

An Eco-Epidemiological Model for Dengue and Yellow Fever. Theoretical biology or applied mathematics?

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Abstract

Dengue and urban Yellow Fever are diseases produced by arbovirus, family *flaviviridae* genus *flavivirus*. The main vector in the Americas is the mosquito *Aedes aegypti* which is now present in the Americas in tropical, subtropical and temperate regions reaching the latitude $38^{\circ}44'S$. Dengue fever follows with some year of delay the expansion of the mosquito. We developed a SEI/SEIR stochastic model for the vector and the disease, intended for use in temperate regions as well as tropical and subtropical regions. The model predicts the possibility of large Dengue epidemics in the city of Buenos Aires $34^{\circ}36'S$, when Dengue-infected people arrive early in the Summer season, while for late arrivals in Summer or Autumn it predicts that the local circulation of the virus will not reach epidemic character. This approach was used to successfully reproduce the daily mortality in the historical Yellow Fever epidemic of 1871. Soon after the model was completed, a stream of Dengue infected people arrived to the area (March-April, i.e., Spring 2009) resulting in the local circulation of the virus as expected by the time of arrival. We will discuss the model and its relation with empirical data. We will also glance at cases in which the model has indicated problems with current (biological) accepted knowledge and pointed out the need of more precise information, contributing to improve biological knowledge.