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An Informatics-based Approach for Sustainable Management of Factors Affecting the Spread of Infectious Diseases

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Abstract. Several of the United Nations’ Sustainable Development Goals (SDGs) are directly or indirectly concerned with improving health and well-being of the world population. This paper presents an informatics-based approach to the management and monitoring of infectious diseases, in the context of one of these SDGs focusing on the eradication of vector-borne diseases such as malaria, Zika and other neglected tropical diseases. Here we outline the challenges faced by many conventional approaches to ecoepidemiological modelling and proposes a distributed interactive architecture for teamwork coordination, and data integration at different levels of information, and across disciplines. This approach is illustrated by an application to the surveillance of Leishmaniasis, a neglected tropical disease, in remote regions.

Keywords: Sustainable Development Goals · agent-based modelling · serious games · mobile games · game engines · vector-borne diseases · tropical neglected diseases.

1 Introduction

The 17 Sustainable Development Goals (SDGs) of the United Nations [21], set as part of its 2030 Agenda for Sustainable Development, “are an urgent call for action by all countries - developed and developing - in a global partnership” towards achieving “peace and prosperity for people and the planet, now and into the future” [21]. Health and well-being clearly play important roles in this global vision of peace and prosperity. Therefore, it is not surprising that at least one of the 17 SDGs – Goal 3 – is related directly to health and well-being, aiming to “ensure healthy lives and promote well-being for all at all ages” [22]. Indeed, target 3.3 of this goal aims to “end the epidemics of AIDS, tuberculosis, malaria and neglected tropical diseases and combat hepatitis, water-borne diseases and other communicable diseases” by 2030.

* Both authors contributed equally to this paper, and are listed in alphabetical order.

Despite these ambitious future goals, the past decade has actually seen the (re)emergence of several vector-borne diseases [23], including malaria and most neglected tropical diseases [10]. The increased spread of such diseases is frequently associated with increased human mobility [1] and climate change [4, 20], which is also related to various environmental factors targeted by several other UN SDGs.

Many neglected tropical diseases are zoonoses, and as such, they spread as a result of the complex interactions and through cycles of transmission between humans and a range of domestic or wild animals [20]. The effectiveness of their related control actions is, therefore, contingent on the availability of consistent, user-friendly and up-to-date epidemiological, environmental and socioeconomic data. However, obtaining and checking the quality of such spatial and temporal data remains challenging, particularly in the case of environmental data, known as Earth Observation [9].

In this paper, we argue that novel approaches to epidemiological surveillance, prevention and control of vector-borne diseases should be considered in order to address these challenges. These approaches should aim to better integrate models of transmission and hitherto fragmented data infrastructures. This paper discusses an informatics-based approach, underpinned by *agent-based modelling* (ABM) methods, which incorporate data gathering and simulations that encompass various *agents* – i.e., vectors, reservoirs, human susceptible populations – and environmental factors, such as micro- and macro-climatic variations, vegetation cover, and sanitation standards under a single platform.

2 Challenges of Dealing with Vector-borne Diseases

As identified by the UN SDG number 3, eradication of vector-borne diseases such as malaria and other neglected tropical diseases is an important step towards global health and well-being. Similarly, in its recent roadmap 2021-2030, the World Health Organization (WHO) also sets global targets for prevention, control, elimination and eradication of neglected tropical diseases by 2030 [26]. Achieving these goals, however, remains a major challenge, as many such diseases are widespread in mostly less-developed parts of the world, with little access to adequate health resources [24].

The Zika crisis of 2017, which affected several developing countries, underscored this challenge. As the crisis unfolded, WHO emphasized the need for new and more efficient instruments to control Zika (re)emergence. Similarly, the Brazilian Association of Collective Health called upon health authorities and funding agencies to provide more support for environmental sanitation and epidemiological surveillance measures that had been neglected in the 2016 Zika emergency [2]. The Zika virus outbreak reached pandemic levels in Latin America and continued to spread in other parts of the world [25]. In these countries, traditional approaches to epidemiological surveillance methods and control strategies based on conventional modelling have long been insufficient to respond to such emergencies.

In Brazil, for instance, although a unified epidemiological surveillance system exists for Zika [18] and other arboviruses, access to up-to-date data is often difficult, with health-planning professionals having to rely on information aggregated at relatively coarse spatial resolutions (e.g., municipal level), and with significant time delays. In addition, relevant vector, climate, geographical and social data usually have to be obtained from separate sources, causing temporal and spatial resolution issues, and highlighting needed multidisciplinary teamwork. These challenges are common to resource-limited countries vulnerable to Zika [3] where, as in the Brazilian case, the available databases are often outdated and fragmented. Low spatial resolution is also a common problem, as is the lack of data on human-induced microgeographic factors influencing potential *Aedes aegypti* breeding habitats [11].

