Integrated Epidemiologic Simulation for Person to Person Contagion through Urban Mobility within GIS

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ABSTRACT
In recent years, advances in Health Geography, Geographical Epidemiology and Public Health Informatics have led to an extensive use of Geographic Information Systems (GIS) to study a variety of public health issues. Considering infectious disease outbreaks, time becomes a critical factor and Public Health officers require tools to support rapid decision making. In this context, GIS technology presents some limits. Mainly, the study of communicable diseases requires the development of complicated spatial-temporal models which is often time and effort consuming. In addition, this type of dynamic analysis is hard to realize by means of the GIS functionalities commonly available. Addressing such limits, we present in this paper a new GIS-based spatial-temporal simulation approach and software to support public health decision making in the context of communicable diseases. Our approach stands out by the integrative perspective and the explicit spatial aspect that it offers. On the one hand, it fully integrates epidemiological, mobility and GIS-data models at an aggregate population level in order to support public health decision making. This is made possible because our approach is built on data automatically processed from transportation surveys that are widely available, at least in North America and Europe. Our approach is thus simple and can be promptly put into use. On the other hand, our approach particularly aims at supporting decision makers with respect to “spatialized” intervention policies. Mainly, it allows for the assessment of different public intervention actions in different spatial locations of the studied area and the evaluation of their effects on the disease spatial evolution and distribution.

Categories and Subject Descriptors
I.6 [SIMULATION AND MODELING]; K.4 [COMPUTERS AND SOCIETY]; K.4.1 Public Policy Issues; J.3 [LIFE AND MEDICAL SCIENCES]: Health

General Terms
Design, Theory.

Keywords
Public Health Decision Support, Spatial-Temporal Simulation. GIS, Communicable Infectious Diseases.

1. INTRODUCTION
In recent years, advances in Health Geography [13], Geographical Epidemiology [13, 1] and Public Health Informatics [10, 24, 25, 29] have led to an extensive use of Geographic Information Systems (GIS) to study a variety of public health issues such as disease mapping, exposure/risk modelling, environmental health analyses and disease diffusion [3] as well as the propagation of infectious communicable diseases [19, 21, 22, etc.]. It has been emphasized that effective public health practice requires timely and accurate information from a wide variety of sources in order to allow policy makers analyze and justify both existing and proposed public health initiatives [25].

Considering infectious disease outbreaks, time becomes a critical factor and Public Health officers require tools to support rapid decision making. In this context, GIS technology presents some limits for two main reasons. First, communicable diseases are multi-dimensional, complex and dynamic phenomena and are best studied from two perspectives: human disease ecology and disease spatial diffusion [23, 12]. Human ecology is the study of how individuals and groups interact with one another. In a simplified way, it studies and models how the disease can be locally transmitted through the contacts between infectious and susceptible individuals. Modeling disease spatial diffusion requires the study and analysis of human activities and movement patterns. Both human disease ecology and spatial diffusion are complex and dynamic depending on several factors such as social, environmental and economical ones. Modeling human mobility is particularly a challenging problem that often requires the collection, integration and analysis of huge amounts of data from different sources. Moreover, it is currently an active research field. Thus, the study of communicable diseases requires the development of spatial-temporal models for both local contact and mobility, which is often time and effort consuming. In addition, this type of dynamic analysis is hard to realize by means of the GIS functionalities commonly available [13, 19] and often requires the use of other models and tools, in addition to GIS. Hence, it is not easy to use current GIS tools to support the rapid decision making process that is required when dealing with communicable disease outbreaks. Moreover, GIS systems are difficult to use by public health decision makers without training in spatial techniques [18], and the lack of trained staff is probably the most serious issue in the field [13].
Addressing such limits, we present in this paper a new GIS-based spatial-temporal simulation approach and software to support public health decision making in the context of communicable diseases. The main idea is to take advantage of available transportation surveys to rapidly model the demographic characteristics and activity/mobility patterns of a significant sample of a urban population at an aggregate level, so that the proposed approach fully integrates human epidemiology, human mobility and public intervention models in a GIS system. The proposed simulation tool allows a user to visualize and to assess the spread of a contagious disease in a geographic area simulated in a GIS and taking into account the spatial locations of the residence and usual activities (work, study, shopping, leisure, etc.) of different population groups (characterized by age groups). The simulation is initialized with a simulated population sampled from the transportation survey in which the user can easily introduce infected or susceptible people. Our tool also allows for the creation and comparison of different intervention scenarios (vaccination of targeted age groups in targeted areas, closure of certain activity locations such as schools or even public transportation) in terms of the spatial evolution and distribution of infected people in the studied area.

