R'
'modeDelta.R'
'readCells.R'
'readEvents.R'
'readGridParams.R'
'readSimulationParams.R'
'splitReverse.R'

R topics documented:

`antennaNeighbours` *Computes a list of neighbouring antennas.*

Description

Computes a list of pairs antennaID1-antennaID2 with neighbouring antennas. Two antennas are considered neighbours if their coverage areas overlap (i.e. their intersection is not void).

Usage

```
antennaNeighbours(coverarea)
```

Arguments

`coverarea`	a data.table object with two columns: `antennaID` and `cell`. The first column contains the ID of each antenna while the second one contains a `sp` object that represents the coverage area of the corresponding antenna. The coverage area is obtained by calling `readCells()` function.

Value

A data.table object with a single column called `nei`. Each element of this column is a pair of the form antennaID1-antennaID2 where the two antennas are considered neighbours.

`aprioriDuplicityProb` *Apriori probability of duplicity.*

Description

Apriori probability of duplicity, i.e. the probability of a device to be in a 2-to-1 correspondence with the person who holds it. It is computed as $2 * (Ndev - Ndev2)/(Ndev * (Ndev - 1))$ where $Ndev$ is the total number of devices and $Ndev2$ is the number of devices that are in a 1-to-1 correspondence with the persons that hold them.

Usage

```
aprioriDuplicityProb(prob2Devices, ndevices)
```

Arguments

`prob2Devices`	The probability of a person to have 2 devices. In case of using simulated data, this parameter is read from the simulation configuration file.
`ndevices`	The number of devices detected by the network during the time horizon under consideration.

Value

Apriori probability of duplicity, i.e. the probability of a device to be in a 2-to-1 correspondence with the person who holds it.

---

apriori0neDeviceProb *Apriori probability of a device to be in a 1-to-1 correspondence with its holder.*

Description

Apriori probability of a device to be in a 1-to-1 correspondence with the holder. It is computed simply as $(2 * Ndev1 - Ndev)/Ndev1$ where $Ndev1$ is the number of devices that are in a 1-to-1 correspondence with the persons that hold them and $Ndev$ is the total number of devices.

Usage

```
apriori0neDeviceProb(prob2Devices, ndevices)
```

Arguments

prob2Devices	The probability of a person to have 2 devices. In case of using simulated data, this parameter is read from the simulation configuration file.
ndevices	The number of devices detected by the network during the time horizon under consideration.

Value

The apriori probability of a device to be in a 1-to-1 correspondence with its holder.

---

checkConnections_step1 *Make the first step of the checks between the connections and the emission model.*

Description

This function obtains the results of the first step of checks for the compatibility between the connections observed and the emission model. It checks if each individual connection is coherent with the probabilities in the emission matrix. In those cases when that connection is not compatible, the connection is imputed with a missing value.

Usage

```
checkConnections_step1(connections, emissionProbs)
```

Arguments

connections	A matrix with the connections, a row per device and a column per time.
emissionProbs	A matrix of emission probabilities resulting from the function getEmissionProbs in **deduplication** package.

Value

A list with two elements: one is the information about the checks and the second is the matrix of connections with imputation in the observations not compatible with the model in emissionProbs.

---

checkConnections_step2 *Make the second step of the checks between the connections and the emission model.*

Description

This function obtains the results of the second step of checks for the compatibility between the connections observed and the emission model. It checks that the transitions from one connections to the following is coherent with the probabilities in the emission matrix. In those cases when the transition is not compatible, a solution to fit the model is given with the needed time padding coefficient.

Usage

```
checkConnections_step2(emissionProbs, connections, gridParams)
```

Arguments

emissionProbs	The matrix of emission probabilities.
connections	A matrix with the connections, a row per device and a column per time.
gridParams	A list with the parameters of the grid: nrow,ncol,tileX,tileY.

Value

A list with two elements" one is the information about the checks with a vector containing all the time padding coefficients and the second is the matrix of connections with the time padding done by using the maximum coefficient.

---

computeDuplicity *Computes the duplicity probability for each device.*

Description

Computes the duplicity probability for each device using three different methods: pairs, 1-to-1 and trajectory. The theory behind these methods is described in detail in WPI Deliverable 3 and in the paper *An end-to-end statistical process with mobile network data for Official Statistics*.

Usage

```
computeDuplicity(
  method,
  gridFileName,
  eventsFileName,
  signalFileName,
  antennaCellsFileName = NULL,
  simulatedData = TRUE,
  simulationFileName,
  netParams = NULL,
  path = NULL,
  gamma = 0.5,
  aprioriProbModel = NULL,
  aprioriProbJointModel = NULL,
  lambda = NULL,
  handoverType = "strength",
  emissionModel = NULL,
  antennaFileName = NULL,
  prefix = NULL
)
```

Arguments

method	The method used to compute the duplicity probability. It could have one of the following values: "pairs", "1to1", "trajectory".
gridFileName	The name of the file with the grid parameters. This file could be the one generated by the simulation software or can be created with any text editor. The grid file generated by the simulation software has the following columns: Origin X,Origin Y,X Tile Dim,Y Tile Dim,No Tiles X,No Tiles Y. We are interested only in the number of rows and columns and the tile size on OX and OY axes. Therefore, the file provided as input to this function should have at least the following 4 columns: No Tiles X ,No Tiles Y, X Tile Dim and Y Tile Dim.
eventsFileName	The name of the file with the network events to be used. Depending on the parameter simulatedData it could be a .csv file coming from the simulation software or from a real MNO. In case the file comes from the simulation software it contains following columns: time,antennaID,eventCode,deviceID,x,y,tile Only the first 4 columns are used, the rest are ignored.
signalFileName	The name of the .csv file that contains the signal strength/quality for each tile in the grid. Depending on the parameter simulatedData it could be a .csv file coming from the simulation software or from a real MNO. In case the file comes from the simulation software the data are organized as a matrix with the number of rows equals to the number of antennas and the the following columns: Antenna ID,Tile 0,Tile 1,... Tile (N-1). On the first column there are the antenna IDs and on the rest of the columns the corresponding signal strength/quality for each tile in the grid.
simulatedData	If TRUE the input data are provided by the simulation software, otherwise real data is used.
simulationFileName	The name of the file used to define a simulation scenario. It is the file that was provided as input for the simulation software. This file is required only if simulatedData is TRUE.

netParams — This parameter is required if simulatedData is FALSE, i.e. the **deduplication** package uses real mobile network data. In this case, netParam is a list with two elements: conn_threshold and prob_sec_mobile_phone. conn_threshold is the minimum value of the signal strength/quality that can be used to connect a mobile device to an antenna. If the signal in a region is below this value the region is considered out of the coverage area. prob_sec_mobile_phone is the probability of a person to have two mobile devices.

path — The path where the files with the posterior location probabilities for each device are to be found. This parameter is needed only if the "trajectory" method is used.

gamma — This value is used only for the "trajectory" method and is the factor used in the compariosn between the mode of Delta X and Delta Y and the dispersion radius. The default value is 0.5.

aprioriProbModel — This parameter is used to initialize the apriori probabilities for the HMM model for each device. The default value is NULL which means that by default the models are initialized with the steady state.

lambda — This parameter is used in combination with the "1-to-1" method. If it is NULL (which is the default value) the computations follow the description given in WPI Deliverable 3, otherwise the computations proceed as they are described in the *An end-to-end statistical process with mobile network data for Official Statistics* paper.

handoverType — The handover mechanism used by the mobile network. It could have two values: "strength" or "quality". The default value is "strength". This parameter is used to compute the emission probabilities for the HMM models using the values from the signal file. If this file contains the signal strength then the handoverType should be set to "strength" and if the file contains the values of the signal quality then the parameter should be set to "quality".

emissionModel — This parameter dictates how the emission probabilities for the HMM models are computed. It can have two values: "RSS" and "SDM". Normally, the emission probabilities are computed using the signal values from the signal file assuming that if the handoverType is set to "strength" then the signal file contains the strength values and if the handoverType is set to "quality" the signal file contains the quality of the signal. For demonstrative purposes the package supports unusual combinations. If handoverType is set to "strength", the signal file contains the signal strength but the emissionModel is set to "SDM" the signal strength values are transformed to signal quality and then the computation of the emission probabilities uses these transformed values. If handoverType is set to "quality", the signal file contains the signal quality but the emissionModel is set to "RSS", the signal quality values are transformed to signal strength and then the computation of the emission probablities uses these transformed values.

antennaFileName — The name of the xml file containing the technical parameters of the antennas needed to transform the signal quality into signal strength and the other way around. This is an input file of the simulation software. An example file is included in this package. The default value is NULL because this file is only needed to make unusual combinations between handoverType and the way the emission probabilities are computed.

prefix — The file name prefix for the files with posterior location probabilities.

cellsFileName — The name of the file where the coverage areas of antennas are to be found. It is a should be a .csv file with two values on each row: the antenna ID and a WKT

string representing a polygon (i.e. it should start with the word POLYGON) which is the coverage area of the corresponding antenna. This area is also called the antenna cell.