Researchers working with standard models of transmission of Zika and related arboviruses acknowledge that lacking or incomplete knowledge of the *A. aegypti* ecoepidemiology constitutes one of the greatest obstacles to effective surveillance and control actions [7]. In standard mathematical models, transmission dynamics is modelled as a system of ordinary differential equations which describe rates of change in measurable human and entomological population variables, as well as population and behaviour estimates. While these models enable researchers to explore how different epidemiological scenarios might develop under alternative parametrizations through numerical methods, their actual use in context is affected by difficulties in incorporating relevant data, such as their inability to accommodate high spatial resolutions, complex boundary conditions, and temporal constraints. Consequently, data which are currently gathered through geo-monitoring, and (increasingly) citizen input and sensor networks, often remain underutilized in epidemiological work.

Novel approaches to epidemiological surveillance and prevention of vector-borne diseases are therefore needed – particularly those which move beyond traditional modelling frameworks [19] and fragmented data infrastructures. Such approaches could also prove relevant for the control of other infectious diseases, as illustrated by the increased interest in alternative methods during the COVID-19 pandemic, including large-scale agent based simulations [17].

3 Agent-Based Modelling Approach

Considering these challenges, we advocate an informatics-based approach underpinned by ABM, with support for data gathering, and simulations encompassing vectors, reservoirs, populations and environment under a single paradigm. The ABM approach differs considerably from other conventional approaches based on Differential Equations Modelling (DEM). Table 1 provides a summary comparison of the main characteristics of these two approaches.

Our research group has adopted an ABM approach in South-western Amazonia (see Figure 1) to coordinate the actions of a multidisciplinary team working on vector-borne neglected tropical diseases research. This work focused on Amer-

Table 1. A summary comparison of ABM and DEM used for modelling the spread of infectious diseases.

	ABM	DEM
Granularity	Individual agent behaviour	System-level properties
Modelling units	Sets of rules, algorithms	Sets of differential equations
Geographical properties	Modelled as agents	Model only high level properties
Complex boundaries	Easily implemented	Non-trivial (e.g., multigrid)
Small populations	Easily modelled	Not suitable for small populations
Robustness to noise	May be affected by noisy data	Robust to noise
Interpretability	Interpretable but transition from local to global patterns often non-trivial	
Realism	Realistic simulations	Abstract simulations

ican Cutaneous Leishmaniasis (ACL) which, in that region, presents complexities shared by several other vector-borne diseases, including:

- increased human mobility due to new roads linking Brazilian soy-beans producing regions to the Pacific ports of Peru;
- climatic changes in a region under intense land use and land cover changes;
- unplanned urbanization and rural occupation, leading to close coexistence of vectors, domestic and sylvatic animals, and infected and susceptible people;
- poor public and private sector support for appropriate preventative measures, with the consequent reliance on old and toxic drugs to mitigate transmission sources; and
- the unique geographical setting, which combines regional ACL hyperendemicity with increasing population vulnerability to Visceral Leishmaniasis, from the Brazilian North-eastern region towards the West, and Bartonellosis, From the Peruvian Western plateaus towards the East.

In this complex research context, our ABM approach has facilitated three broad lines of action:

1. the use of mobile devices for gathering and sharing of ecoepidemiological data from remote areas by local healthcare personnel [13];
2. health education through the use of “serious games” for improving community-level knowledge of transmission and prevention mechanisms; and
3. the use of spatiotemporal data visualization tools [5] to support the identification of critical points in the chain of transmission [16].

The tools that we have developed as part of these lines of action support a combination of online/offline access and database synchronization to overcome connectivity issues in remote areas [13].



Fig. 1. South-western Amazonia, where our multidisciplinary team working on vector-borne neglected tropical diseases has conducted its research.

An ABM describing the relevant environmental (climatic, geographical), entomological (vectors), zoological (reservoirs) and socioeconomic variables provided an infrastructure for incorporation of existing databases, newly gathered data, and expert knowledge, as well as a simulation mechanism for analysis purposes and for the health education application itself. The ABM also supported data validation by highlighting discrepancies between incoming data collected by local personnel and model predictions.

Therefore, in this informatics-based approach, the ABM functioned both as a predictive tool and as a database for integration of surveillance, population and spatiotemporal data. In the case of ACL, for instance, we were able to group municipalities according to statistical similarities – rather than the official grouping based on the river basins of the region – with implications to government policy and interventions. ABMs are better suited to such data-intensive analysis than other frequently used frameworks, even those supporting more detailed biological and environmental information, such as CIMSIM [15].