The paper aims at giving an overview of the proposed approach and tool and is organized as follows. Section 2 introduces the conceptual framework that we propose to integrate human epidemiology and mobility models. In Section 3 we provide an overview of our approach, and in Section 4 we briefly present the simulation tool and some examples that we have implemented. Section 5 concludes the paper emphasizing the advantages and limits of the proposed approach and discussing some future work.

2. THE CONCEPTUAL FRAMEWORK FOR INTEGRATING EPIDEMIOLOGIC AND MOBILITY MODELS

The main idea of our approach is to model the population and the geographic locations of activities and social contact at aggregate levels that are allowed by data available in transportation surveys and are sufficient to provide significant data and results to public health decision makers. We present these aggregate models in the following sub-sections.

2.1 The aggregated spatial model

The aggregated spatial model that we use is based on the concept of container. A container is any location in the studied area in which groups of people can carry out typical activities that can be characterized using a transportation survey. Figure 1 presents the typology of containers that we use in our approach and that allows for a hierarchical description of the studied area. At the more detailed level we use a spatial tessellation of space as a set of ‘zones’ which usually correspond to local administrative boundaries of interest to public health decision makers (such as census tracks). Using the transportation survey we initialize the simulated population by assigning individuals of different age groups (those that are relevant to the epidemiological study) to the different zones called residence containers. In a simplified simulation of their daily activities people will move in the morning from their residence container to an activity container (depending on the characteristics of the individuals) and will return to their residence container at the end of the day. We will have a ‘contact model’ (and hence a contagion model) specific to the residence zone and that reflects typical residential risk factors such as the number of individuals and the characteristics of their contacts.

Indeed, we also need containers to represent the locations where people carry out activities that are relevant with respect to the disease propagation. In Figure 1 they are represented by the ‘anchor activities’ and the ‘other activities’ containers. These containers have been chosen, considering the activity data usually available in (or computable from) transportation surveys and that can be aggregated in a significant way for our simulation purposes. The anchor activities correspond to the activity categories that favor different types of contact between people. We consider the general categories ‘work container’ for the working population, ‘study container’ for the studying population (with the differentiation of elementary schools, secondary schools and university) as well as ‘nursery container’, which introduces a constraint on the mobility of a part of the workforce (parents having infants attending the nursery). As we will see, each of these anchor containers is associated with a different ‘contact model’ (and hence a contagion model). Given that data available in transportation surveys do not usually provide detailed information about anchor locations, we associate these anchor activity containers (the aggregated parameters used in the simulation) to locations called ‘Places’ (Figure 1) that aggregate one or several residential zones. The ‘container of other activities’ aggregates the locations of all the other activities that are different from the anchor activities. For simplification purposes and considering that these activities affect the disease transmission less considerably, the ‘container of other activities’ is currently associated with the regional level of the spatial hierarchy (corresponding to the whole area of study). We associate another contact model to this container.

Finally we aggregate in a ‘Public transit’ container all the activities that are related to individuals’ public transit, since people spend some time with each other in public vehicles where disease transmission is facilitated. For simplification purposes we only use one Public transit container at the regional level, since we can easily compute aggregated contact attributes from transportation surveys. But if more detailed information is available, we could distinguish several public transit containers such as Bus container, Metro container and Regional Train container.
2.2 The spatial-temporal population contact model

The spatial-temporal population contact model aims at proposing a credible mechanism to model the dynamics of the interactions between population groups in local spatial areas and the transmission of the disease from infectious to susceptible individuals. To build such a model we need to address three issues: 1) identify relevant population groups, 2) identify local spatial areas where those population groups should interact with each other and 3) model the dynamics of the disease transmission through groups’ interactions in these areas. As we mentioned in Section 2.1, we use the concept of containers to model the spatial areas where population groups interact with each other and may consequently get infected. In this sub-section we build on the aggregate spatial model presented in Section 2.1 and we progressively present our spatial-temporal population contact model.