`aprioriJointModel`
: This parameter is used to initialize the apriori probabilities for the joint HMM models for each pair of two devices. The default value is NULL which means that by default the models are initialized with the steady state.

Value

a data.table object with two columns: `deviceID` and `dupP`. On the first column there are deviceIDs and on the second column the corresponding duplicity probability, i.e. the probability that a device is in a 2-to-1 correspondence with its holder.

`computeDuplicityBayesian`
: *Computes the duplicity probabilities for each device using a Bayesian approach.*

Description

Computes the duplicity probabilities for each device using a Bayesian approach. It uses two methods: "pairs" and "1to1". The "pairs" method considers the possible pairs of two compatible devices. These devices were selected by `computePairs()` function taking into consideration the antennas where the devices are connected and the coverage areas of antennas. Two devices are considered compatible if they are connected to the same or to neighbouring antennas. Thus, the data set with pairs of devices will be considerable smaller than all possible combinations of two devices. The "1to1" method considers all pairs of two devices when computing the duplicity probability, the time complexity being much greater than that of the "pairs" method. Both methods uses parallel computations to speed up the execution. They build a cluster of working nodes and splits the pairs of devices equally among these nodes.

Usage

```
computeDuplicityBayesian(
  method,
  deviceIDs,
  pairs4dupl,
  modeljoin,
  llik,
  P1 = NULL,
  Pii = NULL,
  init = TRUE,
  lambda = NULL
)
```

Arguments

`method`
: Selects a method to compute the duplicity probabilities. It could have one of the two values: "pairs" or "1to1". When selecting "pairs" method, the `pairs4dupl` parameter contains only the compatible pairs of devices, i.e. the pairs that most

	of the time are connected to the same or to neighbouring antennas. "1to1" method checks all possible combinations between devices to compute the duplicity probabilities.
deviceIDs	A vector with the device IDs. It is obtained by calling the getDevices() function.
pairs4dupl	A data.table object with pairs of devices and pairs of antennas where these devices are connected. It can be obtained by calling computePairs() function.
modeljoin	The joint HMM model returned by getJointModel() function.
llik	A vector with the values of the log likelihoods after the individual HMM models for each device were fitted. This vector can be obtained by calling fitModels() function.
P1	The apriori duplicity probability as it is returned by aprioriDuplicityProb() function. It is used when "pairs" method is selected.
Pii	Apriori probability of a device to be in a 1-to-1 correspondence with the holder as it is returned by aprioriOneDeviceProb() function. This parameter is used only when "1to1" method is selected.
init	A logical value. If TRUE, the fit() function uses the stored steady state as fixed initialization, otherwise the steady state is computed at every call of fit() function.
lambda	It is used only when "1to1" method is selected and a non NULL value mean that the computation of the duplicity probabilities is performed according to the method described in *An end-to-end statistical process with mobile network data for Official Statistics* paper.

Value

a data.table object with two columns: deviceID and dupP. On the first column there are deviceIDs and on the second column the corresponding duplicity probability, i.e. the probability that a device is in a 2-to-1 correspondence with the holder.

`computeDuplicityTrajectory` *Computes the duplicity probabilities for each device using the trajectory approach.*

Description

Computes the duplicity probabilities for each device using the trajectory approach described in WPI Deliverable 3.

Usage

```
computeDuplicityTrajectory(
  path,
  prefix,
  devices,
  gridParams,
  pairs,
  P1,
```

```
  T,
  gamma
)
```

Arguments

path	The path where the files with the posterior location probabilities for each device are to be found.
devices	A vector with device IDs.
gridParams	A list with the number of rows and columns of the grid and the tile dimensions on OX and OY axes. The items of the list are named nrow, ncol, tileX and tileY.
pairs	A data.table object containing pairs with the IDs of compatible devices. It is obtained calling buildPairs() function.
P1	The apriori probability for a device to be in 1-to-1 correspondence with its owner.
T	The sequence of time instants in the data set.
gamma	A coefficient needed to compute the duplicity probability. See WPI Deliverable 3.

Value

a data.table object with two columns: deviceID and dupP. On the first column there are deviceIDs and on the second column the corresponding duplicity probability, i.e. the probability that a device is in a 2-to-1 correspondence with the holder.

---

computePairs *Builds pairs of devices and corresponding connections.*

Description

Builds a data.table object that contains pairs of antenna IDs in the form "antennaID1-antennaID2", where antennaID1 corresponds to a device while antennaID2 corresponds to another device, for each time instant over a time period when the network events are registered. These pairs are build for each distinct combination "deviceID1-deviceID2" of devices. The rows of the data.table object corresponds to a combination of devices and the columns corresponds to different time instants. The first two columns contains the device IDs of each pair of devices and the rest of the columns correspond to a time instant and contains the pairs antennaID1-antennaID2 where the two devices are connected at that time instant.

Usage

```
computePairs(
  connections,
  ndevices,
  oneToOne = TRUE,
  P1 = 0,
  limit = 0.05,
  antennaNeighbors = NULL
)
```

Arguments

`connections`	A matrix with the antenna IDs where the mobile devices are connected at every time instant. Each row corresponds to a device and each column to a time instant. This matrix is obtained by calling `getConnections()` function.
`ndevices`	The number of devices registered by the network. A vector with device IDs can be obtained by calling `getDevices()` function and the number of devices is simply the lenght of this vector.
`oneToOne`	If TRUE, the result is built to apply the method "1to1" to compute the duplicity probability for each device. This means that the result will contain all combinations of devices. If FALSE, the result will consider the proximity of antennas through the parameter `antennaNeighbors` and remove all the combinations of devices that are impossible to belong to a single person. If most of the time instants two devices are connected to two antennas that are not neighbors (i.e. their cells don't overlap) we consider that these two devices belong to different persons and remove this combination of devices from the result. The term "most of the time instants" is implemented like this: we add how many times during the time horizon two devices are connected to neighboring antennas and than keep in the final result only those combinations of devices with this number greater than the quantile of the sequence 0...(Number of time instants) with probability 1-P1-limit. In this way we reduce the time complexity of the duplicity probability computation.
`P1`	The apriori probability of duplicity. It is obtained by calling `aprioriDuplicityProb()` function.
`limit`	A number that stands for the error in computing apriori probability of duplicity.
`antennaNeighbors`	A data.table object with a single column `nei` that contains pairs of antenna IDs that are neighbors in the form antennaID1-antennaID2. We consider that two antennas are neighbors if their coverage areas has a non void intersection.

Value

a data.table object. The first two columns contain the devices indices while the rest of the columns contains pairs antennaID1-antennaID2 with antenna IDs where the devices are connected. There is one column for each time instant for the whole time horizon.

`deduplication` *deduplication: A package for computing the duplicity probability for mobile device detected by the network.*

Description

This package contains functions to compute the duplicity probability for mobile device detected by the network. It has three methods for this purpose: pairs, 1-to-1 and trajectory. The theory behind these methods is described in detail in WPI Deliverable 3 and in the paper *An end-to-end statistical process with mobile network data for Official Statistics*. For an example on how to use this package please read example1, example2 and example3.

Details

deduplication: A package for computing the duplicity probability for mobile devices.

example1 *Example of using* **deduplication** *package - the simple way*

Description

This is just an example on how to compute duplicity probabilities using simulated data. All the files used in this example are supposed to be produced using the simulation software. The "simulation.xml" file is an exception and it is an input file for the simulation software. The files used in this example are provided with the **deduplication** package.

