

Dengue Epidemiology

Modeling in Dengue: PRONEX Network

Jair Koiller, Fundação Getúlio Vargas

A brief presentation will be made about the PRONEX Network - Modeling in Dengue and its goals.

TerraME: Computer Science for the modelling and simulation of human-nature interactions

Tiago Garcia de Senna Carneiro, Universidade Federal de Ouro Preto

The lecture will address some of the major contributions of Computer Science for the modelling and simulation of biophysical and socioeconomics systems and their interactions. TerraME is a software environment for the modelling and simulation of geographical phenomena spatial dynamics. Its use in the development of models real case studies will be discussed: Land use and cover change (LUCC) in Amazonian region, fire propagation in the Emas National Park - GO, and spatial dynamics of *Aedes aegypti* populations in Rio de Janeiro - RJ. TerraME is fully integrated with geographic database. It allows the development of multiple scale models that consider several temporal, spatial and behavioral resolutions and extents. Complex models can be built from the hierarchical composition of simpler models. Models can be represented through the simultaneous use of several modelling paradigms: Discrete Event Simulation, General Systems Theory, Cellular Automata Theory or Agent Theory. The main methodological and computational challenges encountered in modeling and simulation of interactions between society and environment will be discussed.

Simulation of population dynamics of *Aedes aegypti*

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Aedes aegypti population dynamics have been studied to understand the transmission dynamics of the Dengue disease. The mosquito dynamics is influenced by environmental factors as temperature, humidity, precipitation and space. In accordance to these factors, a spatially-explicit model of *Aedes aegypti* population dynamics was proposed and evaluated for a neighborhood in Rio de Janeiro, Brazil. A temporal series of weekly egg collections and temperature data were used. The spatial model is coupled to the population dynamics model from Ferreira e Yang (2003) and integrated to a Geographical Database. The population dynamics model was modified based on recent literature. The spatial model was constructed using the TerraME environmental modeling platform. An average kernel map was necessary to estimate the egg density surface as an input to spatial model. The model was parameterized, calibrated and validated at three spatial scales. Sensibility tests of key model variables were done to understand problems in the model related to the bad fit.

Individual based model for dengue transmission: Interactions between humans, mosquitoes and serotypes

Líliam César de Castro Medeiros, Instituto Nacional de Pesquisas Espaciais

Dengue is the most rapidly spreading mosquito-borne viral disease in the world and there may be 50 million Dengue infections worldwide every year. It is a disease of great complexity, due to interactions between humans, mosquitoes and various virus serotypes as well as efficient vector survival strategies. In Brazil it is mainly transmitted by *Aedes aegypti* mosquitoes. The spread and dramatic increase in the incidence of Dengue has been blamed on uncontrolled urbanization, population growth and international traveling. Mathematical and computational models have been developed to help understand the disease's epidemiology, expanding the capacity of phenomena explanation. Knowledge gained on different scenarios generated by the models can help in the formulation of custom intervention plans. In this work will be presented a spatially explicit individual based model for the simulation of Dengue transmission in a densely populated area. The model involves the dynamic interactions between humans, mosquitoes and distinct serotypes. It will be

shown the importance of human mobility, human renewal and asymptomatic individuals in disease spread and persistence, as well as different scenarios generated by the coexistence of two serotypes.

Diffusive SIR-like epidemiological models

Reginaldo Aparecido Zara, Universidade Estadual do Oeste do Paraná

In this work are presented numerical studies of epidemiological models based on the Susceptible-Infected-Removed (SIR) model for epidemics. Some of the results are discussed and the limitations in their computational solutions are presented in the context of spreading diseases. The discussed SIR-like models are derived from cellular automata models whose solutions, when simulated for homogeneous populations randomly distributed and using a spatiotemporal dynamics, provide results showing concentrically spreading centered at the source of the disease. The results indicate that such approach can simulate the dynamics of a variety of ecological, biological and physical phenomena when aspects purely diffusive are taken into account. Moreover, the results also indicate that solutions more consistent with actual data depend on the detailed specification of the models considering, for example, other characteristics such as interaction between individuals and the environment and the heterogeneity of the relational system of contacts.

Modelling urban arboviral epidemics

Max Souza, Universidade Federal Fluminense

Data from Dengue epidemics suggest that the transport of population can be very important in the infection dynamics. We shall describe a meta-population model that seems to be able to capture the qualitative dynamics of the data. Also we shall show some results on vector/host dynamics and global stability for this and related models.