In epidemiology, it is considered that disease events “do not occur randomly in a population, but are more likely to occur in some members of the population than others because of risk factors that may not be distributed randomly in the population” [11]. An important effort in epidemiology is concerned with identifying the factors that classify individuals at different risk levels. The “triangle of human ecology” (also called epidemiological triangle) is one of the conceptual frameworks that are applied for this purpose [12]. In this model, a disease results from the interaction between an external agent and a susceptible host in an environment that supports the transmission of the agent from a source to that host [11].

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<td>Pop5MG</td>
<td>Infants of less than 5 years old who attend a nursery</td>
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<tr>
<td>Pop6_15P</td>
<td>Young people between 6 and 15 years old who attend a primary school</td>
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<tr>
<td>Pop6_15S</td>
<td>Young people between 6 and 15 years old who attend a secondary school</td>
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<tr>
<td>Pop6_15A</td>
<td>Young people between 6 and 15 years old who carry out other studies</td>
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<tr>
<td>Pop16_64U</td>
<td>Adults between 16 and 64 years old who carry out (pre) universitary studies</td>
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<tr>
<td>Pop16_64T</td>
<td>Adults between 16 and 64 years old who work</td>
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<tr>
<td>Pop16_64A</td>
<td>Adults between 16 and 64 years old who are neither workers nor students</td>
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<td>Pop65P</td>
<td>Retired people of more than 65 years old</td>
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In our approach, we were inspired by this triangle model to identify relevant population groups and to model how they locally interact and communicate the disease to each other. The agent is a virus that can be communicated by contacts between infectious and susceptible humans. Consequently, we consider that the first risk factor is the virus virulence. The second risk factor is the population vulnerability to the virus. Assuming that the vulnerability depends on the age attribute, we classify a population into four groups (children, young, adult and elder). A population is active and mobile: individuals do have activities and daily move between their homes and various activity places.

Therefore, we establish a correspondence between the environment - the third dimension of the epidemiologic triangle - and the different containers presented in Section 2.1. Hence, in our model the environmental risk factors are derived from the characteristics of these containers, mainly as a result of crowding and poor hygiene attributes [28] (containers with high crowding and poor hygiene correspond to high environmental risk).

Considering the combination of these three dimensions (i.e., the virus virulence, the population vulnerability and the containers risk level) and the data available in transportation surveys we identified the nine socio-demographic population groups illustrated in Table 1.

In our approach containers correspond to the spatial locations where population groups interact with each other, and they therefore represent the locations of the disease transmission from infectious to susceptible individuals. Thus, we associate a local contagion model to every container, and we use a simplified compartmental epidemiologic model where each population group is subdivided into five compartments (susceptible, exposed, infected, protected, dead) corresponding to the different disease epidemiologic stages (Figure 2). The transitions between these stages are associated with different rates that are computed using stochastic functions (except for the infection model which is deterministic). More specifically, we use a stochastic contamination model to compute the local contagion rate in each container taken into consideration its specific environmental risk factors (i.e., crowding and hygiene attributes). Detailing the whole epidemiologic model is out the scope of this paper, and Figure 2 illustrates its global logic.

2.3 The spatial-temporal mobility model

Whereas the model presented in Section 2.2 allows for modeling the contagion of the communicable disease locally inside containers, it does not allow for studying the disease spatial spread over different containers. A mobility model is required for this purpose.
In our approach we use real data compiled from the Canadian Origin-Destination (OD) transportation survey to build our mobility model (our examples are carried out with Quebec City’s 2008 OD Survey). The survey data are statistically adjusted and weighted, so they constitute a credible representation of the whole population of the region targeted by the survey. Some pre-processing allowed us to enrich the survey data as for example the estimation of daily multi-modal commuting movement times (i.e., bus, car and walk) [20].