Usage

```
example1()
```

Details

This is just an example on how to compute duplicity probabilities using simulated data. All the files used in this example are supposed to be produced using the simulation software. The "simulation.xml" file is an exception and it is an input file for the simulation software. The files used in this example are provided with the **deduplication** package.This example showsthe simplest way of using this package. It reads the necessary input data and then calls `computeDuplicity` function.

References

https://github.com/MobilePhoneESSnetBigData

Examples

```
# set the folder where the necessary input files are stored
path_root      <- 'extdata'

# set the grid file name, i.e. the file where the grid parameters are found
gridfile <-system.file(path_root, 'grid.csv', package = 'deduplication')

# set the events file name, i.e. the file with network events registered during
# a simulation
eventsfile<-system.file(path_root, 'AntennaInfo_MNO_MNO1.csv',
package = 'deduplication')

# set the signal file name, i.e. the file where the signal strength/quality
# for each tile in the grid is stored
signalfile<-system.file(path_root, 'SignalMeasure_MNO1.csv',
package = 'deduplication')

# set the antenna cells file name, i.e. the file where the simulation software
# stored the coverage area for each antenna
# This file is needed only if the duplicity probabilities are computed using
# "pairs" method
antennacellsfile<-system.file(path_root, 'AntennaCells_MNO1.csv',
package = 'deduplication')

# set the simulation file name, i.e. the file with the simulation parameters
# used to produce the data set
```

```
simulationfile<-system.file(path_root, 'simulation.xml',
package = 'deduplication')

# compute the duplicity probabilities using the "pairs" method
out1<-computeDuplicity("pairs", gridFileName = gridfile,
eventsFileName = eventsfile, signalFileName = signalfile,
antennaCellsFileName = antennacellsfile, simulationFileName = simulationfile)

# compute the duplicity probabilities using the "1to1" method
out2<-computeDuplicity("1to1", gridFileName = gridfile,
eventsFileName = eventsfile, signalFileName = signalfile,
simulatedData = TRUE, simulationFileName = simulationfile)

# compute the duplicity probabilities using the "1to1" method with lambda
out2p<-computeDuplicity("1to1", gridFileName = gridfile,
eventsFileName = eventsfile, signalFileName = signalfile,
simulatedData = TRUE, simulationFileName = simulationfile, lambda = 0.67)

# compute the duplicity probabilities using the "trajectory" method
prefix <- 'postLocDevice'
out3<-computeDuplicity("trajectory", gridFileName = gridfile,
eventsFileName = eventsfile, signalFileName = signalfile,
antennaCellsFileName = antennacellsfile, simulationFileName = simulationfile,
path= system.file(path_root, package='deduplication'), prefix = prefix)
```

`example2` *Example of using* **deduplication** *package - the long way*

Description

This is just an example on how to compute duplicity probabilities using simulated data. All the files used in this example are supposed to be produced using the simulation software. The "simulation.xml" file is an exception and it is an input file for the simulation software. The files used in this example are provided with the **deduplication** package.

Usage

```
example2()
```

Details

This is detailed example on how to compute duplicity probabilities using simulated data. All the files used in this example are supposed to be produced using the simulation software. The "simulation.xml" file is an exception and it is an input file for the simulation software. The files used in this example are provided with the **deduplication** package. This example shows step by step all intermediate computations performed before calling one the functions that computes the duplicity probabilities. All three methods are used in this example: "1-to-1", "pairs" and "trajectory".

References

https://github.com/MobilePhoneESSnetBigData

Examples

```
# set the folder where the necessary input files are stored

path_root      <- 'extdata'

# 0. Read simulation params

simParams <-readSimulationParams(system.file(path_root, 'simulation.xml',
package = 'deduplication'))

 # 1. Read grid parameters

gridParams <-readGridParams(system.file(path_root, 'grid.csv',
package = 'deduplication'))

 # 2.Read network events

events <- readEvents(system.file(path_root, 'AntennaInfo_MNO_MNO1.csv',
package = 'deduplication'))

 # 3. Get a list of detected devices

devices <- getDeviceIDs(events)

#4. Get connections for each device

connections <- getConnections(events)

#5. Emission probabilities are computed from the signal strength/quality file

emissionProbs <- getEmissionProbs(gridParams$nrow, gridParams$ncol,
system.file(path_root, 'SignalMeasure_MNO1.csv', package = 'deduplication'),
simParams$conn_threshold)

#6. Build joint emission probabilities

jointEmissionProbs <- getEmissionProbsJointModel(emissionProbs)

#7. Build the generic model

model <- getGenericModel(gridParams$nrow, gridParams$ncol, emissionProbs)

#8. Fit models

ll <- fitModels(length(devices), model,connections)

#9. Build the joint model

modelJ <- getJointModel(gridParams$nrow, gridParams$ncol, jointEmissionProbs)

#10. Read antenna cells and build a matrix of neighboring antennas

coverarea <- readCells(system.file(path_root, 'AntennaCells_MNO1.csv',
package = 'deduplication'))

antennaNeigh <- antennaNeighbours(coverarea)
```

```
#11. Apriori probability of duplicity

P1 <- aprioriDuplicityProb(simParams$prob_sec_mobile_phone, length(devices))

#12. Build a matrix of pairs of devices to compute duplicity probability

pairs4dupP<-computePairs(connections, length(devices), oneToOne = FALSE, P1=P1,
limit = 0.05, antennaNeighbors = antennaNeigh)

#13. Compute duplicity probabilities using the "pairs" method (faster)

out1 <- computeDuplicityBayesian("pairs", devices, pairs4dupP, modelJ, ll, P1)

#14. Apriori probability of 2-to-1

Pii <- aprioriOneDeviceProb(simParams$prob_sec_mobile_phone, length(devices))

#15. Build a matrix of pairs of devices to compute duplicity probability

pairs4dupO<-computePairs(connections, length(devices), oneToOne = TRUE)

#16. Compute duplicity probabilities using "1to1" method

out2 <- computeDuplicityBayesian("1to1", devices, pairs4dupO, modelJ, ll,
P1 = NULL, Pii=Pii)

#17. Compute duplicity probabilities using "trajectory method"

T<-sort(unique(events[,1][[1]]))

out3 <-computeDuplicityTrajectory(path=system.file(path_root, package = 'deduplication'),
"postLocDevice", devices, gridParams, pairs4dupP, P1 = P1, T, gamma = 0.5)
```

`example3` *Example of using* **deduplication** *package - the case of incompatibility*

Description

Example of using **deduplication** package - showing the case of incompatibility between the type of connection in the network and the emission model.

Usage

```
example3()
```

Details

This is an example of how to force the use of an emission model that differs from the type of connection done by the network. Thanks to the information from the simulator and the flexibility of the functions of this package, it is possible to make the assumption of a kind of emission model different from the real type of connection. Obviously, this incoherence has consequences. It could cause to type of problems. Firstly there are events to antennas without signal under the assumption made to build the emission probability matrix. Secondly, there are transitions between pairs of

antennas which are not possible in consecutive times because there is some tile without signal between those antennas under the assumption made to build the emission probability matrix. These two problems can be detected by two functions in this package: checkConnections_step1() and checkConnections_step2(). In the following example, one of these kinds of cases is shown.

