Developing a Framework for Modeling and Simulating Aedes aegypti and Dengue Fever Dynamics

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Abstract. Dengue fever is a challenging complex transmissible disease due to its unstable temporal and spatial dynamics. Modeling is a powerful tool to understand disease dynamics and to evaluate costs, benefits and effectiveness of control strategies. In order to assist decision-makers and researchers in the evaluation and proposition of new strategies, we present DengueME, a collaborative open source platform for dengue modeling. It provides an environment for easy implementation of compartmental and individual-based models over a geographic database, combining modules describing Aedes aegypti's life cycle, human demography, human mobility, urban landscape and dengue transmission.

1. Introduction

Dengue fever is a vector borne disease characterized by a complex temporal-spatial dynamic which emerges from the interaction of multiple agents in a complex ecological and social landscape. Dissecting the contribution of specific variables to the observed dynamics as well as the effect of control strategies require modeling and simulation tools that integrate the several components of this system: ecological, social, demographic, mobility, immunological components, etc.

Several models have been developed aiming at understanding the dengue vector population dynamic and spread [Yang and Ferreira 2008] [Otero et al. 2006] [Otero et al. 2008] [Lana et al. 2011] [Lana et al. 2013], as well as the disease transmission dynamic [Santos et al. 2009] [Pinho et al. 2010] [Medeiros et al. 2011]. However, in general they represent homogeneous populations and scaling them up to several populations (metapopulation models) or introducing spatial heterogeneity demands a high dosage of efficient programming. One barrier in using these models to help in decision making is the time and effort usually required to implement and adapt these models to specific contexts, which requires parameterization with local spatial and temporal data, when data is often available at different spatial and/or temporal resolutions. A tool for modeling-based decision making should provide a variety of built-in models to attend the user as well as allow easy parameterization (eg. with meteorological data of a specific region) supporting the development of specific scenarios.

In this context, this work presents the conception and the initial state of development of the DengueME (Dengue Modeling Environment) framework, an open source tool for modeling and simulation of dengue models on geographical landscapes. DengueME is designed to simulate and compare site-specific and population-specific control strategies for dengue, offer a basic library of epidemiological and entomological spatio-temporal models that are easily configured and parameterized to attend the needs of the user and applied to real case studies. The framework seeks to provide an open environment for user contribution and sharing as well to foster the development of an active community.

2. DengueME framework overview

2.1. Framework requirements and design

DengueME was designed to attend the following requirements: (a.1) to allow efficient simulation of spatio-temporal dengue models; (a.2) to support efficient communication with geographical databases for storage of input and output data; (b) to allow easy implementation of multi-scale models as well as models based on different paradigms (compartmental, agent-based, cellular automata, hybrids); (c) to provide a common and easy language for model implementation; (d) to provide a rich library of built-in modular models which can be customized and combined to generate specific models; (e) to offer a friendly graphical user interface for creating, configuring and running built-in and user defined models; (f) to provide standard data protocols for integration of models within the framework.

DengueME is developed over the TerraME platform [Carneiro et al. 2013], an open source programming environment for spatial dynamic modeling. This is a software architecture for building models with multiple scales that provides a rich modeling

language for the development of compartmental, individual and agent based modeling. It also provides an interface to TerraLib geographical databases, allowing direct access of models to geospatial data (http://www.terrame.org/).

Within DengueME, model implementation, parameterization and configuration use TerraML (Terra Modeling Language), a high level programming language for modeling which offer many data structures and services to support a rich description and simulation of environmental models [Carneiro et al. 2013].

As not all potential users of DengueME knows how to program in TerraML, we invested from the beginning in the design of a Visual Development Environment, which provides a graphical interface for users to configure built-in or imported models and create their own scenarios through the selection and combination of sub-models and their parameterization with data from geographic databases and tabular data. Its graphical user interface (GUI) currently provides wizards that guide users in performing the steps required for modeling 1. It allows users to select a model from a set of built-in models; to define values for the model parameters; to set the options for output visualization and storage. The user defined settings and parameters (designed scenarios) may be stored and retrieved for later use. After finishing all customization and parametrization, the GUI drives the creation of the corresponding TerraML source code.

2.2. Current built-in models

Currently, DengueME's library contains a dengue model as developed by Medeiros et al. (2011) in the form an agent-based model, and an *Aedes aegypti* population model as described in Lana et al. (2011). These models illustrate the main features of the DengueME platform, which include customization and comparison of transmission control scenarios.