In the ABM framework, models are built by describing the behaviour of relevant “agents” (representing algorithmic abstractions of humans, vectors, and the environment), gathering data to instantiate their behaviour and characteristics through computer simulation, and exploring different scenarios by tracking system-level properties under varied parameters. These parameters can be set at the agent level – e.g., diversity in behaviours for male and female mosquitoes, in bloodmeal search by females according to lifecycle, in human exposure according to socioeconomic and neighbourhood-specific environmental factors – so that system-level properties emerge from the local interactions among heteroge-

neous agents. Therefore, modelling individuals along with spatial and temporal constraints becomes straightforward, allowing the incorporation of various data sources [12] and input from different disciplines and stakeholders. Homogeneity assumptions can also be relaxed or eliminated by, for instance, explicit specification of agent contact graphs [6], which can be defined using novel data sources, such as those accessible through the internet or collected using mobile devices.

Although ABMs are bottom-up models, they can incorporate features of top-down *Ross-MacDonald models* [19] through pattern-oriented modelling techniques now commonly employed in ecological research [8]. An overall informatics-based approach can thus be employed to support the work of personnel involved in the different facets of data gathering, in order to supply the model with the required information for use in context. Furthermore, a game-based ABM approach can support data gathering through community participation, with potential for feeding considerable amounts of population and environmental data into large-scale simulations. This could enhance modelling capabilities by interpolation and extrapolation from available data with increasing accuracy as more detailed local information is supplied.

It has been pointed out that agent-based models tend to have a large number of parameters, which could limit their analytic power [8]. However, while simpler models may lend themselves better to macro-level analyses under assumptions of population homogeneity and size, agent-based modelling provides greater realism and specificity, accounting for spatial and populational heterogeneity. In fact, at one extreme (still beyond the reach of current technological capabilities) one could conceive of a maximally realistic ABM as a detailed monitoring system capable of integrating data on households and public areas, and delivering information to epidemiological surveillance personnel in real time. Currently, these systems open up possibilities for gathering data through community participation, with potential for feeding considerable amounts of population and environmental data into large-scale simulations. This would enhance modelling capabilities by interpolation and extrapolation from available data with increasing accuracy as more detailed local information is supplied. In our view, these are characteristics of a promising tool for timely responses to public health emergencies such as the present Zika outbreak.

4 Serious Game Simulation

To investigate the feasibility of using an ecoepidemiological ABM as part of a game engine – to be deployed as a unifying mechanism for health promotion and data gathering by local citizens – we developed a module encompassing several variables that influence the spread of infectious vector-borne diseases. Table 2 gives an example of our ABM approach and a typical example of a DEM approach to allow their comparison.

Figure 2 provides an overview of the architecture of the overall game engine, which consists of the BADAGUA ABM simulator [14], a GUI-based game client, and a “gatekeeper” module that keeps track of the users and coordinates their

Table 2. Typical examples of ABM and DEM approaches to the modelling of infectious disease spread.

	Example
ABM	<p>Modelling an individual vector in Badagua/Mason:</p> <pre> public static double DEFattToWater = .3; public static double DEFattToLeaves = .4; public static double DEFattToAnimal = .6; public static double DEFattToSandfly = .7; [...] public double attractionToAnimal = 0; public void step(SimState state) { Badagua bagua = (Badagua)state; if (age++ > longevity) { this.die(bagua); return; } if (this.isFemale()){ Bag fb = bagua.map.getObjectsAtLocation(location.x, location.y); if (fb != null){ Sandfly sf; Animal an; for (int i = 0; i < fb.numObjs; i++) { if (fb.objs[i] instanceof Sandfly){ if (this.isPregnant()) continue; sf = (Sandfly) fb.objs[i]; if (sf.isMale()) { this.setPregnant(true); this.attractionToSandfly = 0; this.attractionToLeaves = 0; this.attractionToWater = 0; this.attractionToAnimal = DEFattToAnimal; } } else if (fb.objs[i] instanceof Animal) { an = (Animal) fb.objs[i]; this.suckBlood(an); } } } // end for } // end if fb != null } // end if this.isFemale() // [etc ...] </pre>
DEM	<p>Susceptible-Infective-Recovered (SIR) modelling</p> <p>Transmission dynamics modelled as a system of ordinary differential equations which describe rates of change in measurable human and entomological population variables, such as susceptible (S), infective (I), and recovered (R) individuals in a population of size N. Let S_t, I_t, R_t denote numbers at time t, and $s(t) = \frac{S_t}{N}$ etc, s.t. $s(t) + i(t) + r(t) = 1$ For parameters probabilities of transmission (β) and recovery (γ) a DEM could be set out as follows:</p> $\frac{ds(t)}{dt} = -\beta s(t)i(t) \tag{1}$ $\frac{di(t)}{dt} = \beta s(t)i(t) - \gamma i(t) \tag{2}$ $\frac{dr(t)}{dt} = \gamma i(t) \tag{3}$ <hr/> <p>There is an epidemic \iff “reproductive number” $R_0 = \beta/\gamma > 1$</p>