References

https://github.com/MobilePhoneESSnetBigData

Examples

```
###    READ DATA    ####

# Set the folder where the necessary input files are stored

path_root <- 'extdata'

 # 0. Read simulation params

simParams <- readSimulationParams(system.file(path_root, 'simulation.xml',
package = 'deduplication'))

 # 1. Read grid parameters

gridParams <- readGridParams(system.file(path_root, 'grid.csv',
package = 'deduplication'))

 # 2. Read network events

events <- readEvents(system.file(path_root, 'AntennaInfo_MNO_MNO1.csv',
package = 'deduplication'))

# 3. Set the signal file name, i.e. the file where the signal strength/quality
# for each tile in the grid is stored

signalFileName <- system.file(path_root, 'SignalMeasure_MNO1.csv')

 # 4. Set the antennas file name

antennasFileName <- system.file(path_root, 'antennas.xml')

####    PREPARE DATA    ####

 # 5. Initial state distribution (prior)

nTiles <- gridParams$ncol * gridParams$nrow
initialDistr_RSS_uniform.vec <- initialDistr_SDM_uniform.vec <- rep(1 /
nTiles, nTiles)

 # 6. Get a list of detected devices

 devices <- getDeviceIDs(events)

 # 7. Get connections for each device

connections <- getConnections(events)
```

```
# 8. Emission probabilities are computed from the signal strength/quality file.
# In this case handoverType is strength then the emission model should be RSS.

emissionProbs_RSS <- getEmissionProbs(nrows = gridParams$nrow,
ncols = gridParams$ncol, signalFileName = signalFileName,
sigMin = simParams$conn_threshold, handoverType = simParams$connection_type[[1]],
emissionModel = "RSS", antennaFileName = antennasFileName)

 # We also try to use the emission model with the SDM assumption.

emissionProbs_SDM <- getEmissionProbs(nrows = gridParams$nrow,
ncols = gridParams$ncol, signalFileName = signalFileName,
sigMin = simParams$conn_threshold, handoverType = simParams$connection_type[[1]],
emissionModel = "SDM", antennaFileName = antennasFileName)

 # 9. Build joint emission probabilities for both options: RSS and SDM.

jointEmissionProbs_RSS <- getEmissionProbsJointModel(emissionProbs_RSS)

jointEmissionProbs_SDM <- getEmissionProbsJointModel(emissionProbs_SDM)

 # 10. Build the generic model for both cases and the a priori
 # uniform (by default)

model_RSS_uniform <- getGenericModel( nrows = gridParams$nrow,
ncols = gridParams$ncol, emissionProbs_RSS, initSteady = FALSE,
aprioriProb = initialDistr_RSS_uniform.vec)

model_SDM_uniform <- getGenericModel( nrows = gridParams$nrow,
ncols = gridParams$ncol, emissionProbs_SDM, initSteady = FALSE,
aprioriProb = initialDistr_SDM_uniform.vec)

 # 11. Fit models.

ll_RSS_uniform <- fitModels(length(devices), model_RSS_uniform, connections)

ll_SDM_uniform <- fitModels(length(devices), model_SDM_uniform, connections)

# The log likelihood is infinity for those connections that are impossible
# under the model SDM (ll_SDM_uniform).


 # 12. Make the checks and corresponding imputations to force the fit of SDM model.

### check1: connections incompatibles with emissionProbs are imputed as NA

check1_SDM <- checkConnections_step1(connections, emissionProbs_SDM)

check1_SDM$infoCheck_step1 connections_ImpSDM0 <-check1_SDM$connectionsImp

### check2: jumps incompatibles with emissionProbs are avoid by making time padding.

check2_SDM <- checkConnections_step2(emissionProbs = emissionProbs_SDM,
connections = connections_ImpSDM0, gridParams = gridParams)

connections_ImpSDM <- check2_SDM$connections_pad
```

```
 # 13. Fit models.

ll_SDM_uniform <- fitModels(length(devices), model_SDM_uniform, connections_ImpSDM)

 # 14. Build the joint model.

modelJ_RSS_uniform <- getJointModel( nrows = gridParams$nrow,
ncols = gridParams$ncol, jointEmissionProbs = jointEmissionProbs_RSS,
initSteady = FALSE, aprioriJointProb = initialDistr_RSS_uniform.vec)

modelJ_SDM_uniform <- getJointModel( nrows = gridParams$nrow,
ncols = gridParams$ncol, jointEmissionProbs = jointEmissionProbs_SDM,
initSteady = FALSE, aprioriJointProb = initialDistr_SDM_uniform.vec)

 # 15. Apriori probability of 2-to-1

Pii <- aprioriOneDeviceProb(simParams$prob_sec_mobile_phone, length(devices))

 # 16. Build a matrix of pairs of devices to compute duplicity probability

pairs4dup_RSS <- computePairs(connections, length(devices), oneToOne = TRUE)

pairs4dup_SDM <- computePairs(connections_ImpSDM, length(devices), oneToOne = TRUE)


####    COMPUTE DUPLICITY    ####


# 17. Compute duplicity probabilities using "1to1" method

duplicity1to1_RSS_uniform.dt <- computeDuplicityBayesian("1to1", devices,
pairs4dup_RSS, modelJ_RSS_uniform, ll_RSS_uniform, P1 = NULL, Pii=Pii)

duplicity1to1_SDM_uniform.dt <- computeDuplicityBayesian("1to1", devices,
pairs4dup_SDM, modelJ_SDM_uniform, ll_SDM_uniform, P1 = NULL, Pii=Pii)
```

`fitModels` *Fits the HMM model for each device.*

Description

Fits the HMM model for each device using the `fit()` function from **destim** package. The computations are done in parallel to reduce the running time using all the available cores. This function creates a cluster of working nodes, splits the devices equally among the working nodes and assigns a partition of devices to each node in the cluster. For Unix-like operating systems, this functions uses a "FORK" cluster while for Windows it uses a "SOCK" cluster.

Usage

```
fitModels(ndevices, model, connections)
```

Arguments

ndevices	The number of devices.
model	The HMM model returned by getGenericModel() function. This model is fitted for each device.
connections	A matrix whose elements are the antenna ID where a device is connected at every time instant. This matrix is returned by getConnections() function.

Value

A vector of log likelihoods computed using the fitted model for each device.

---

getConnections *Builds a matrix object containing the IDs of the antennas to which devices are connected.*

Description

Builds a matrix object containing the IDs of the antennas to which devices are connected. The number of rows equals the number of devices and the number of columns equals the number of time instants when the network events were recorded. An element [i,j] in the returned matrix equals the ID of the antenna where the mobile device with index i in the ordered list of device IDs (returned by getDeviceIDs()) is connected at the time instant with index j in the sequence of time instants when the network events were recorded.

Usage

```
getConnections(events)
```

Arguments

events	A data.table object returned by readEvents() function.

Value

A matrix object with the antenna IDs where devices are connected for every time instants in the events file. If a device is not connected to any antenna at a time instant, the corresponding element in the matrix will have the value NA.

---

getDeviceIDs *Builds a vector with the IDs of the mobile devices.*

Description

Builds a vector with the IDs of the mobile devices by taking the unique values from the events data set.

Usage

```
getDeviceIDs(events)
```

Arguments

events	A data.table object that contains the events generated by the mobile network. It is returned by the readEvents() function. The device IDs are on the second column of this data.table object.

Value

A vector with the IDs of the mobile devices detected by the network.

---

getEmissionProbs *Builds the emission probabilities for the HMM used to estimate the posterior location probabilities.*

Description

Builds the emission probabilities needed for the HMM used to estimate the posterior location probabilities. In case of using simulated data, these probabilities are build using the signal strength or signal quality saved by the simulation software for each tile in the grid.

Usage

```
getEmissionProbs(
  nrows,
  ncols,
  signalFileName,
  sigMin,
  handoverType = "strength",
  simulatedData = TRUE,
  emissionModel = NULL,
  antennaFileName = NULL
)
```

Arguments

signalFileName	The name of the .csv file that contains the signal strength/quality for each tile in the grid. This file is one of the outputs of the data simulator. The data are organized as a matrix with the number of rows equals to the number of antennas and the the following columns: Antenna ID,Tile 0,Tile 1,... Tile (N-1). On the first column there are the antenna IDs and on the rest of the columns the corresponding signal strength/quality for each tile in the grid.
sigMin	The minimum value of the signal strength/quality that allow a connection between a device and an antenna.
handoverType	The handover mechanism used by the mobile network. It could have two values: "strength" or "quality". It should match the types of the values in the signal file, otherwise the results are impredictible.
simulatedData	If TRUE, the input data provided to this function come from the simulator otherwise the data come from a real mobile network.

emissionModel A parameter that can take two values: "RSS" or "SDM". It indicates how the emission probabilities are computed. This parameter is needed to force computing the emission probabilities with a "wrong" model. For example, the signal file contains the values of the signal strength, the handoverType parameter is set to 'strength' but the emissionModel is set to "SDM", the values of the signal strength are transformed in signal quality and the emission probabilities are computed using the signal quality. Such a combination should never be used in practice but it is allowed only for demonstrative purposes: it can be use to demonstrate that if the emission probabilities are not correctly computed then the resulted duplicity probabilities are wrong.

antennaFileName This parameter is needed to read the technical parameters of antennas.These parameters are used to transform the signal strength in signal quality and the other way around. They are needed only in the case the emission probabilities are computed using the signal quality when the handoverType is "strength" or when they are computed using signal quality when the handoverType is "quality".

nrow the number of rows in the grid. It can be obtained by calling readGridParams().

ncol the number of columns in the grid. It can be obtained by calling readGridParams().