The vector (entomological) model describes the population dynamics of *Ae. ae-gypti* with differential equations modeling the variation of the stock at each life stage (eggs, larvae, pupae and adults) under the influence of to the environmental carrying capacity and the climate [Lana et al. 2013]. The vector model may be used stand alone, or integrated with the other models.

The transmission process between humans and mosquitoes depends on the local amount of susceptible people (or mosquitoes) and infected people (or mosquitoes). Immune people act as barriers to transmission, since they absorb some of the bites from infected mosquitoes, without subsequent spread of the virus. Dengue models describe this dynamic through the classification of the stock of people and mosquitoes in states (susceptible, exposed, infected and recovered).

Future models to be implemented include a mobility model, which describes the mobility and commutation of humans and vectors through space. The spread of viruses and vectors is facilitated by the flow of individuals through the network of air and land transportation. Moreover, the urban landscape interferes in the dynamics of dengue transmission as it introduces heterogeneity in the availability of breeding sites for *Ae. aegypti*. The landscape component will provide a landscape classification model to describe the space and may be used to obtain input parameters for the models. DengueME will implement the landscape classification model suited to dengue issues developed by [Reis 2010].



Figure 1. Diagram showing the modeling process using the DengueME Visual Development Environment.

3. Results and Final Remarks

Despite the variety of mathematical models for *Ae. aegypti* spatial dynamics and dengue transmission, there is still a need to stimulate model usage to assist the planning of dengue control interventions. Fast model reuse is still a challenge. Moreover, the application of models and tools should not require extensive experience in programming techniques or great expertise in modeling development, database management and and model-data integration (although it is required to understand the model assumptions to correctly use them).

These challenges motivated the development of the DengueME framework, which aims at supporting the modeling and simulation of the spatio-temporal dynamics of dengue and its vector in urban environments.

This work remains under development. Partial results were obtained, analyzed, and positively evaluated, motivating its continuity. Future work includes: (i) performing further framework evaluations with potential users, (ii) developing and incorporating new models into the framework, (iii) developing case studies, (iv) making a stable and documented version of the DengueME framework publicity available, (v) providing tutorials and demo applications to support users.

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References

- Carneiro, T. G. d. S., Andrade, P. R. d., Câmara, G., Monteiro, A. M. V., and Pereira, R. R. (2013). An extensible toolbox for modeling nature–society interactions. *Environmental Modelling & Software*, 46:104–117.
- Lana, R. M., Carneiro, T. G., Honório, N. A., and Codeço, C. T. (2011). Multiscale Analysis and Modelling of Aedes aegyti Population Spatial Dynamics. *Journal of Information and Data Management*, 2(2):211.
- Lana, R. M., Carneiro, T. G., Honório, N. A., and Codeço, C. T. (2013). Seasonal and nonseasonal dynamics of Aedes aegypti in Rio de Janeiro, Brazil: fitting mathematical models to trap data. *Acta Tropica*. Accepted for publication in 07/23/2013.
- Medeiros, L. C. d. C., Castilho, C. A. R., Braga, C., de Souza, W. V., Regis, L., and Monteiro, A. M. V. (2011). Modeling the dynamic transmission of dengue fever: investigating disease persistence. *PLOS neglected tropical diseases*, 5(1):e942.
- Otero, M., Schweigmann, N., and Solari, H. G. (2008). A stochastic spatial dynamical model for Aedes aegypti. *Bulletin of mathematical biology*, 70(5):1297–1325.
- Otero, M., Solari, H. G., and Schweigmann, N. (2006). A stochastic population dynamics model for Aedes aegypti: formulation and application to a city with temperate climate. *Bulletin of Mathematical Biology*, 68(8):1945–1974.
- Pinho, S. T. R. d., Ferreira, C. P., Esteva, L., Barreto, F., e Silva, V. M., and Teixeira, M. (2010). Modelling the dynamics of dengue real epidemics. *Philosophical Transactions of the Royal Society A: Mathematical, Physical and Engineering Sciences*, 368(1933):5679–5693.
- Reis, I. C. (2010). Caracterização de paisagens urbanas heterogêneas de interesse para a vigilância e controle da dengue com o uso de sensoriamento remoto e mineração de padrões espaciais: um estudo para o Rio de Janeiro. Master in remote sensing, National Institute of Spatial Research.
- Santos, L., Costa, M., Pinho, S., Andrade, R., Barreto, F., Teixeira, M., and Barreto, M. (2009). Periodic forcing in a three-level cellular automata model for a vectortransmitted disease. *Physical Review E*, 80(1):016102.
- Yang, H. M. and Ferreira, C. P. (2008). Assessing the effects of vector control on dengue transmission. *Applied Mathematics and Computation*, 198(1):401–413.