The use of the enriched OD data allowed for the elaboration of our population mobility model illustrated in Figure 3. All containers are instantiated from the OD data. We computed the number of individuals of every home (residence) container, which allows for a realistic initialization of the population groups (aggregated at the census track level in the case of Quebec City). The OD data is also used to determine the specific activity container of every resident population group, which allows for the computation of daily relative mobility flows between home containers on one hand and activity and public transit containers on the other hand.

Consequently, we designed our approach around three main integrated and explicitly spatialized dimensions: the Contact and Mobility dimension, the Contagion dimension and the Intervention dimension (Figure 4).

Figure 3. The population mobility model

Taking advantage of the aggregate spatial model (Section 2.1) and of the conjunction of the spatial-temporal population contact (Section 2.2) and mobility (Section 2.3) models, we have been able to model the local disease transmission between population groups of the same container as well as its spatial diffusion over other containers. These models are the foundation of our GIS-based spatial-temporal simulation approach and software to support public health decision making in the context of communicable diseases which are presented and illustrated in the next sections.

3. OUR APPROACH

Our approach stands out by the integrative perspective and the explicit spatial aspect that it offers. On the one hand, it fully integrates epidemiological, mobility and GIS-data models at an aggregate population level in order to support public health decision making. On the other hand, the proposed approach is particularly aimed to support decision makers with respect to “spatialized” intervention policies. Mainly, our approach allows for the assessment of different public intervention actions in different spatial locations of the studied area and the evaluation of their effects on the disease spatial evolution and distribution.

Figure 4. Our three-spatialized dimension model

The Spatialized Contact and Mobility dimension (dashed rectangle in Figure 4) integrates the models that describe daily activities and commuting of population groups. This dimension results from the conjunction of the Population, the Activity & Mobility and the Spatial-Temporal Simulation models. Derived from transport surveys data, the Population model specifies the composition of the whole population in terms of socio-demographic groups discussed in Section 2.2. Every population group is further subdivided into five compartments that correspond to the disease infection stages illustrated in Figure 2. Population groups are initially assigned to their residence containers, but they daily move to their activity containers - possibly using the public transit container - where they carry out their activities and meet population groups coming from other residential containers. In addition, daily activity and mobility flows are constrained by several activity parameters such as daily presence and quarantine rates. All these data are specified in the population Activity & Mobility model, in accordance to the models discussed in Sections 2.2 and 2.3. The Spatial-Temporal Simulation module is the piece that makes the link between the Population and Activity & Mobility models and effectively simulates the population groups’ daily activities and mobility. At every simulation step (corresponding to one day), the simulation engine moves the different groups from their residential containers to their activity and public transit containers where they spend time and interact with other groups. These interactions offer occasions for disease transmission from infectious to
susceptible individuals, and constitute the Spatialized Contagion dimension with both its individual and environmental risk factors discussed in Section 2.2. Therefore, the spatial-temporal simulation module applies the local contagion model in order to simulate the disease transmission inside every activity container and inside the public transit container. At the end of the day, the simulation engine moves all the active population groups back to their residence containers where they spend the night. It also applies a local contagion model in order to simulate the disease transmission inside residential containers and then carries out all the computations required for the initialization of the next simulation day (computation of the numbers of susceptible, exposed, infectious, protected and dead people of the day at each residence container).

With respect to the third dimension (the Spatialized Intervention), our approach offers a variety of scenarios illustrated in Figure 5. The ‘External Flows’ scenario is used to specify the arrival of infectious individuals from outside the area of study. These arrivals represent either the arrival of tourists or the return of resident individuals back to their homes (from extra-regional or international travels). In an external flow scenario a user can specify the number of infectious individuals (and their age groups) arriving in specific places (residential containers) on a daily basis. As a simplification, we assume that arrivals of external infectious individuals occur only at the residential containers, and external flows scenarios are therefore associated to the zone spatial level (Figure 5).

**Figure 5. Typology of spatialized intervention scenarios**

Considering the intervention scenarios, we distinguish Population-Oriented and Activity & Mobility-Oriented scenarios.