Value

Returns a Matrix object with the emission probabilities for the HMM. The number of rows equals the number of tiles in the grid and the number of columns equals the number of antennas. An element (i,j) of this matrix corresponds to the probability of a device being in tile i to be connected to antenna j. The row names of the matrix are the tile indexes and the column names are the antenna IDs.

---

getEmissionProbsJointModel

Builds the emission probabilities for the joint HMM.

Description

Builds the emissions probabilities needed for the joint HMM used to estimate the posterior location probabilities.

Usage

```
getEmissionProbsJointModel(emissionProbs)
```

Arguments

emissionProbs the emission probabilities (the location probabilities) computed by calling getEmissionProbs() for each individual device.

Value

Returns a matrix with the joint emission probabilities for the HMM. The number of rows equals the number tiles and the number of columns equals the number of combinations between antenna IDs. Before the combination between antenna IDs are build, the NA value is added to the list of antenna IDs. An element in this matrix represents the transition probability from an antenna to another, computed for each tile in the grid.

`getGenericModel` *Builds the generic HMM model.*

Description

Builds the generic HMM model using the emission probabilities given by `getEmissionProbs()`.

Usage

```
getGenericModel(
  nrows,
  ncols,
  emissionProbs,
  initSteady = TRUE,
  aprioriProb = NULL
)
```

Arguments

`nrows`	Number of rows in the grid.
`ncols`	Number of columns in the grid.
`emissionProbs`	A matrix with the event location probabilities. The number of rows equals the number of tiles in the grid and the number of columns equals the number of antennas. This matrix is obtained by calling `getEmissionProbs()` function.
`initSteady`	If TRUE the initial apriori distribution is set to the steady state of the transition matrix, if FALSE the apriori distribution should be given as a parameter.
`aprioriProb`	The apriori distribution for the HMM model. It is needed only if `initSteady` is FALSE.

Value

Returns an HMM model with the initial apriori distribution set to the steady state of the transition matrix or to the value given by `aprioriProb` parameter.

`getJointModel` *Builds the joint HMM model.*

Description

Builds the joint HMM model using the emmission probabilities given by `getEmissionProbsJointModel()`.

Usage

```
getJointModel(
  nrows,
  ncols,
  jointEmissionProbs,
  initSteady = TRUE,
  aprioriJointProb = NULL
)
```

Arguments

`nrows`	Number of rows in the grid.
`ncols`	Number of columns in the grid.
`jointEmissionProbs`	A (sparse) matrix with the joint event location probabilities. The number of rows equals the number of tiles in the grid and the number of columns equals the number of antennas. This matrix is obtained by calling `getEmissionProbsJointModel`.
`initSteady`	If TRUE the initial apriori distribution is set to the steady state of the transition matrix, if FALSE the apriori distribution should be given as a parameter.
`aprioriJointProb`	The apriori distribution for the HMM model. It is needed only if initSteady is FALSE.

Value

Returns an HMM model with the initial apriori distribution set to the steady state of the transition matrix or to the value given by `aprioriJointProb` parameter.

`modeDelta` *Returns the mode of delta distribution.*

Description

Returns the mode of the deltaX or deltaY distribution.

Usage

```
modeDelta(deltaDistribution)
```

Arguments

deltaDistribution
: A data.table object that could be Delta X or Delta Y distribution. The table has two columns: delta and p. It is obtainded from calling buildDeltaProb() function.

Value

Rhe mode of the delta distribution.

---

readCells *Reads the coverage areas of antennas.*

Description

Reads the coverage areas of antennas from a .csv file.

Usage

```
readCells(cellsFileName, simulatedData = TRUE)
```

Arguments

cellsFileName
: It is the name of the file where the coverage areas of antennas are to be found. The data have two columns, the first one is the antenna ID and the second one is a WKT string representing a polygon (i.e. it should start with the word POLYGON) which is the coverage area of the corresponding antenna. This area is also called the antenna cell.

simulatedData
: If TRUE it means that the file with the coverage areas is produced by the data simulator

Value

A data.table object with 2 columns: the antenna ID and an sp geometry object which is the coverage area of the corresponding antenna.

---

readEvents *Reads the network events file.*

Description

Reads the network events file. This file can come from the network simulator or it ca be a file with real mobile network events provided by an MNO.

Usage

```
readEvents(eventsFileName, simulatedData = TRUE)
```

Arguments

eventsFileName	The name of the file with the network events to be used. Depending on the parameter simulatedData it could be a .csv file coming from the simulation software or from a real MNO. In case the file comes from the simulation software it should contain following columns: time,antennaID,eventCode,deviceID,x,y,tile. Only the first 4 columns are used, the rest are ignored.
simulatedData	If TRUE it means that the input data are simulated data, otherwise the data come from a real MNO.

Value

Returns a data.table object that contains the events generated by the mobile network. The number of rows equals the number of connection events recorded by the network. The returned object has the following columns: time,deviceID,eventCode,antennaID,x,y,tile,obsVar. obsVar stands for observed variable and is a concatenation between the antenna ID and the event code.

---

readGridParams *Reads the parameters of the grid.*

Description

Reads the parameters of the grid overlapped on the geographical of interest from a .csv file.

Usage

```
readGridParams(gridFileName)
```

Arguments

gridFileName	The name of the file with the grid parameters. This file could be the one generated by the simulation software or can be created with any text editor. The grid file generated by the simulation software has the following columns: Origin X,Origin Y,X Tile Dim,Y Tile Dim,No Tiles X,No Tiles Y. We are interested only in the number of rows and columns and the tile size on OX and OY axes. Therefore, the file provided as input to this function should have at least the following 4 columns: No Tiles X ,No Tiles Y,X Tile Dim,Y Tile Dim.

Value

Returns a list with the following items: nrow - the number of rows, i.e. the number of tiles in a column of the grid, ncol - the number of columns, i.e. the number of tiles in a row of the grid, tileX - the dimension of a tile on OX axis, tileY - the dimension of a tile on OY axis.

readPostLocProb *Reads a file with the posterior location probabilities.*

Description

Reads a .csv file with the posterior location probabilities. Each row of the file corresponds to a tile and each column corresponds to a time instant.

Usage

```
readPostLocProb(path, prefixName, deviceID)
```

Arguments

path	The path to the location where the posterior location probabilities are stored. The file with the location probabilities should have the name postLocDevice_ID.csv where ID is replaced with the device ID.
prefixName	The file name prefix. The whole file name is composed by a concatenation of prefixName, _ and deviceID.
deviceID	The device ID for which the posterior location probabilities are read.

Value

A Matrix object with the posterior location probabilities for the device with ID equals to deviceID. A row corresponds to a tile and a column corresponds to a time instant.

readSimulationParams *Reads the parameters of the simulation used to generate a data set.*

Description

Reads the parameters of the simulation used to generate a data set from an .xml file used by the simulation software. The following parameters are needed by this package: the connection threshold which is the minimum signal strength/quality that can be used by a mobile device to connect to an antenna and the probability of having a two mobile devices.

Usage

```
readSimulationParams(simFileName)
```

Arguments

simFileName	The name of the file used to define a simulation scenario. It is the file that was provided as an input for the simulation software.

Value

A list with all the parameters read from the file: start_time, end_time, time_increment, time_stay, interval_between_stays, prob_sec_mobile_phone, conn_threshold.

`tileEquivalence` *Transforms the tiles indices from the notation used by the simulation software to the one used by the* **raster** *package.*

Description

In order to perform the population estimations, the area of interest is overlapped with a rectangular grid of tiles. Each tile is a rectangle with predefined dimensions. This function is a utility function which transform the tiles indexes from the numbering system used by the simulation software to the one used by the **raster** package. The simulation software uses a notation where the tile with index 0 is the bottom left tile while the **raster** package uses another way to number the tiles, tiles being numbered starting with 1 for the upper left tile.