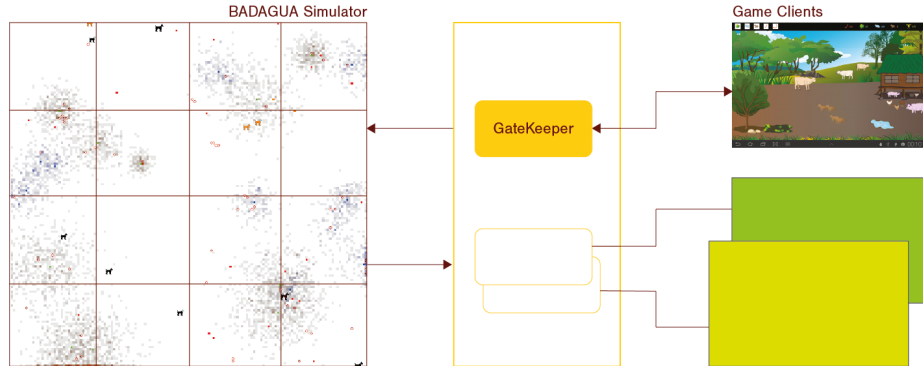


Fig. 2. Architecture of the BADAGUA serious game simulation.

access to different regions of the simulation, as well as game-specific tasks. This game setup combines features of two game genres, namely, life simulation and construction and management simulation. The underlying game mechanics leads players to manage virtual environments inhabited by avatars of themselves and, while doing so, receive information about disease prevention, and subsequently act on such information during the game. The simulator represents a physical environment in an area of interest for disease surveillance, consisting of human and animal habitats, and populated by humans, disease vectors and animals. Players can input information pertaining to the actual physical environment, and therefore, update the simulator running on a remote server.

The environment is represented as a sparse 2-dimensional grid where positions can be occupied by different agents – i.e., humans, vectors or animals. Each cell on the grid contains a score which determines the likelihood that an agent will move into that cell. Such scores can be specific to different types of agents. For instance, sand-flies in the Dr Ludens’ LSG simulation [14] are attracted to accumulated leaves, water and rubbish, as well as nearby humans and animals. Each of these elements is modelled as an independent feature of the environment on a separate grid. Similarly, regularities in human behaviour can be modelled through superimposed grids with different attractiveness scores.

The simulator uses a discrete event schedule to control the activation of the various agents in the simulation as well as the dynamics of the environment. Disease spread thus emerges as a dynamic process that results from the interactions of several ABM variables, including population features, vector feeding behaviour, geographical distribution, and agent mobility patterns.

In addition to being useful as a health education tool, the game simulation facilitates the integration of ecoepidemiological information into a single platform. Such information could comprise the characteristics of the human, animal (i.e., reservoirs) and vector populations, and of the environment – initially specified by a multidisciplinary team of experts, and subsequently refined and validated

as the simulation evolves and local information gets incorporated into the central system database.

5 Evaluation

We have conducted a preliminary evaluation of the proposed serious game among healthcare professionals, through questionnaires and interviews [14]. The overall perception was that the integration of a serious game and ABM has the potential to raise awareness of broader ecological issues implicated in the spread of Leishmaniasis and to promote behaviour change among community members. Perhaps not surprisingly, the respondents expressed concern regarding the need to balance the fun elements of the game component against the accuracy levels needed to make the ABM useful as a modelling and policy-informing tool. The study participants also highlighted a potential role for extending the game into a tool for training of health professionals as well.

6 Conclusions

In this paper, we outlined an approach to sustainable ecoepidemiological management based on ABM and informatics methods, and illustrated its use through the description of a serious game simulator used in the context of ACL monitoring. We argued that this approach is capable of simplifying the aggregation of the relevant vector, climate, geographical and social data continuously and at scale in a distributed, interactive environment, thus addressing temporal and spatial resolution, and multidisciplinary teamwork challenges involved in the eradication of vector-borne diseases. By doing so, we aim to assist healthcare professionals and local citizens in remote regions to work towards achieving one of the United Nations' SDGs.

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