Population-Oriented interventions target population groups and correspond to Vaccination and Quarantine scenarios. Both scenario types are considered to be regional and characterized by occurrence days and targeted population groups. In contrast, Activity & Mobility-Oriented scenarios target the population activities, and they are currently supported by the ‘Public Settings Closure’ scenarios, where the decision maker can specify the closure of certain activity locations (such as schools or even public transit) on certain days. Similarly, ‘Public Settings Closure’ scenarios are currently associated with the regional level.

In the simulation, intervention scenarios are handled as constraints applied to the daily activity and movement flows of the population, which explains the direct link between the ‘Spatio-Temporal Simulation’ and the ‘Intervention’ modules in Figure 4.

Constrained by the paper length, our approach cannot be further detailed and formalized without loss of clarity. However, in the next section we present some examples which further illustrate the interest for public health decision makers to use these categories of intervention scenarios.

**4. IMPLEMENTATION AND ILLUSTRATIVE INTERVENTION SCENARIOS**

As a proof of concept of our proposed approach, we implemented the P2PCoDiGeosim tool (Person to Person Communicable Disease Geosimulation) within the MapInfo GIS using the MapBasic programming language. The software architecture (Figure 6) is directly derived from the three dimensions of the approach presented in Section 3. The Population and Activity & Mobility modules implement the interfaces that allow a typical GIS user to feed the system with the data relevant to the Spatialized Contact and Mobility dimension (Section 3). Contagion and Environmental risk modules are interfaces designed to allow a typical “epidemiologist” user calibrate and parameterize the models of the Spatialized Contagion dimension.

The intervention module implements all the graphic interfaces that allow a Public Health decision maker specify the different intervention scenarios presented in Section 3 (the Spatialized Intervention dimension). The Spatio-Temporal simulation module is the heart of the software and carries out the simulations. It is fully integrated within the GIS system and coupled with a Graphic Display Module that allows the graphic visualization of the simulation results.

**Figure 6. Architecture of the P2PCoDiGeosim simulation software**

In our software, the population activity and mobility data are compiled from the 2008 OD survey of Quebec metropolitan area. The compiled and enriched data correspond to a total adjusted and weighted population of 724378 individuals, which constitutes a credible representation of the whole population of Quebec area at that time. Residential zones are associated with census tracks: there are about 180 census tracks in the simulated area.
Figure 7. Spatial distribution of exposure rates for Scenario 1 (left) and Scenario 2 (right).

Figure 8. Evolution of the infection rates by category of containers for Scenario 1 (left) and Scenario 2 (right).
5. CONCLUSION
The spread of infectious diseases has been simulated using two major classes of models: multi-agent models which aim at studying the phenomenon at the individual level [26, 27] and meta-population models that operate at an aggregate level [2]. The plausibility and usefulness of individual-based models and simulations can be questioned since it is a quasi-impossible task to try to plausibly model and simulate the activities and mobility behaviours of individuals in an urban area. And even if such models were available, they would require too much data and processing time that can be afforded by public health agencies. For these reasons, the use of multi-agent models has been limited to regional and country levels [7, 14, 15, 17].

Meta-population models, on the other hand, tried to address the limits of agent based models by studying the phenomenon at the population level, while coarse-grained techniques are used to model individual interactions. The world is divided into geographical regions or urban areas that define a sub-population network. The infection evolves inside each urban area, i.e., sub-population, and spreads out through fluxes of movement modeled as connections between the sub-populations of the network [8, 2].

The fluxes of movement are usually compiled from national and/or international transport databases like in the GLEaM model [8, 6]. While meta-population models are suitable for studying the spread of the disease at a global level, their techniques of modeling local individual interactions inside sub-populations oversimplify the reality. In fact, transport databases don’t usually contain sufficient data about daily mobility, and to address this incompleteness, meta-population models commonly assume that 1) individuals behave identically and have the same probability to contact each other and 2) individuals move randomly between sub-populations [4]. However, recent studies about daily mobility showed that individuals don’t move randomly; they follow simple movement patterns and typically commute between a limited number of places, such as homes, work places and other few locations [16]. Except some few recent works [4], meta-population models usually don’t take into consideration these commuting patterns.