Usage

```
tileEquivalence(nrows, ncols)
```

Arguments

`nrow`	Number of rows in the grid overlapping the area of interest.
`ncol`	Number of columns in the grid overlapping the area of interest.

Value

Returns a data.frame object with two columns: on the first column are the tile indexes according to the **raster** package numbering and on the second column are the equivalent tile indexes according to the simulation software numbering.

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Appendix D

Reference manual for the `destim` package

Package 'destim'

October 30, 2020

Type Package

Title R package for mobile devices position estimation

Version 0.1.0

Author David Salgado <david.salgado.fernandez@ine.es>, Luis Sanguiao Sande <luis.sanguiao.sande@ine.es>

Maintainer Bogdan Oancea <bogdan.oancea@gmail.com>

Description R package for mobile devices position estimation

License GPL3, EUPL

Imports Rcpp,
Matrix,
raster,
RColorBrewer,
ggplot2

LinkingTo Rcpp, RcppEigen

Encoding UTF-8

LazyData true

RoxygenNote 7.1.0

Suggests knitr,
rmarkdown

VignetteBuilder knitr

R topics documented:

`addconstraint` *Adds constraints to the model.*

Description

The specified constraints are added to the model. If parameter `ct` is a vector, it is expected to be a set of transition probabilities indexed as in field transitions of the model. In this case the constraint added is the equality between the referred probabilities of transition. If parameter `ct` is a matrix, it is expected to be a system of additional linear equalities that the model must fulfill. Thus, the new equations are added to the field constraints of the model. While it is possible to use a matrix to add equality constraints, it is not recommended because of performance. Previous constraints of the model are preserved.

Usage

```
addconstraint(x, ct)
```

Arguments

`x`	A HMM object.
`ct`	The additional constraints, which can be either a matrix or a vector (see details).

Value

A HMM object similar to the input but with the additional constraints.

See Also

HMM, addtransition

Examples

```
model <- HMM(3)
model <- addtransition(model, c(1,2))
model <- addtransition(model, c(2,3))
model <- addtransition(model, c(3,1))
transitions(model)
constraints(model)
model <- addconstraint(model,c(2,4,5))
constraints(model)
```

`addtransition` *Adds a transition to the model.*

Description

The specified transition is added to the model as a transition with non zero probability. Since the transition probabilities from the initial state of the newly specified transition still have to sum up to one, the correspondent constraint is modified accordingly. It is not recommended to use this function to define a big model, as it is much slower than specifying all transitions in advance.

Usage

```
addtransition(x, t)
```

Arguments

`x`	A HMM object.
`t`	The transition, as a two dimensional integer vector. The first element is the number of the initial state and the second one the number of the final state.

Value

A HMM object similar to the input but with the additional transition.

See Also

HMM, addconstraint

Examples

```
model <- HMM(3)
model <- addtransition(model, c(1,2))
model <- addtransition(model, c(2,3))
model <- addtransition(model, c(3,1))
transitions(model)
constraints(model)
```

constraints *Matrix of constraints.*

Description

Returns the matrix of constraints from a HMM object.

Usage

```
constraints(x)

## S3 method for class 'HMM'
constraints(x)
```

Arguments

x	the HMM object.

Value

A row major sparse matrix as in HMM.

See Also

HMM, nconstraints, transitions

Examples

```
model <- HMMrectangle(3,3)
constraints(model)
nconstraints(model)
nrow(constraints(model)) # should agree
```

createEM *Creates the events matrix.*

Description

Creates the events matrix for a rectangular grid according to the location of the towers and the S function.

Usage

```
createEM(size, towers, S)
```

Arguments

size	The number of rows and columns in the grid.
towers	The towers(antenna) positions. This parameter is a matrix with two rows and the number of columns equals to the number of antennas. On the first row we have the X coordinate of the towers and on the secnd row the Y coordinate.
S	A function to compute the signal strength.

Value

The events matrix.

`destim` *A package for mobile devices position estimation using HMM.*

Description

This package contains functions to compute the posterior location probability for each device over a grid of tiles covering the geographical area under consideration. It uses Hidden Markov Models. The theory behind the method is described in detail in WPI Deliverable 3 and in the paper *An end-to-end statistical process with mobile network data for Official Statistics*. For an example on how to use this package please read example1 and example2.

Details

destim: A package for mobile devices position estimation.

`emissions` *Emissions matrix*

Description

Returns the matrix of emissions from a HMM object.

Usage

```
emissions(x)

## S3 method for class 'HMM'
emissions(x)
```

Arguments

x	the HMM object.

Value

A column major sparse matrix as in HMM.

See Also

HMM, emissions<-, getTM

Examples

```
model <- HMM(2)
emissions(model)<-diag(2)
emissions(model)
```

---

emissions<- *Set the emissions of the model*

Description

Sets the emissions of the model.

The number of rows must match the number of states. If a matrix is provided, it is converted to column major sparse matrix (dgCMatrix).

Usage

```
emissions(x) <- value
```

Arguments

x	A HMM model.
value	A (sparse column major) matrix with the likelihoods of each emission (column) conditioned on the state (row).

Value

Changes the emissions matrix in the model.

See Also

HMM, emissions

Examples

```
model <- HMMrectangle(10,10)
tws <- matrix(c(3.2, 6.1, 2.2, 5.7, 5.9, 9.3, 5.4,
4.0, 2.9, 8.6, 6.9, 6.2, 9.7, 1.3),
nrow = 2, ncol = 7)
S <- function(x) if (x > 5) return(0) else return(20*log(5/x))
emissions(model)<-createEM(c(10,10), tws, S)
emissions(model)
```

`fit` *Fits a HMM model*

Description

Fits the transition probabilities of the model by maximum likelihood. The transition probabilities are fitted by ML, subject to the linear constraints specified in the model. The argument retrain can be used to avoid local minima. It is possible to specify additional non linear constraints, passing the suitable arguments to the optimizer.

Usage

```
fit(x, e, init = FALSE, method = "solnp", retrain = 1, ...)
```

Arguments

`x`	A HMM model.
`e`	A vector with the observed events. It admits missing values.
`init`	Logical specifying whether the initial state found in x is going to be used. Defaults to FALSE, which means that steady state initialization will be used instead.
`method`	The optimization algorithm to be used. Defaults to `solnp` from package **Rsolnp**. The other possible choice is `constrOptim` from package **stats**.
`retrain`	The times the optimizer will be launched with different initial parameters. The model with higher likelihood will be returned.
`...`	Arguments to be passed to the optimizer.

Value

The fitted model.

See Also

logLik, initparams, minparams

Examples

```
model <- HMMrectangle(20,20)
S <- function(x) if (x > 5) return(0) else return(20*log(5/x))
emissions(model) <- createEM(c(20,20), towers, S)
model <- initparams(model)
model <- minparams(model)
logLik(model,events)
model <- fit(model,events)
logLik(model,events)
```

`fstates` *This function returns the filtered states whenever an observation is present and predicted states otherwise.*

Description

This function returns the filtered states whenever an observation is present and predicted states otherwise.

Usage

```
fstates(P, E, e)
```

Arguments

`P`	Transition matrix P(will go to i | is in j)
`E`	Event observation matrix P(detection event j | is in i)
`e`	Sequence of observation events. Since we are taking time increase small, it is expected to have mostly missing values. The first value is expected to have an observation.

Value

The filtered states.

`getTC` *Gets the column of the transition matrix.*

Description

Gets the column of the transition matrix corresponding to a point from a rectangular grid according to the mask

Usage

```
getTC(point, size, mask)
```

Arguments

`point`	We are setting the transition probabilities starting from this point. It corresponds to the column (point[2] - 1) * size[1] + point[1] of the transition matrix.
`size`	Size of the grid. It is expected to be a 2 dimensional vector, containing the number of rows and columns respectively.
`mask`	Transition probabilities to the contiguous tiles. It is expected to be a 3x3 matrix where the (2,2) element represents the probability of staying in the current tile.

`getTM` *Transition matrix.*

Description

Returns the transition matrix from a HMM object. The transition matrix is represented as row major. This way its transpose matrix which is used to left multiply the state is column major.

Usage

```
getTM(x)

## S3 method for class 'HMM'
getTM(x)
```

Arguments

x	the HMM object.

Value

A row major sparse matrix which is the transition matrix of the model.

See Also

HMM, linkemissions

Examples

```
model <- HMM(2)
model <- addtransition(model,c(1,2))
model <- initparams(model)
getTM(model)
```

`gettransmatrix` *Transformation matrix*

Description

Returns the transformation matrix that transforms the minimal parameters into the probabilities of transition. The transformation matrix allows obtains the probabilities of transition from the minimal set of parameters. If we append an one at the end of the vector of parameters, the product of this matrix by such vector is the probabilities of transition vector.

Usage

```
gettransmatrix(x)

## S3 method for class 'HMM'
gettransmatrix(x)
```

Arguments

x	the HMM object.

Value

A matrix.

See Also

minparams, ptransition, rparams, fit

Examples

```
model <- HMMrectangle(3,3)
model <- initparams(model)
model <- minparams(model)
# Should be close to zero
range(ptransition(model) - gettransmatrix(model) %*% c(rparams(model), 1))
```

HMM *Class constructor for Hidden Markov models*

Description

Creates a HMM object, as specified.

The HMM object contains five fields: states, transitions, constraints, emissions and parameters.

The field states contains a character vector with the names of the states. If the constructor is given a number S, it sets the names as follows: as.character(1:S). An additional field, called coordinates is provided too, were in the future the geolocation of the states will be specified. Note that state determines geolocation, but different states might share geolocation.

The field transitions contain a matrix which is a list of the transitions with non-zero probability. It is a two row integer matrix where each column represents the transition from first row state to second row state. The columns of the matrix are ordered by first row and then by second row. This order corresponds to a row major representation of the transition matrix. The states are referenced in the same order as they appear in field states. While (number of states)^2 transitions are possible, a much smaller number is expected. It defaults to still transitions for all states.

The field constraints is the augmented matrix of the system of linear equalities that the model must fulfill. The variables of the system correspond to the probabilities of transition, in the same order as in field transitions. It is a row major sparse matrix. The first rows should have equalities between pairs of transition probabilities, which are rows with just two non zero elements. Next, we have the sum up to one conditions, which are rows with constant term equal to one. Finally, the remaining constraints are expected to have constant term different from one (otherwise multiply the constraint by a constant). This structure, allows an efficient treatment of constraints that are equalities between pairs of transition probabilities.They are expected to be the most frequent constraints.

The field emissions consists in a matrix that contains the emission probabilities, where the number of rows is the number of states and each column correspond to a possible output. EM is a column major sparse matrix. Unlike usual, the emission probabilities are fixed, do not have parameters to estimate.

The field parameters contain additional information about the probabilities of transition and the initial state of the model. Also some auxiliary information to reduce the number of parameters of the model. See `initparams`, `minparams` and `initsteady`.

Usage

```
HMM(...)

## S3 method for class 'integer'
HMM(S, TL, CT, EM = NULL, checks = TRUE)

## S3 method for class 'numeric'
HMM(S, ...)

## S3 method for class 'character'
HMM(S, ...)
```

Arguments

`S`	Number or names of states. It can be either a numeric or a character.
`TL`	Matrix of integers that lists non-zero transitions. The matrix corresponds to the field transitions of the object (see details).
`CT`	Matrix of constraints. It corresponds to the field constraints of the object (see details).
`EM`	Matrix of emissions. It corresponds to the field emissions of the object (see details).

Value

A HMM object.

See Also

initparams, minparams, initsteady

Examples

```
model1 <- HMM(5)
model2 <- HMM(c("a","b","c"),
            TL = matrix(c(1, 1,
                          1, 2,
                          2, 1,
                          2, 2,
                          2, 3,
                          3, 2,
                          3, 3), nrow = 2))
nstates(model1)
ntransitions(model1)
nstates(model2)
ntransitions(model2)
```

HMMrectangle *Basic HMM grid model.*

Description

Creates a basic rectangular grid model as specified. This model is a rectangular grid where the only transitions allowed are those between contiguous tiles. Moreover, horizontal and vertical transition probabilities are equal for all tiles. Diagonal transition probabilities are equal between them too, but different from the former. These constraints mean that there are only two parameters to estimate. The emissions field is left unassigned.

Usage

```
HMMrectangle(x, y)
```

Arguments

x	length of the rectangle in tiles.
y	width of the rectangle in tiles.

Value

A HMM object.

See Also

emissions, minparams

Examples

```
model <- HMMrectangle(3,3)
nstates(model)
ntransitions(model)
nconstraints(model)
```

initparams *Initializer for HMM objects*

Description

Sets initial parameters for a HMM object, as specified. The field parameters of the HMM object, which includes both initial state and transition probabilities, is initialized at random.

The initial states probabilities are set to an uniform (0,1) distribution and then divided by their sum.

The initial probabilities of transition are also set to an uniform (0,1) and in this case, projected on the constrained space. After the projection some probability might result greater than one or less than zero. Those probabilities are then set to uniform (0,1) again and the process is repeated until all probabilities of transition are in (0,1) and the constraints are satisfied.

Usage

```
initparams(x)
```

Arguments

x	A HMM object.

Value

An initialized HMM object.

See Also

HMM, minparams, initsteady

Examples

```
model <- HMMrectangle(3,3)
model <- initparams(model)
range(constraints(model) %*% c(ptransition(model), -1)) # It should be close to zero
```

---

initsteady *Sets the initial state to the steady state*

Description

The initial a priori distribution is set to the steady state of the transition matrix.

The Markov Chain is expected to be irreducible and aperiodic. The first because otherwise the devices would not have freedom of movement. The second because some probabilities from one state to itself are expected to be non zero. This implies that there exists one unique steady state.

The steady state is computed by solving the sparse linear system (TM - I)x = 0, where TM is the matrix of transitions I is identity and x the steady state. As it is an homogeneous system, and because of the uniqueness of the steady state, the solution is a one dimensional vector space, and the generator does not have any coordinate equal to zero. Then the last coordinate is set to 1 / number of states, so the sparse linear system becomes inhomogeneous with unique solution. Finally the solution is normalized so that the components of x sum up to 1.

Usage

```
initsteady(x)
```

Arguments

x	A HMM object.

Value

The same HMM object of the input with its initial state set to steady state.

See Also

HMM, initparams, minparams

Examples

```
model <- HMM(2)
model <- addtransition(model, c(1,2))
model <- addtransition(model, c(2,1))
model <- initparams(model)
istates(model)
model <- initsteady(model)
istates(model)
(istates(model) %*% getTM(model))
```

---

istates *Initial state probabilities.*

Description

Returns the initial state probabilities from a HMM object. The object has to be initialized with initparams, which generates a random initial state. The vector of probabilities follows the same order as the states, so ptransition(model)[i] is the probability of state i. Of course, the probabilities sum up to one.

Usage

```
istates(x)

## S3 method for class 'HMM'
istates(x)
```

Arguments

x	the HMM object.

Value

A numeric vector with the probabilities.

See Also

initparams, fit, nstates, initsteady

Examples

```
model <- HMM(2)
model <- addtransition(model,c(1,2))
model <- addtransition(model,c(2,1))
model <- initparams(model)
istates(model)
sum(istates(model)) # should be one
```

`istates<-` *Set the initial states*

Description

Sets the initial distribution of states.

The length must match the number of states, and the sum of the vector must be one.

Usage

```
istates(x) <- value
```

Arguments

`x`	A HMM model.
`value`	A numeric vector with a probability for each state that represents the initial distribution of states.

Value

Changes the initial distribution of states in the model.

See Also

HMM, initparams, initsteady, fit

Examples

```
model <- HMMrectangle(3,3)
model <- initparams(model)
istates(model)
istates(model) <- (1:9) / sum(1:9)
istates(model)
```

`logLik` *Minus logLikelihood*

Description

Returns the minus logarithm of the likelihood given a model and a set of observations.

A slightly modified version of the forward algorithm is used to compute the likelihood, to avoid store unneeded data. The sign is changed because it is usual to minimize instead maximize.

Usage

```
logLik(...)

## S3 method for class 'HMM'
logLik(x, e)
```

Arguments

x	A HMM model.
e	A vector with the observed events. It admits missing values.

Value

The minus logarithm of the likelihood of the events given the model.