Hence, there is a need for an alternative ‘light approach’ that takes full advantage of mobility and epidemiological data currently available in order to plausibly model individuals commuting mobility and interactions (and consequently, infectious diseases propagation). Our work attempts to propose such an approach and associated GIS-based simulation tool. Indeed, our approach operates at an aggregated level which is plausible since it is based on a significant sample of the real population whose characteristics are computed from transportation surveys’ data, in contrast to common meta-population models.

Yet, our approach is simple and can be promptly put into use, since it does not require lengthy processing of population and mobility data. Transportation surveys are widely available, at least in North America and Europe and our approach and tool can be adapted to local variations of these data sets. Our contagion models are simple and agree with typical epidemiological models. Hence, epidemiologists should not have difficulties to set the relevant parameters for the communicable diseases they desire to simulate.

Our approach and tool innovate in offering a complete integration of mobility and infection models in a GIS–based software for decision support in the public health domain. The full integration of our simulator in a GIS allows a public health decision maker to

For illustrative purposes, we considered a 30-day simulation period and we defined and simulated one ‘External Flows’ scenario and two intervention scenarios. The external flows scenario enacts the arrival of 95 infectious individuals in three specific residence containers (in three different census sectors) in the first day of simulation. The external flows scenario initializes the simulation and is used in conjunction with the two intervention scenarios.

In the first intervention scenario (Scenario 1) called No Intervention Scenario, no public intervention is carried out.

In the second intervention scenario (Scenario 2), called Vaccination Scenario, the decision maker decided to organize a regional vaccination campaign that targets about 30.17% of the youth population groups (between 6 and 15 years old persons). The vaccination is scheduled from simulation days 2 to 8, inclusively. The simulation software takes advantage of the GIS spatial visualization functionalities and provides the decision maker with a wide range of graphic displays that facilitate the exploration and comparison of the simulation outcomes of different scenarios. In this paper we only present few illustrative screen captures.

For example, Figure 7 illustrates the spatial distribution of the exposure rates for scenario 1 (left-side) and scenario 2 (right side) during the 30-day simulation period. We can see that the vaccination campaign has reduced the exposure rates in the different census tracks (residential zones), and the total number of exposed persons has decreased from 180960 (scenario 1) to 140877 (scenario 2).

Moreover, we can see in Figure 8 that the vaccination campaign has substantially reduced the infections rates in primary and secondary schools, but less in university, public transit and residence containers.

Finally, the simulated scenarios showed that a targeted vaccination of a small part of the population (about 30.17% of youth between 6 and 15 years old) has reduced the total deaths number by about 24%. Table 2 illustrates the final simulation outcomes of the two scenarios.

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<th>Table 2. Final simulation outcomes of Scenario1 and Scenario2</th>
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Regarding the software’s efficiency, we executed our simulations on a laptop equipped with 4 Intel Core I7-2677M (1.80 GHz) processors, 4GB of RAM and an integrated solid-state drive. Even though MapInfo is not multi-threaded, the 4 processors have boosted the performance of machine, which consequently has increased the performance of the simulation tool. With this configuration, the simulation of 30-day scenarios takes less than 17 minutes. Certainly, further tests are required in the future in order to have a more precise evaluation of the software’s efficiency.

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simply set various intervention scenarios and to view simulation results in different display formats authorized by the GIS. This facilitates the comparison of the outcomes of different scenarios. Our system also offers the option of visualizing the spatial spread of the disease in an animated way.

However, in the near future we intend to improve some limits of our work, mainly with respect to the epidemiological model. In fact, our model currently does not take into consideration complex epidemiologic situations, such as possible vaccinations’ complications. We intend to collaborate with experts in epidemiology in order to improve, calibrate and validate our epidemiological model.

In addition, and for simplification purposes, some intervention scenarios are currently possible only at the regional level. One of our future priorities is to provide the decision maker with more flexibility by allowing the experimentation of intervention scenarios at other spatial scales.

6. ACKNOWLEDGMENTS

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7. REFERENCES


[6] Broeck, W.V, Gioannini C. Gonçalves B., Quaggiotto M., Colizza V. and Vespignani A. (2011), The GLEaMviz computational tool, a publicly available software to explore realistic epidemic spreading scenarios at the global scale. BMC Infectious Diseases, Vol 11(37)