See Also

fit, HMM, initparams

Examples

```
model <- HMMrectangle(20,20)
S <- function(x) if (x > 5) return(0) else return(20*log(5/x))
emissions(model) <- createEM(c(20,20), towers, S)
model <- initparams(model)
model <- minparams(model)
logLik(model,events)
```

---

minparams *Reparametrizes a HMM model with a minimal set of parameters.*

Description

Finds a minimal set of parameters that fully determine the probabilities of transition.

This function avoids to solve a high dimensional optimization problem with many constraints, parametrizing the probabilities of transition with as few parameters as possible: the number of degrees of freedom.

A pivoted QR decomposition of the constraints matrix is done, to get both the free parameters and the matrix that transforms them back into the probabilities of transition.

Many constraints are expected to be equalities between two probabilities of transition, so the function is optimized for this special kind of constraints.

Usage

```
minparams(x)
```

Arguments

x	A HMM object.

Value

The same HMM object of the input with some additional fields that store the new parameters and the matrix that transforms these parameters in the probabilities of transition.

See Also

rparams, rparams<-

Examples

```
model <- HMMrectangle(2,2)
model <- initparams(model)
ntransitions(model)
nconstraints(model)
model <- minparams(model)
rparams(model)
range(ptransition(model) -
  gettransmatrix(model) %*% c(rparams(model), 1))
```

---

nconstraints *Number of constraints.*

Description

Returns the number of constraints from a HMM object.

Usage

```
nconstraints(x)

## S3 method for class 'HMM'
nconstraints(x)
```

Arguments

x	the HMM object.

Value

An integer with the number of constraints of the model.

See Also

constraints, nstates, ntransitions

Examples

```
model <- HMM(5)
nconstraints(model)
model <- HMMrectangle(3, 3)
nconstraints(model)
```

nstates *Number of states.*

Description

Returns the number of states from a HMM object.

Usage

```
nstates(x)

## S3 method for class 'HMM'
nstates(x)
```

Arguments

x	the HMM object.

Value

An integer with the number of states of the model.

See Also

ntransitions, nconstraints

Examples

```
model <- HMM(5)
nstates(model)
```

ntransitions *Number of transitions.*

Description

Returns the number of possible transitions from a HMM object.

Usage

```
ntransitions(x)

## S3 method for class 'HMM'
ntransitions(x)
```

Arguments

x	the HMM object.

Value

An integer with the number of possible transitions of the model.

See Also

transitions, nstates, nconstraints

Examples

```
model <- HMM(5)
ntransitions(model)
model <- addtransition(model, c(1,2))
ntransitions(model)
```

---

ptransition *Probabilities of transition.*

Description

Returns the probabilities of transition from a HMM object. The object has to be initialized with initparams, otherwise it will return numeric(0). The order is row major.

Usage

```
ptransition(x)

## S3 method for class 'HMM'
ptransition(x)
```

Arguments

x	the HMM object.

Value

A numeric vector with the probabilities of transition.

See Also

HMM, initparams, transitions, ntransitions

Examples

```
model <- HMM(2)
model <- addtransition(model,c(1,2))
model <- addtransition(model,c(2,1))
model <- initparams(model)
ptransition(model)
```

rparams *Reduced parameters.*

Description

Returns the values of the minimal set of parameters. The minimal set of parameters are selected by minparams. They are a few probabilities of transition that determine the remaining ones because of the constraints. They are used to fit the model.

Usage

```
rparams(x)

## S3 method for class 'HMM'
rparams(x)
```

Arguments

x	the HMM object.

Value

A numeric vector with the values of the parameters.

See Also

minparams, ptransition, gettransmatrix, fit

Examples

```
model <- HMMrectangle(3,3)
model <- initparams(model)
model <- minparams(model)
rparams(model)
ntransitions(model)
length(rparams(model)) # A much smaller parameter space!
```

rparams<- *Set reduced parameters*

Description

Sets the parameters selected by minparams function.

The function minparams selects a minimal set of parameters, that fully determine the transition probabilities. This function sets those parameters and recalculates all transition probabilities from them.

The model is initialized with initparams and minparams when required.

Usage

```
rparams(x) <- value
```

Arguments

x	A HMM model.
value	A numeric vector with the new parameters.

Value

Changes parameters$reducedparams$params and parameters$transitions in the object x.

See Also

minparams, rparams, initparams

Examples

```
model <- HMMrectangle(3,3)
rparams(model)<-c(0.3, 0.03)
ptransition(model)
```

---

scpstates *Returns ξ like in the Baum-Welch algorithm.*

Description

Returns the smooth joint probability mass function for consecutive states, which is usually called ξ in the Baum-Welch algorithm. Smooth states are marginal but as they are far to be independent it is convenient to have some information about their dependence. This function returns the joint probability mass function for two time consecutive states, conditional on the observations. This agrees with the so called ξ from the Baum-Welch algorithm.

It is returned as a matrix, so that the said joint probability for time instants i - 1 and i are the columns from i - 1 times the number of states plus one, to i times the number of states.

Usage

```
scpstates(...)

## S3 method for class 'HMM'
scpstates(x, e)
```

Arguments

x	A HMM model.
e	A vector with the observed events. It admits missing values.

Value

A sparse matrix. The number of rows is the number of states, and the number of columns is the number of states times the number of observed events minus one. Each full row square slice of the output matrix corresponds to a joint probability mass function, so it sums up to one.

See Also

HMM, sstates, backward

Examples

```
model <- HMMrectangle(10,10)
tws <- matrix(c(3.2, 6.1, 2.2, 5.7, 5.9, 9.3, 5.4,
4.0, 2.9, 8.6, 6.9, 6.2, 9.7, 1.3),
nrow = 2, ncol = 7)
S <- function(x) if (x > 5) return(0) else return(20*log(5/x))
emissions(model)<-createEM(c(10,10), tws, S)
obs <- c(1,2,NA,NA,NA,NA,7,7)
model <- fit(model, obs)
scpstates(model, obs)
```

---

setsnames<- *Set the names of the states.*

Description

Sets the names of the states.

The length of the character vector must match the number of states of the model.

Usage

```
setsnames(x) <- value
```

Arguments

x	A HMM model.
value	A character vector with the names.

Value

Changes states names in the object x.

See Also

HMM

Examples

```
model <- HMM(3)
setsnames(model) <- c("a","b","c")
model$states$names
```

sstates *Smooth states*

Description

Returns the smooth states from the forward-backward algorithm.

Smooth states are the marginal of the state conditional on the observations, for each time. This agrees with the so called γ from the Baum-Welch algorithm.

It is returned as a matrix, so that the smooth state for time instant i is the column i of the matrix.

Usage

```
sstates(...)

## S3 method for class 'HMM'
sstates(x, e)
```

Arguments

x	A HMM model.
e	A vector with the observed events. It admits missing values.

Value

A sparse matrix. The number of rows is the number of states, and the number of columns is the number of observed events. Each column of the output matrix corresponds to the probability mass function for the state, so it sums up to one.

See Also

HMM, scpstates, backward

Examples

```
model <- HMMrectangle(10,10)
tws <- matrix(c(3.2, 6.1, 2.2, 5.7, 5.9, 9.3, 5.4,
4.0, 2.9, 8.6, 6.9, 6.2, 9.7, 1.3),
nrow = 2, ncol = 7)
S <- function(x) if (x > 5) return(0) else return(20*log(5/x))
emissions(model)<-createEM(c(10,10), tws, S)
obs <- c(1,2,NA,NA,NA,NA,7,7)
model <- fit(model, obs)
sstates(model, obs)
```

`transitions` *Transitions.*

Description

Returns the list of possible transitions from a HMM object. Each column represents a transition, the first row is the initial state and the second row is the final state. The transitions are ordered, first on the initial state and then on the final state. Any transition not listed in the matrix is supposed to be not possible (zero probability).

Usage

```
transitions(x)

## S3 method for class 'HMM'
transitions(x)
```

Arguments

x	the HMM object.

Value

An integer matrix with two rows as in HMM.

See Also

HMM, ntransitions, constraints, ptransition

Examples

```
model <- HMM(2)
transitions(model)
model <- addtransition(model,c(1,2))
model <- addtransition(model,c(2,1))
transitions(model)
```

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